PCT (43) International Publication Date 31 October 2002 (31.10.2002)

(10) International Publication Number WO 02/086443

(8) COIN PCT/US02/12476 (21) International Application Number: (51) International Patent Classification?; (22) International Filing Date:

18 April 2002 (18.04.2002) (25) Filing Language:

M. Designated States (mational): AE, AG, AL, AM, AT, AU, AZ, BA, BB, RG, BR, BY, BZ, CA, CH; CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ST, GB, GD, GE, GH, GM, IR, HU, ID, L, M; S, P, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, AZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TI, TM, TN, TR, TZ, LU, UG, US, UZ, VN, YU, ZA, ZM, ZW, ZW, English

(26) Publication Language:

English

222222 13 November 2001 (13.11.2001) 29 November 2001 (29.11.2001) 18 April 2001 (18,04,2001) 10 May 2001 (10.05.2001) 9 November 2001 (09.11.2001) 12 April 2002 (12.04.2002) Priority Data: 60/290,492 60/339,245 60/350,666 60/334,370 60/372,246 (71) Applicant (for all designated States except US): EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

Inventors; and

Inventora/Applicants for US only): AZIZ, Natasha [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). MURRAY, Richard [US/US]; 22643 Woodbridge Court, Cupertino, CA 95014 (US). 58

(74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center,

Burasian patent (AM, AZ, BY, RCI, KZ, MD, RU, TI, TM), Usurpean patent (AH, AZ, BY, RCI, KZ, MD, RU, TI, TH, Usurpean patent (AT, BU, CH, CY, DU, DK, ES, IH, IH, GB, GR, EL, FL, LU, MC, NL, PT, SE, TR), OAPI patent (BH, BL, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NR, SN, TD, TG). Designated States (regional): ARIPO patent (GII, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), **F** 

of Inventorship (Rule 4.17(iv)) for US only Declaration under Rule 4.17:

2

report and to be republished without international search upon receipi of that report Published:

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Lighth Floor, San Prancisco, CA 94111-3834 (US).

WO 02/086443

PCT/US02/12476

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

# CROSS-REFERENCES TO RELATED APPLICATIONS

60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN This application is related to USSN 60/284,770, filed April 18, 2001; USSN

.)} USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety. 2

#### FIELD OF THE INVENTION

and to the use of such expression profiles and compositions in diagnosis and therapy of lung profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; cancer. The invention further relates to methods for identifying and using agents and/or The invention relates to the identification of nucleic acid and protein expression argets that inhibit lung cancer or related conditions.

### BACKGROUND OF THE INVENTION

20

Lang cancer is the second most commonly occurring cancer in the United States and cancer in men and accounts for nearly one third of all cancer deaths in both men and women cases of lung cancer in the United States every year. Of those who are diagnosed with lung the leading cause of cancer-related death. It is estimated that there are over 160,000 new cancer, 86 percent will die within five years. Lung cancer is the most common visceral

22

In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women. Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,

(nomicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines. 3

## BEST AVAILABLE COPY

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and

similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

(\$4) THE: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MOD-ULATORS OF LUNG CANCER

E++980/70 OM

12/0864413 PCT/US02/12476 Tobacco-epecific nitrosamines are formed during tobacco curing and processing, and

and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas lung adenocarcinomas in rodents.

S

important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling concentrations in second hand smoke. For this and other reasons, "passive smoking" is an concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the each year

2

the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards In addition to smoking, other factors thought to be causes of lung cancer include onsuch as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

15

different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid Tumours (International Histological Classification of Tumours, No 1. Four major cell types called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Histological classification of various lung cancers define the types of cancer that carcinoids, bronchial gland tumors, and other rarer types. The various cell types have the first step of effective treatment.

2

rapidly than non-small cell lung cancer. In general, at the time of prosentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent less frequently than non-small cell lung cancers, and generally spread to distant organs more can be undertaken. Hoever, if identified early enough, these cancers are often responsive to Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs chemotherapy and thoracic radiation treatment.

30

25

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized usually are not identified until significant metastasis has occurred, which are typically not at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but WO 02/086443

very responsive to surgical, chemotherapy, or radiation treatment..

The screening of asymptomatic persons at high risk for lung cancer has often proven detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease

because of the lack ofv effective curative treatments, early detection does not necessarily alter spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, the total death rate from lung cancer. 2

in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

13

### SUMMARY OF THE INVENTION

ಣ

antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy The present invention provides nucleotide sequences of genes that are up- and downmonitoring and early detection of relapse following treatment of lung cancers, monitoring regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as can be used for a number of purposes. Examples include early detection of lung cancers, of lung cancers, selecting patients for postoperative chemotherapy or rudiation therapy, largets for screening for therapeutic compounds that modulate lung cancer, such as 25

selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early

8

detection of precancerous lesions of the lung. Examples of benign or precancerous lesions

include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis,

hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

WO 02/086443
bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

'n

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

2

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a humah

2

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

2

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an analyse.

25

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evalated for comparison of protein.

9

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

WO 02/086443
biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

efficacy of the thorapy.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical

to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

ន

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

~

WO 02/086443

In another aspect, the present invention provides a method of detecting antibodies

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

2

S

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

2

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

2

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

25

be of lung cancer or related condition itself, or treatment of metastasis.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

30

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

WO 02/086443

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

# DETAILED DESCRIPTION OF THE INVENTION

filed March 29, 2002), each of which is incorporated herein by reference. The treatment may non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, screening for compositions which modulate lung cancer. "Treatment, monitoring, detection that the subject is more likely to have disease. In particular, while these targets are identified nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating In accordance with the objects outlined above, the present invention provides novel carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, modulation of lung disease in those patients who have lung disease (whether malignant or primarily from lung cancer samples, these same targets are likely to be similarly found in or modulation of lung disease or cancer" includes treatment, monitoring, detection, or pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, methods for diagnosis and treatment of lung disease or cancer, as well as methods for analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung 2 13 2

for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to PCT/US02/12476

similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have

but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

S

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide

sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are <u>의</u>

as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung

2

(e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain chronically diseases lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples analyses, the ratio for the "chron" category was determined using the 70th percentile of divided by the 90th percentile of normal lung samples.

2

Definitions

mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-

22

more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 32%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or 22

comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) ജ

the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, PCT/US02/12476 or 99% or greater amino sequence identity, preferably over a region of over a region of at other mammal. A "Jung cancer polypeptide" and a "Jung cancer polynucleotide," include least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence polynucleotide or polypeptide sequence is typically from a mammal including, but not both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide polypeptide sequences. The "full length" may be prior to, or after, various stages of postcontained in one or more naturally occurring, wild type lung cancer polynucleotide or or polynucleotide sequence, or a variant thereof, that contains the elements normally ranslational processing or splicing, including alternative splicing. 2

transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; derived from patient tissues. A biological sample is typically obtained from a eukaryotic contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or 'Biological sample" as used herein is a sample of biological tissue or fluid that Biological samples also include explants and primary and/or transformed cell cultures archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. fish. Livestock and domestic animals are of interest. 15 2

isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using proviously isolated cells (e.g., "Providing a biological sample" means to obtain a biological sample for use in history, will be particularly useful. 39

acids or polypeptide sequences, refer to two or more sequences or subsequences that are the The terms "identical" or percent "identity," in the context of two or more nucleic

WO 02/086413
same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%,

95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the

complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

2

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequencess are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

ន

15

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) I. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFTT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

23

30

W0 03/086413
Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) <u>Current Protocols in Molecular Biology</u>.

words of length W in the query sequence, which either match or satisfy some positive-valued described in Altschul, et al. (1977) <u>Nuc. Acids Res.</u> 25:3389-3402 and Altschul, et al. (1990) LMol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described threshold score T when aligned with a word of the same length in a database sequence. T is sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., neighborhood word hits act as seeds for initiating searches to find longer HSPs containing due to the accumulation of one or more negative-scoring residue alignments; or the end of sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) them. The word hits are extended in both directions along each sequence for as far as the for nucleotide sequences, the parameters M (reward score for a pair of matching residues; quantity X from its maximum achieved value; the cumulative score goes to zero or below, either sequence is reached. The BLAST algorithm parameters W, T, and X determine the always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid nerein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This hits in each direction are halted when: the cumulative alignment score falls off by the uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=.4 and a S 2 13 20 23

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) <u>Proc. Nat'l. Acad. Sci. USA</u> 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

(see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of

50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

2

defaults a wordlength of 3, and expectation (B) of 10, and the BLOSUM62 scoring matrix

comparison of both strands. For amino acid sequences, the BLASTP program uses as

WO 02/086443
two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

\$

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

9

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

15

2

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

25

3

WO 02/086443
In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% nure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally

- 10 occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine,
  - norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.
- Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

2

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino

acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can

polypeptide. Such nucleic acid variations are "silent variations," which are one species of

be altered to another of the corresponding codons described without altering the encoded

codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each encodes a polypeptide is implicit in a described sequence with respect to the expression functionally similar molecule. Accordingly, a silent variation of a nucleic acid which TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a product, but not necessarily with respect to actual probe sequences.

Ś

2

alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine homologs, and alleles of the invention. Typically conservative substitutions include for one As to amino acid sequences, one of skill will recognize that individual substitutions, (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)). providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which of an amino acid with a chemically similar amino acid. Conservative substitution tables (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S),

2

20

Macromolecular structures such as polypeptide structures can be described in terms of Alberts, et al. (1994) Molecular Biology of the Cell (3<sup>rd</sup> ed.) and Cantor and Schimmel (1980) refers to locally ordered, three dimensional structures within a polypeptide. These structures compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. are commonly known as domains. Domains are portions of a polypeptide that often form a Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary Iypical domains are made up of sections of lesser organization such as stretches of  $\beta$ -sheet structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" and  $\alpha$ -helices. "Tertiary structure" refers to the complete three dimensional structure of a formed, usually by the noncovalent association of independent tertiary units. Anisotropic polypeptide monomer. "Quaternary structure" refers to the three dimensional structure various levels of organization. For a general discussion of this organization, see, e.g., terms are also known as energy terms.

22

30

WO 02/08/6443 PCT/US02/1141/6 "Nucleic acid" or "oligonucleotide" or grammatical equivalents

typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any used herein means at least two nucleotides covalently linked together. Oligonucleotides are

although in some cases, nucleic acid analogs are included that may have at least one different length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, ctc. A nucleic acid of the present invention will generally contain phosphodiester bonds, inkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-S

methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A 2

5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones, non-ionic aackbones, and non-ribose backbones, including those described in U.S. Patent Nos.

Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing

Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring increase the stability and half-life of such molecules in physiological environments or as one or more carbocyclic sugars are also included within one definition of nucleic acids. 2

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids This results in two advantages. First, the PNA backbone exhibits improved hybridization acid analogs. These backbones are substantially non-ionic under neutral conditions, in

nucleic acids and analogs may be made.

ಜ

backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded kinetics. PNAs have larger changes in the melting temperature  $(T_m)$  for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T<sub>m</sub> for an Similarly, due to their non-ionic nature, hybridization of the bases attached to these internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. by cellular enzymes, and thus can be more stable. 25 3

portions of both double stranded or single stranded sequence. As will be appreciated by those The nucleic acids may be single stranded or double stranded, as specified, or contain in the art, the depiction of a single strand also defines the sequence of the complementary

WO 02/086443

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guamine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally

hypoxenthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pro-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

2

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include <sup>32</sup>P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) L. Immunol. Meth., 40:219-230; and Nygren (1982) L. Histochem, and Cytochem, 30:407-412.

15

2

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

22

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

೫

WO 02/08/6413
using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases target sequences lacking complete complementarity with the probe sequence depending upon linkage other than a phosphodiester bond, preferably one that does not functionally interfere As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of binding to a target nucleic acid of complementary sequence through one or more types of the stringency of the hybridization conditions. The probes are preferably directly labeled, bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind biotin to which a streptavidin complex may later bind. By assaying for the presence or (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a absence of the probe, one can detect the presence or absence of the select sequence or RNA or protein expression. 10 13

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express a tail. By the term "recombinant nucleic acid" herein is meant nucleic acid, expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is

30 understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

or more subsequences that are not found in the same relationship to each other in nature (e.g., typically recombinantly produced, having two or more sequences, e.g., from unrelated genes coding region from another source. Similarly, a heterologous protein will often refer to two indicates that the nucleic acid comprises two or more subsequences that are not normally arranged to make a new functional nucleic acid, e.g., a promoter from one source and a The term "heterologous" when used with reference to portions of a nucleic acid found in the same relationship to each other in nature. For instance, the nucleic acid is a fusion protein).

2

Ś

promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor environmental and developmental conditions. An "inducible" promoter is a promoter that is elements, which can be located as much as several thousand base pairs from the start site of active under environmental or developmental regulation. The term "operably linked" refers promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, ranscription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type A "promoter" is typically an array of nucleic acid control sequences that direct to a functional linkage between a nucleic acid expression control sequence (such as a e.g., wherein the expression control sequence directs transcription of the nucleic acid transcription. A "constitutive" promoter is a promoter that is active under most corresponding to the second sequence.

15

2

particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or synthetically, with a series of specified nucleic acid elements that permit transcription of a An "expression vector" is a nucleic acid construct, generated recombinantly or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be ranscribed in operable linkage to a promoter.

22

23

duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., The phrase "selectively (or specifically) hybridizes to" refers to the binding, total cellular or library DNA or RNA).

30

ಜ

acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and lower than the thermal melting point  $(T_m)$  for the specific sequence at a defined ionic strength "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen ,400004445 The phrase "stringent hybridization conditions" refers to conditions under which a Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10°C higher temperatures. An extensive guide to the hybridization of nucleic acids is found in (1993) Techniques in Biochemistry and Molecular Biology.--Hybridization with Nucleic probe will hybridize to its target subsequence, typically in a complex mixture of nucleic will be different in different circumstances. Longer sequences hybridize specifically at 'n

occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 2 13

nucleotides). Stringent conditions may also be achieved with the addition of destabilizing typically at least two times background, preferably 10 times background hybridization. agents such as formamide. For selective or specific hybridization, a positive signal is

SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency depending on primer length. For high stringency PCR amplification, a temperature of about Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% amplification, although annealing temperatures may vary between about 32° C and 48° C

2

62° C is typical, although high stringency annealing temperatures can range from about 50° C both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for to about 65° C, depending on the primer length and specificity. Typical cycle conditions for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols. A Guide to Methods and

substantially identical if the polypeptides which they encodo are substantially identical. This Nucleic acids that do not hybridize to each other under stringent conditions are still

parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in WO 02/086413 PCT/US02/12476 occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, permitted by the genetic code. In such cases, the nucleic acids typically hybridize under background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization moderately stringent hybridization conditions. Exemplary "moderately stringent

Molecular Biology Lippincott.

2

marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and modulate activity of a lung cancer protein includes the determination of a parameter that is decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft The phrase "functional effects" in the context of assays for testing compounds that indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific protein expression in cells undergoing metastasis, and other characteristics of lung cancer physiological, enzymatic, functional, physical, or chemical effect, such as the ability to cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

15

2

compound on lung cancer can also be performed using lung cancer assays known to those of increases or decreases a parameter that is indirectly or directly under the influence of a lung effects. Such functional effects can be measured by many means known to those skilled in refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for cellular transformation; growth factor or serum dependence; tumor specific marker levels; cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a the protein, measuring inducible markers or transcriptional activation of the lung cancer dependence; contact inhibition and density limitation of growth; cellular proliferation; By "determining the functional effect" is meant assaying for a compound that the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein skill in the art such as an in vitro assays, e.g., cell growth on soft agar, anchorage 25 30

sequences set out in Tables 1A-16.

WO 02/086443

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of RNA stability, identification of downstream or reporter gene expression functional effects can be evaluated by many means known to those skilled in the art, e.g., measurement of changes in RNA or protein levels for lung cancer-associated sequences, (CAT, lucifcrase, p-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory Inhibitors", "activators", and "inodulators" of lung cancer polynucleotide and nucleic acids may seem to inhibit expression and subsequent function of the protein. 2

or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, identified by incubating lung cancer cells with the test compound and determining increases modulators also include genetically modified versions of lung cancer proteins, e.g., versions effects on activity, as described above. Activators and inhibitors of lung cancer can also be agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and membranes, applying putative modulator compounds, and then determining the functional 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or with altered activity, as well as naturally occurring and synthetic ligands, antagonists, activators include, e.g., expressing the lung cancer protein in vitro, in cells, or cell 13 2 22

is achieved when the activity value relative to the control is about 80%, preferably 50%, more value relative to the control (untreated with activators) is 110%, more preferably 150%, more inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide activator, or modulator to examine the extent of inhibition. Control samples (untreated with Samples or assays comprising lung cancer proteins that are treated with a potential preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity activator, inhibitor, or modulator are compared to control samples without the inhibitor,

ဓ္က

WO 02/086443
preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3<sup>rd</sup> ed.).

. S "Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

2

"Cancer cells," 'transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3" ed.)).

13

ຊ

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

25

25

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

8

WO 02/086413
for antigen recognition. The terms variable light chain (V<sub>L</sub>) and variable heavy chain (V<sub>H</sub>)
refer to these light and heavy chains respectively.

using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552converting the F(ab)'s dimer into an Fab' monomer. The Fab' monomer is essentially Fab reduced under mild conditions to break the disulfide linkage in the hinge region, thereby fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an which itself is a light chain joined to V<sub>H</sub>-C<sub>H</sub>1 by a disulfide bond. The F(ab)'<sub>2</sub> may be antibody fragments either produced by the modification of whole antibodics, or those S 15 2

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodics, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy: Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies. A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990)

ನ

A "chimeric antibody" is an antibody molecule in which, e.g. (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

30

Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

WO 02/086443

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

## Identification of lung cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample, while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

2

13

2

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, by comparing patient samples with the known expression profiles. Malignant diseasemay be remote primary site. Furthermore, these gene expression profiles (or individual genes) allow profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. done on the protein basis; that is, protein expression levels of the lung cancer proteins can be destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed which can then be used in these screens. PCR methods may be applied with selected primer evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-This may be done by making biochips comprising sets of the important lung cancer genes, Alternatively, a treatment step may induce other markers which may be used as targets to screening of drug candidates with an eye to mimicking or altering a particular expression pairs, and analysis may be of RNA or of genomic sequences. These methods can also be the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a regulate lung cancer, and thus tumor growth or recurrence, in a particular patient.

25

ဓ္က

WO 02/086443
nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer, as well as those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; o.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

8

obtained using the techniques outlined below.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization

23

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, 30 cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

WO 02086443.

PCT/US02/12476
etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to

commercially available, e.g., from Affymotrix, Santa Clara, CA. Gene expression profiles as biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and although in some embodiments, this is not necessary (e.g., where organs may be dispensible ung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, disease states are compared to genes expressed in other normal tissues, preferably normal at a later stage of life). That is, when screening for drugs, it is usually preferable that the significant amounts in other tissues (e.g., essential organs) are removed from the profile, embodiment, those genes identified during the lung cancer screen that are expressed in target expression be disease specific, to minimize possible side effects on other organs. prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred

2

accession numbers are hereby expressly incorporated by reference. GenBank is known in the lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonlung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a In a preferred embodiment, lung cancer sequences are those that are up-regulated in accession numbers herein are for the GenBank sequence database and the sequences of the number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more malignant conditions relative to normal. Unigene cluster identification numbers and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and 2 15

ಜ

available sequences or be predicted from genomic DNA using exon prediction algorithms, situations, sequences have been derived from cloning and sequencing of isolated nucleic such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ) Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of 25 2

regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue In another preferred embodiment, lung cancer sequences are those that are down-

greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

#### Informatics

additionally provide high-resolution, high-sensitivity datasets which can be used in the areas The ability to identify genes that are over or under expressed in lung cancer can of diagnostics, therapeuties, drug development, pharmacogenetics, protein structure,

example, subcellular toxicological information can be generated to better direct drug structure (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA biosensor development, and other related areas. For example, the expression profiles can be sensor device to predict the likely toxicological effect of chemical exposures and likely used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets. 2 15

tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

at least one set of assay data. The data contained in the database is acquired, e.g., using array database of the invention can be maintained on any electronic device allowing for the storage Thus, in another embodiment, the present invention provides a database that includes analysis either singly or in a library format. The database can be in a form in which data can of and access to the database, such as a personal computer, but is preferably distributed on a be maintained and transmitted, but is preferably an electronic database. The electronic wide area network, such as the World Wide Web.

23

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

30

WO 01/086413
pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genc-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

S

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S.

Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene

2

sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) <u>Biological</u>
Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Ocullette (eds., 1998) <u>Bioinformatics</u>: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) <u>Bioinformatics</u>: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) <u>Introduction to Computational Molecular Biology</u>; Miserier and Krawetz (eds, 2000) <u>Bioinformatics</u>: Methods and Protocols; Higgins and Taylor (eds., 2000) <u>Bioinformatics</u>. Structure, and Databanks; A Practical

3

WO 02/086443
WO 02/086443
Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps. Sequences. and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of farget-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at loast one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit patterm encoding a protein expression fingerprint record comprising unique identifiers for at least 10

2

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

ಜ

arget data records cross-tabulated with target source.

52

fields stored in a hierarchical topological map which can be viewed as a tree structure or as

22

the merger of two or more such tree structures.

record are divided into two classes, navigational and informational data, with navigational

Patent 5,295,261 reports a hybrid database structure in which the fields of each database

WO 02/086443

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences
determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, ALX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

Ś

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

2

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

2

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

22

ಜ

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

8

WO 02/086443
MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a 10 collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

# 15 Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphalase activity, proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting

2

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

3

proteins to various subcellular localizations, and are involved in maintaining the structural

ntegrity of organelles.

23

ಜ

WO 02/086413 PCT/US02/12476

domains, also bind tyrosine phosphorylated targets: SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be

involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple

S

One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains.

10 Versions are available via the internet from Washington University in St. Louis, the Sanger Center in Enpland, and the Karnlinska Institute in Sweden (see e.g. Bateman et al 2000).

Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) <u>Proteins</u> 28:405-420; Bateman, et al. (1999) <u>Nuc. Acids Res.</u> 27:260-262; and Sonnhammer, et al. (1998) <u>Nuc. Acids Res.</u> 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

8

53

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

39

WO 02/086443

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conscrved domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their may be peptides, proteins, or small molecules such as adenosine and the like. For example, cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may and/or functions have been ascribed to different extracellular motifs. Many extracellular also associate with the extracellular matrix and contribute to the maintenance of the cell motifs are found repeatedly among various extracellular domains. Conserved structure structure. 2 2

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic

ន

25 markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods.

Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

PCT/US02/12476

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a

distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

10 Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

### Use of lung cancer nucleic acids

12

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene).

conditions, as outlined herein.

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

3

WO 02/086443
other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications.

Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the pair mismatches which will interfere with hybridization between the target sequence and the complementary" herein is meant that the probes are sufficiently complementary to the target outlined below, this complementarity need not be perfect; there may be any number of base single stranded nucleic acids of the present invention. However, if the number of mutations conditions, the sequence is not a complementary target sequence. Thus, by "substantially sequences to hybridize under appropriate reaction conditions, particularly high stringency complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target nucleic acid sequences outlined in the figures and/or the complements thereof) are made. is so great that no hybridization can occur under even the least stringent of hybridization sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As The nucleic acid probes attached to the biochip are designed to be substantially 2 :2 ន

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

WO 02/086443
particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

S

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

2

2

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochin.

20

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polybethylene, polybutylene, polybutylene, polybutomanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

23

30

WO 02/086443
Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

ຊ

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

25 Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116, WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of the Affymetrix GeneChip<sup>TM</sup> technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

WO 02/086443 PCT/US02/12476

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols. A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Pcrkin-Elmer, e.g., www2.perkin-elmer.com).

2

2

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) <u>Genomics</u> 4:560, Landegren, et al. (1988) <u>Science</u> 241:1077, and Barringer, et al. (1990) <u>Gene</u> 89:117), transcription amplification (Kwoh, et al. (1989) <u>Proc. Natl. Acad. Sci. USA</u> 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) <u>Proc. Nat. Acad. Sci. USA</u> 87:1874), dot PCR, and linker adapter PCR, etc.

ឧ

# Expression of lung cancer proteins from nucleic acids

25

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

3

WO 02/086443
sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Bukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

ឧ

known in the art for a variety of host cells.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

25

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

homologous sequence for inclusion in the vector. Constructs for integrating vectors are well PCT/US02/12476 vector may be directed to a specific locus in the host cell by selecting the appropriate known in the art (e.g., Fernandez and Hoeffler, supra). WO 02/086413

marker gene to allow the selection of transformed host cells. Selection genes are well known In addition, in a preferred embodiment, the expression vector contains a selectable in the art and will vary with the host cell used.

S

Ś

choice of the expression vector and the host cell, and will be easily ascertained by one skilled growth conditions for induction. In addition, in some embodiments, the timing of the harvest The lung cancer proteins of the present invention are usually produced by culturing a cancer protein. Conditions appropriate for lung cancer protein expression will vary with the proliferation of the host cell, while the use of an inducible promoter requires the appropriate is important. For example, the baculoviral systems used in insect cell expression are lytic cancer protein, under the appropriate conditions to induce or cause expression of the lung host cell transformed with an expression vector containing nucleic acid encoding a lung constitutive promoters in the expression vector will require optimizing the growth and in the art through routine experimentation or optimization. For example, the use of viruses, and thus harvest time selection can be crucial for product yield.

2

15

animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

2

25

promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and to the translation stop codon and thus, together with the promoter elements, flank the coding polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR cells. Mammalian expression systems are also known in the art, and include retroviral and sequence. Examples of transcription terminator and polyadenylation signals include those mammalian viral genes, since the viral genes are often highly expressed and have a broad In a preferred embodiment, the lung cancer proteins are expressed in mammalian promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV adenoviral systems. Of particular use as mammalian promoters are the promoters from

30

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated other hosts, is well known in the art, and will vary with the host cell used. Techniques transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of efficient ribosome binding site is desirable. The expression vector may also include a signal the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. polymerase and initiate transcription. In addition to a functioning promoter sequence, an peptide sequence that provides for secretion of the lung cancer protein in bacteria. The Promoters from bacteriophage may also be used and are known in the art. In addition, occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA protein is either secreted into the growth media (gram-positive bacteria) or into the 2

bacteria). The bacterial expression vector may also include a selectable marker gene to allow biosynthetic pathways. These components are assembled into expression vectors. Expression periplasmic space, located between the inner and outer membrane of the cell (gram-negative chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and using techniques well known in the art, such as calcium chloride treatment, electroporation, Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells vectors for bacteria are well known in the art, and include vectors for Bacillus subtilts, E. for the selection of bacterial strains that have been transformed. Suitable selection genes also include biosynthetic genes, such as those in the histidine, tryptophan and leucino include genes which render the bacteria resistant to drugs such as ampicillin, 2 ຂ χ.

vectors for the transformation of insect cells, and in particular, baculovirus-based expression In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast Saccharonyces cerevisiae, Candida albicans and C. maliosa, Hansenula polymorpha, expression systems are well known in the art, and include expression vectors for 2

PCT/US02/12476 Kluyveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris,

Schizosaccharoniyces pombe, and Yarrowia lipolytica.

known in the art. Thus, e.g., for the creation of monocional antibodies, if the desired epitope Alternatively, the lung cancer protein may be made as a fusion protein to increase expression protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other The lung cancer protein may also be made as a fusion protein, using techniques well for affinity purification purposes, or for other reasons. For example, when the lung cancer is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. nucleic acid for expression purposes.

2

ways. Standard purification methods include electrophoretic, molecular, immunological and phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverseexpression. Lung cancer proteins may be isolated or purified in a variety of appropriate The degree of purification necessary will vary depending on the use of the lung cancer In a preferred embodiment, the lung cancer protein is purified or isolated after protein. In some instances no purification will be necessary.

13

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc. 2

#### Variants of lung cancer proteins 25

derivative lung cancer peptide will often contain at least one amino acid substitution, deletion proteins as compared to the wild-type sequence. That is, as outlined more fully below, the In one embodiment, the lung cancer proteins are derivative or variant lung cancer substitution, insertion or deletion may occur at a particular residue within the lung cancer or insertion, with amino acid substitutions being particularly preferred. The amino acid peptide.

ဓ္က

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

4

the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant lung cancer protein fragments having up to about 100-150 residues may be allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants predetermined nature of the variation, a feature that sets them apart from naturally occurring ypically exhibit a similar qualitative biological activity as the naturally occurring analogue, protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer although variants can also be selected which have modified characteristics as will be more WO 02/086443 eCT/US02/12 classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by in vitro synthesis. Amino acid sequence variants are characterized by the fully outlined below. S 2

mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung conducted at the target codon or region and the expressed lung cancer variants screened for While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer optimize the performance of a mutation at a given site, random mutagenesis may be cancer protein activities. 13

Amino acid substitutions are typically of single residues; insertions usually will be on occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although the order of from about 1 to 20 amino acids, although considerably larger insertions may be in some cases deletions may be much larger. ន

at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When Substitutions, deletions, insertions or any combination thereof may be used to arrive small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section. 23

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

ಜ

WO 02/086443
variant may be designed or reorganized such that a biological activity of the lung cancer
protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacety))-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioinidate.

2

S

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the  $\gamma$ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) <u>Proleins: Structure and Molecular Properties,</u> pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

8

:2

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

23

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid scquence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at presolected bases such that codons are generated that will translate into the desired amino acids.

23

WO 02/086443

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem. pp. 259-306.

- Semoval of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.
- 10 Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

2

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or

ន

another type of affinity matrix that binds to the epitope tag. In an alternative embodiment,

23

immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the

chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

3

the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags, HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

WO 02/086413
Horeto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) L Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, supra).

2

### Antibodies to lung cancer proteins

2

2

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

22

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

9

WO 02/086443
being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce 10 or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an

15 human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103)
 Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate onigin. Usually, rat or mouse myeloma cell lines are employed.
 20 The hybridoma cells may be cultured in a suitable culture medium that preferably contains

The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

25

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reascents.

02/086443
In a preferred embodiment, the antibodies to lung cancer protein are capable of

reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

S

2

13

method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. immunoglobulins (recipient antibody) in which residues from a complementary determining framework sequences. In general, a humanized antibody will comprise substantially all of at antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. sequence derived from non-human immunoglobulin. Humanized antibodies include human region (CDR) of the recipient are replaced by residues from a CDR of a non-human species In a preferred embodiment the antibodies to the lung cancer proteins are humanized immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et replaced by corresponding non-human residues. Humanized antibodies may also comprise regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, least one, and typically two, variable domains, in which all or substantially all of the CDR al. (1986) <u>Nature</u> 321:522-525; Riechmann, et al. (1988) <u>Nature</u> 332:323-329; and Presta (1992) Cur. Op. Struct, Biol. 2:593-596). Humanization can be performed following the (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', residues which are found neither in the recipient antibody nor in the imported CDR or substituting rodent CDRs or CDR sequences for corresponding sequences of a human capacity. In some instances, Fv framework residues of a human immunoglobulin are F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal humanized antibody optimally also will typically comprise at least a portion of an (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by

ຊ

23

WO 02/086443

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) <u>I. Mol. Biol.</u> 227:381; Marks, et al. (1991) <u>I. Mol. Biol.</u> 222:581). The techniques of Cole, et al. and Boemer, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985)

Monoclonal Antibodies and Cancer Therapy, p. 77 and Boemer, et al. (1991) L. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992)

BioTechnology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994)

Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

2

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

25

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

ဣ

4,816,567), wherein substantially less than an intact human variable domain has been

3

substituted by corresponding sequence from a non-human species

antibody may cause down-regulation of the transmembrane lung cancer protein. The

antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of

the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or

prevents growth of the cell. The antibody may also be used to target or sensitize the cell to antibody prevents the binding of other molecules to the lung cancer protein, the antibody cytotoxic agents, including, but not limited to TNF-a, TNF-\beta, IL-1, INF-\eta, and IL-2, or may induce or suppress a particular cellular pathway. In some embodiments, when the S

complement when complexed with the transmembrane protein thereby mediating cytotoxicity and the like. In some instances the antibody may belong to a sub-type that activates serum or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by 2

chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate,

administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide

15

means to locally ablate cells.

The effector moiety can be various molecules, including labeling moieties such as radioactive In another preferred embodiment, the antibody is conjugated to an effector moiety. moiety is a small molecule that modulates the activity of a lung cancer protein. In another labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic

close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or aspect the therapeutic moiety may modulate an activity of molecules associated with or in signaling activity such as protease or collagenase activity associated with lung cancer.

ឧ

this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In in the number of afflicted cells, thereby reducing symptoms associated with lung cancer.

25

crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer or toxins or active fragments of such toxins. Suitable toxins and their corresponding

ဓ္က

the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not

only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein In another preferred embodiment, the lung cancer protein against which the antibodies or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a a nuclear localization signal. S

The lung cancer antibodies of the invention specifically bind to lung cancer proteins By "specifically bind" herein is meant that the antibodies bind to the protein with a Kd of at better, and most preferably, 0.01 µM or better. Selectivity of binding to the specific target least about 0.1 mM, more usually at least about 1 µM, preferably at least about 0.1 µM or and not to related other sequences is also important.

2

Detection of lung cancer sequence for diagnostic and therapeutic applications

15

cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., or point of development is essentially a "fingerprint" of the state of the cell. While two states not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities evaluated to provide expression profiles. A gene expression profile of a particular cell state of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are In one aspect, the RNA expression levels of genes are determined for different may have a particular gene similarly expressed, the evaluation of a number of genes

. 20.

simultaneously allows the generation of a gene expression profile that is reflective of the state regarding which genes are important (including both up- and down-regulation of genes) in determine whether a tissue sample has the gene expression profile of normal or cancerous of the cell. By comparing expression profiles of cells in different states, information each of these states is obtained. Then, diagnosis may be performed or confirmed to tissue. This will provide for molecular diagnosis of related conditions. 25

qualitatively have its expression altered, including an activation or inactivation, in, e.g., 'Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can

PCT/US02/12476 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but ranscript. The degree to which expression differs need only be large enough to quantify via expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of not in both. Alternatively, the difference in expression may be quantitative, e.g., in that standard characterization techniques as outlined below, such as by use of Affymetrix

S

GeneChip<sup>TM</sup> expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about expressly incorporated by reference. Other techniques include, but are not limited to, 2

preferred. 2

expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein those identified as being important in a lung cancer or disease phenotype, can be evaluated in and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., gene transcript, and the quantification of gene expression levels, or, alternatively, the final Bvaluation may be at the gene transcript or the protein level. The amount of gene a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

ន

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for he detection and quantification of lung cancer sequences in a particular cell. The assays are sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, further described below in the example. PCR techniques can be used to provide greater these assays may be performed on an individual basis as well.

25

particular interest are methods wherein an mRNA encoding a lung cancer protein is detected. detected. Although DNA or RNA encoding the lung cancer protein may be detected, of In a preferred embodiment nucleic acids encoding the lung cancer protein are

to hybridize with the target mRNA. Following washing to remove the non-specifically bound and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to remove the non-specifically bound probe, the label is detected. In another method detection probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that of the mRNA is performed in stiu. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe RNA. Probes also should contain a detectable label, as defined herein. In one method the is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue as nylon membranes and hybridizing the probe with the sample. Following washing to tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate. S 2

containing lung cancer sequences are used in diagnostic assays. This can be performed on an described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic In a preferred embodiment, various proteins from the three classes of proteins as assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells expression profiles are used, preferably in conjunction with high throughput screening individual gene or corresponding polypeptide level. In a preferred embodiment, the techniques to allow monitoring for expression profile genes and/or corresponding polypeptides. 15 ಜ

detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gol, including protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art. isoelectric focusing gels and the like). Following separation of proteins, the lung cancer of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer As described and defined herein, lung cancer proteins, including intracellular, 9 23

In another preferred method, antibodies to the lung cancer protein find use in in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

WO 02/086443

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody binding, the presence of the antibody or antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

'n

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

2

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including BLISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

15

ຊ

In a preferred embodiment, *in stiu* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In stiu* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

22

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays.

As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

WO 02/086413
genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) <u>Science</u> 279:84-8; Heid (1996) <u>Genome Res.</u> 6:986-94.

2

modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired, similarly, a 10-fold decrease in lung

WO 02/086443

PCT/US02/12476
cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

Ś

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

2

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

13

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

20

The term 'test compound" or "drug candidate" or ''modulator'' or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or, indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator

25

another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

30

suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In

WO 02/086443

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity.

Conventionally, new chemical cutities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as

2

conventional "lead compounds" or can themselves be used as potential or actual therapeutics. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) L.Med. Chem., 37(9):1233-1251).

೧

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept Prot. Res. 37:487-493, Houghton, et al. (1991) Mature. 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1992) J. Amer. Chem. Soc. 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small

(Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) L. Med. Chem. 37:1385, nucleic compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates

Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S.

No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent 2

U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see,

Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, 2

e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin,

A number of well known robotic systems have also been developed for solution phase apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek chemistries. These systems include automated workstations like the automated synthesis systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, present invention. In addition, numerous combinatorial libraries are themselves Biosciences, Columbia, MD, etc.).

ន

23

Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide The assays to identify modulators are amenable to high throughput screening. expression, and polypeptide activity. High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

23

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding. In addition, high throughput screening systems are commercially available (see, e.g., Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.): These systems assay. These configurable systems provide high throughput and rapid start up as well as a typically automate procedures, including sample and reagent pipetting, liquid dispensing, high degree of flexibility and customization. The manufacturers of such systems provide timed incubations, and final readings of the microplate in detector(s) appropriate for the Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene ranscription, ligand binding, and the like. 2

preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or useful test compound will be directed to the class of proteins to which the target belongs, e.g., ibraries of proteins may be made for screening in the methods of the invention. Particularly with the latter being preferred, and human proteins being especially preferred. Particularly In one embodiment, modulators are proteins, often naturally occurring proteins or random or directed digests of proteinaccous cellular extracts, may be used. In this way substrates for enzymes or ligands and receptors. 13 8.

amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring In a preferred embodiment, modulators are peptides of from about 5 to about 30

nucleotide or amino acid at any position. The synthetic process can be designed to generate proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical quivalents herein is meant that the nucleic acid or peptide consists of essentially random nucleic acids, discussed below) are often chemically synthesized, they may incorporate a sequences of nucleotides and amino acids, respectively. Since these random peptides (or 23

combinations over the length of the sequence, thus forming a library of randomized candidate randomized proteins or nucleic acids, to allow the formation of all or most of the possible bioactive proteinaceous agents. 2

sterically biased (either small or large) residues, towards the creation of nucleic acid binding In one embodiment, the library is fully randonitzed, with no sequence preferences or positions within the sequence are either held constant, or are selected from a limited number PCT/US02/12476 randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, constants at any position. In a preferred embodiment, the library is biased. That is, some domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are threonines, tyrosines or histidines for phosphorylation sites, etc.

S

Modulators of lung cancer can also be nucleic acids, as defined above.

2

Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins. naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. As described above generally for proteins, nucleic acid modulating agents may be

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15

with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids amplification such as PCR performed as appropriate. For example, an in vitro transcription sequence is prepared using known techniques. For example, the sample may be treated to period of time, the sample containing a target sequence is analyzed. If required, the target After a candidate agent has been added and the cells allowed to incubate for some lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or are labeled with biotin-FITC or PE, or with cy3 or cy5.

20

or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled target sequence's specific binding to a probe. The label also can be an enzyme, such as, is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

22

assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos Nucleic acid assays can be direct hybridization assays or can comprise "sandwich

20

which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization formamide concentration, salt concentration, chaotropic salt concentration, pH, organic complex only in the presence of target. Stringcircy can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, solvent concentration, etc. 9

outlined in U.S. Patent No. 5,681,697: Thus it may be desirable to perform certain steps at These parameters may also be used to control non-specific binding, as is generally higher stringency conditions to reduce non-specific binding. 15

The reactions outlined herein may be accomplished in a variety of ways. Components assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be specific or background interactions. Reagents that otherwise improve the efficiency of the other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. used as appropriate, depending on the sample preparation methods and purity of the target. preferred embodiments outlined below. In addition, the reaction may include a variety of which may be used to facilitate optimal hybridization and detection, and/or reduce nonof the reaction may be added simultaneously, or sequentially, in different orders, with

ຊ

expression levels as between states, of individual genes, forming a gene expression profile. The assay data are analyzed to determine the expression levels, and changes in

22

embodiment, e.g., for diagnostic applications, having identified differentially expressed genes expression of individual genes. In an another embodiment, screening is performed to identify particular expression profile, thus preferably generating the associated phenotype. In another Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a important in a particular state, screens can be performed to identify modulators that alter expressed gene. Again, having identified the importance of a gene in a particular state, modulators that alter a biological function of the expression product of a differentially 2

WO 02/086443
screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

2

15

2

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

2

23

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

8

WO 02/086443

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g.,

Assays to identify compounds with modulating activity can be performed in vitro.

For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, BLISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

mouse, preferably human.

2

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or \(\beta\)-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

52

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

WO 02/086443

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

'n

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

10

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

13

or nitrocellulose, teflon<sup>TM</sup>, etc. Microtiter plates and arrays are especially convenient because long as it is compatible with the reagents and overall methods of the invention, maintains the and samples. The particular manner of binding of the composition is typically not crucial so a large number of assays can be carried out simultaneously, using small amounts of reagents beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon Generally, in a preferred embodiment of the methods herein, the lung cancer protein supports may be made of a composition to which the compositions can be bound, is readily activity of the composition, and is nondiffusable. Preferred methods of binding include the screening. The surface of such supports may be solid or porous and of a convenient shape. or the candidate agent is non-diffusably bound to an insoluble support, preferably having Examples of suitable insoluble supports include microtiter plates, arrays, membranes and ase of antibodies (which do not sterically block either the ligand binding site or activation separated from soluble material, and is otherwise compatible with the overall method of isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble 2 25 ဓ္က

PCINOSOLISTATE
sequence when the protein is bound to the support), direct binding to "sticky" or ionic
supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc.
Following binding of the protein or agent, excess unbound material is removed by washing.
The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, nonnatural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cella. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

15

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., <sup>125</sup>I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

2

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Bither the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

. 39

WO 02/086413

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

S

2

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

2

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

29

25

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

WO 02/08/443
Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

ನ

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

25

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

30

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

WO 02/086443 PCT/US02/12476

A variety of cell growth, proliferation, viability, and metastasis assays are known to hose of skill in the art, as described below.

## Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with turnor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

2

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3<sup>rd</sup> ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

2

# 20 Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (<sup>3</sup>H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

25

In this assay, labeling index with (<sup>3</sup>H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

3

WO 02/086443 PCT/US02/12476 non-limiting medium conditions. The percentage of cells labeling with (<sup>2</sup>H)-thymidine is determined autoradiographically. See, Freshney (1994), supra.

### Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>I. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al. (1970) <u>I. Exp. Med.</u> 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

### Tumor specific markers levels

2

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (sec, e.g.,

15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in <u>Sem Cancer Biol.</u>).

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) <u>I. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>I. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Minich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

20

#### Invasiveness into Matrigel

25

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancerassociated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

ജ

WO 02/086443

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with <sup>12</sup>f and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

#### Tumor growth in vivo

2

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the cadogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

2

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) <u>Science</u> 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) <u>Manipulating the Mouse Embryo: A Laboratory Manual</u>, Cold Spring Harbor Laboratory and Robertson (ed. 1987) <u>Teratocarcinomas and Embryonic Stem Cells: A Practical Approach</u>, IRL Press, Washington, D.C.

2

23

Alternatively, various innune-suppressed or imnune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) L. Natl. Cancer Inst., 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10<sup>6</sup> cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

3

WO 02/086443
preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

### 5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

2

In the context of this invention, antisense polynucleotides can comprise naturallyoccurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothicate and other sulfur containing
species which are known for use in the art. Analogs are comprehended by this invention so
long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g.,
Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art. Antisense molecules as used herein include antisense or sense oligonucleotides.

8

Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense

30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence eucoding a given protein

WO 02/086443 is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dey</u>, 13:139-141; and Cathew (2001) <u>Curt. Op. Cell Biol.</u> 13:244-248. In manmalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ś

5

## Ribozymes

In addition to antisense polymucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNaso P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

2

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

ನ

22

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

2

wo ususes.

Formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer ncorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer are provided. In one embodiment, the methods comprise administering to a cell an anti-lung recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous Thus, in one embodiment, methods of modulating lung cancer in cells or organisms number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is downlung cancer gene or administering a gene encoding the lung cancer sequence, using known cancer protein. Alternatively, the methods comprise administering to a cell or organism a cancer antibody that reduces or eliminates the biological activity of an endogenous lung as described in PCT/US93/03868, hereby incorporated by reference in its entirety. antisense or RNAi nucleic acid. S 2 13

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

## 30 Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

PCT/US02/12476

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e.,

S

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

2

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

2

## Administration of pharmaceutical and vaccine compositions

25

In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art. Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

ဓ

WO 02/086443
drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intransally, iransdermally, intraperitoneally, intramuscularly, or intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. substituted amines including naturally occurring substituted amines, cyclic amines and basic acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acctic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic protein in a form suitable for administration to a patient. In the preferred embodiment, the The pharmaceutical compositions of the present invention comprise a lung cancer "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the pharmaccutically acceptable salts, which is meant to include both acid and base addition such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, manganese, aluminum salts and the like. Particularly preferred are the ammonium, biological effectiveness of the free bases and that are not biologically or otherwise pharmaceutical compositions are in a water soluble form, such as being present as 13 2 25

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine,

tripropylamine, and ethanolamine.

lactose, com and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules constructs, ribozymes, small organic molecules, etc.) when administered orally, should be The pharmaceutical compositions can be administered in a variety of unit dosage protection barrier. Means of protecting agents from digestion are well known in the art. packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a forms depending upon the method of administration. For example, unit dosage forms protected from digestion. This is typically accomplished either by complexing the

2

13

are sterile and generally free of undesirable matter. These compositions may be sterilized by A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. accordance with the particular mode of administration selected and the patient's needs (e.g., The compositions for administration will commonly comprise a lung cancer protein conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate pharmaccutically acceptable auxiliary substances as required to approximate physiological and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) conventional, well known sterilization techniques. The compositions may contain Goodman and Gilman: The Pharmacologial Basis of Therapeutics).

2

23

the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per Thus, a typical pharmaceutical composition for intravenous administration would be Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis day may be used, particularly when the drug is administered to a secluded site and not into dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g.,

8

Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition ozuso443
The compositions containing modulators of lung cancer proteins can be administered use will depend upon the severity of the disease and the general state of the patient's health. administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this for therapeutic or prophylactic treatments. In therapeutic applications, compositions are cure or at least partially arrest the disease and its complications. An amount adequate to should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in or in a mammal who is suspected of having a significant likelihood of developing cancer the mammal, the particular cancer being prevented, as well as other factors such as age, either a DNA vaccine form, or protein vaccine. 2 13

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapcutic agent, e.g., other anti-cancer agents or treatments.

20

invention provides methods, reagents, vectors, and cells useful for expression of lung cancerassociated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi In numerous embodiments, one or more nucleic acids, e.g., polynucleotides organism-based) recombinant expression systems.

25

introducing foreign nucleotide sequences into host cells may be used. These include the use plasma vectors, viral vectors and other well known methods for introducing cloned genomic of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for

WO 02/086443

Berger and Kimmel, <u>Guide to Molecular Cloning Techniques. Methods in Enzymology</u>
volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through
1999), and Sambrook, et al. (1989) <u>Molecular Cloning - A Laboratory Manual</u> (2nd ed., Vol.

<u>1.3</u>

In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

2

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) LClin\_Invest\_95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec\_Immunol\_28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol\_113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc\_Natl\_Acad\_Sci\_U.S.A. 85:5409-5413; Tam (1996) L.Immunol\_Methods 196:17-32), peptides formulated as multivalent peptides; peptides, viral delivery

2

Chalcrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) ADS Bio/Technology 4:790; Top, et al. (1971) L'Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) L Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1993) Annu. Rev. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

ജ

25

vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development;

2

WO 02/086443

delivery technologies, also known as receptor mediated targeting, such as those of Avant
Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvant (Difco Laboratorica, Detroit, MJ); Merck Adjuvant 65 (Merck and Complete Adjuvant (Difco Laboratorica, Detroit, MJ); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxido gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) <u>Science</u> 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include 'haked DNA'', facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, c.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S.

22

Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the

ike, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) I. Leukge. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter encodes portions of the lung cancer proteins including peptides derived from the lung cancer or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a

and an ability to generate cytotoxic T cell responses. This procedure provides for production plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancerassociated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC of cytotoxic T cell responses against cells which present antigen, including intracellular

2

molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant Additional or alternative adjuvants are available.

2

metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or desired, tissue-specific expression or knockout of the lung cancer protein may be necessary. models of lung cancer. When the lung cancer gene identified is repressed or diminished in vector, will result in the absence or increased expression of the lung cancer protein. When In another preferred embodiment lung cancer genes find use in generating animal 2 25

Depending on the desired expression level, promoters of various strengths can be employed It is also possible that the lung cancer protein is overexpressed in lung cancer. As to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. such, transgenic animals can be generated that overexpress the lung cancer protein.

င္က

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer WO 02/086443

PCT/US02/12476

## Kits for Use in Diagnostic and/or Prognostic Applications

also provided by the invention. In diagnostic and research applications such kits may include For use in diagnostic, research, and therapeutic applications suggested above, kits are antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi. dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or another pharmaceutically acceptable emulsion and suspension base. 2 Ś

protocols) for the practice of the methods of this invention. While the instructional materials capable of storing such instructions and communicating them to an end user is contemplated In addition, the kits may include instructional materials containing instructions (e.g., by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such typically comprise written or printed materials they are not limited to such. A medium media may include addresses to internet sites that provide such instructional materials. 15

reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated sequences. Such kits can be prepared from readily available materials and Diagnosis would typically involve evaluation of a plurality of genes or products. The genes cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer typically will be selected based on correlations with important parameters in disease which invention, depending upon the intended user of the kit and the particular needs of the user. protein. A wide variety of kits and components can be prepared according to the present The present invention also provides for kits for screening for modulators of lung may be identified in historical or outcome data. 2 25

8

စ္ဆ

PCT/US02/12476

EXAMPLES

Example 1: Gene Chip Analysis

described (Glymne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-5 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as Molecular profiles of various normal and cancerous tissues were determined and 993).

WO 02/086443

PCT/US02/12476

Tables 14 and 18 were proviously filed on April 18, 2001 in USSH 60/284,770 (18501-0015/0US) and on November 29, 2001 in USSH 60/334,570 (18501-001520US)

70% SOAD/90 0.74	87. 60 - 62 63 - 63 - 63 63 - 63 - 63 63 - 63 - 63 63 - 63 -	88555	83242 83242 83242 83242 83242 8324 8324	345 0.23 0.45 0.45 0.45 0.45	12333	22228 2000	0.0 0.0 0.0 0.0 0.0 0.0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.25 0.46 0.61	22 22 25 25 25 25 25 25 25 25 25 25 25 2	0.23 0.24 0.24 0.24 0.24	0.22 0.03 1 0.62 0.24	882 822 72	22222	0.91 0.04 0.08 0.78
70% chron/80% M. 1.61	882 882 882 982 983 983 983 983 983 983 983 983 983 983	0.00 0.55 0.83 1.33 1.33	1821.00 1821.00 1821.00	281 200 1.77 8.1.77 8.1.77	52555	2.12 2.23 2.12 5.23	0.82 0.82 1.1. 84.	8 8 8 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	102 102 183 183	25.5 25.5 25.6 2.6 3.1 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	1.01 0.81 1.44 1.01	1.1 1.26 3.06 0.97	1.22 1.06 1.16 1.18	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	57.1 88.5 8.5 8.5 8.7 7.7 8.1 8.1
Unigene Tille macrophage scenenger receptor 1	"Temanogictudin Heavy Chain, Vilpa Reg and the did birding probain 4 adipocyta acida carrier family 6 (neurobrassmita branstaming grown lactor, bela recepto G protein-coupled receptor kinasa 6	intercultritis-sestockards protein 4 methors of figurantiples (i.cs-tha do FBJ murhin catacterioria virtualization) calcibrain receptor-file calci	a sub-caeutr-portury protest AA (section mystold call nuclear differentiation and mannote receipts; C type I mannote receipts; C type I gustalise nucleotide binding protein 11 enrine codesse; copper containing 3 (vasc	potasskim hvædfy-redfyng chenek e progastiskin poestingen ( potah hvædie plotejningen redgjor ( cadhen il, VE-cadhen (vascular epithe deh ordnight protocyptense 2 (2)XX anhan ferforde R (nymbroder)	carecian i, cavedee protein 22:0 CAA3200 protein ESTs ESTs	ESTS ESTS, Wasky similar to PHOSPHOLEMAAN PR ESTS calcilonin receptor REM	ESTs, Weatly surfar to dipopitioses pred ESTs Hone suppers mRUA; cDNA DK72,65846076 (h ESTs ESTs	ESTs sperm respondand antgen 6 searun deprivation response (phosphaticy) ESTs	ESTR, Woodly sinter in addictive-stress ESTS Human DNA sequence from clone 141HS on a ESTs ESTs	macrophage receptor with callagenous str ESTs ESTs ESTs	ESTA ESTA ESTA ESTA ESTA	ESTR, Weaky dinilar b semaphorin F pH. Homo sapiens mRUM, cDNA DK-ZpoSkiEXOS // ESTs ESTs		ESTs ESTs ESTs, Moderately strifes to MT chterido ESTs	ESTS ESTS FOATIVOS probabi ESTS ESTS
UnigenalD Hs.49		1.16223 1.80261 1.75678 1.152175 18.2161	h.153637 h.76162 h.83361 h.198241	Hs.193044 Hs.1857 Hs.123841 Hs.123821 Hs.132821	Ha.74034 78 Ha.173035 78 Ha.37744 13 Ha.141863 19 Ha.19058			H.16943 H.168213 H.26530 H.204038 H.1438	Hs.4789 Hs.166030 Hs.87223 Hs.61957 Hs.40545		Hs.28792 Hs.30484 Hs.10299 Hs.23748	Hs. 17424 Hs. 16762 Hs. 22483 Hs. 16355 Hs. 9218	Hs.163613 Hs.16757 Hs.16028 Hs.17125		FG0 Hs.63671 D53 Hs.43877 S61 Hs.17223 S58 Hs.272940 77 Hs.57362
_	100780 HG373 100871 J02874 101088 L05564 101102 L07594 101168 L15383			102507 U52154 102598 U75272 103026 X54131 102280 X79881 103496 Y09267 103431 Z11697	14444						109613 F03031 109837 H00656 10993 H04768 109984 H09594 110099 H16568				115278 AA278760 115568 AA38003 115368 AA416681 116178 AA416573 116279 AA416073
8	91	15	70	25	30	35	04	45	20	55	99	65	70	75	80

	2:	Š-	29 <b>-</b>	470		5.5	i		_6,	0.74	<u>.</u> -	25	200	2 S.	0.52 0.91		-,-	<b>5</b> .		7.5 7.15	_!	8 -	£;_	<b>9</b> ;	ra-	8 E	25		689	25 25 25	889	35	15:	0.95	- 5	<b>2</b>	3.0	5 <b>5</b> 3.	0.87	0.83 0.83	8	55	22		60 <b>-</b>			35 .
	keralla 14 (aptiemotysk bullosa struck	Achacta metanoproteinas a (peracusas Achacta ecide complex (Drosophilg) homol	"Probase Inhibitor 3, strinderhed (GKA "Metanoma antigen, family A, Z.	Alecto-telangectasis group D-esseciated Small prefiles 4th perion 19 (perion)	haratin 5 (epidemotysts buttosa simplex	Certinoembryonic antigen-ratated call ad	Human parathyroid homone-related pept	butious periodistration 1 (23024010)	Desmoglein 3 (pemphigus vulgaris satigan Soluts carter family 7 (calonto amino	1 TK protein kinase 3 6100 catclum-binding protein A7 (psortas	"Homo sapiens conneron 26 (GJB2) mRNA, o "Protein brosine phosphatasa, receptor-	Middine (neurite growth-promoting factor Interdesifin enhancer Motine factor 2	Lemins, beta 3 (nices) (125/Q), kallel	decrees programme to (rest homolog)	Aldehyde dehydrogenase 8 Enhancer of zeste (Drosochila) homotoo 2	Preferentially expressed entition in mela	Netranoma amagen, taminy A, 9 (MALICE-8) Eyes absent (Drosophita) homolog 2	Forthead box MI	Ubiquifin carboxyl-terminal esterase L1	kerain 15 Matrix Metalleardelmase 10 (Stromobali	*Cetcltorincatcitonin-related polypepi	magne, bera 4. Matrix metalloprotesse 1 (interstital o	Streigh matrix materials are 11 (strometrals)	"Cathern 3, P-cadhern (placents)"	monotine induced by gamma interferon *Atchol dehydrogenasa 7 (dass IV), mu	"Lymphocyte artigen 6 complex, focus D, 8100 carbing harden property A2	keralin 17	514 Oncoletal antigen	ESTs, Agrity similar to Integral membre			Protein tinase domains containing protein			ESTs 8-phase kinase-associated protein 2 (p45							ESTs; procedagen I:N proteinse		ig superfamily receptor LNIR procursor Hypothetical protein FL/21620			"RABS Interacting, kinestn-like (rebibne Hysturanen synthese 3	
2773	E 1172	Hs.1619	#.1524 #.15980	Hs. 82237	Ha.195850 He.287319	Hs. 22052		Ha.620	Ha. 1925 Ha. 184801	H-112/0	Ha.78867	Hs.82045	FF.75517	Hs.90073	H.87538	Hs.30743	Hs.29279	Hs.239	Ha.78118	Ha. 80342	Ha.37058	Hs.83168	Ha. (845)0	Hs.2877	H-383	H.3185	H. 2785	H-82128	12.318	Ha.8127 He.88959	11 22014	H-26902	Hs.9029	Hs.6682	H-26369 H-23349	Hs.38733	Hs.8895	Hs.28114	Hs. 11950	Hs.34045 Hs.222024	Hs.23044	Hs.8687	Ha.91539	Hs.51450 Hs.18978	15.70823 15.62150	Hs.129911 Hs.72045	Hs.73625 Hs.85962	Hs.27027 Hs.13234
277760/CU O/M	100960 J00124		101124 (10343						101748 M76482 101759 M80244																																	107161 AA621169						
			S			20		31	C		20			22			က္က			35			40	!		45	2		20			22		9	8		44	3		70			75		ć	2		82
92FC					•																																					•						٠
PCT/11503/13476																											-																					
	£8	878	200	. S. S.	0.37	55	0.69	933	- 03s	. 25	9.4	99	6.08 4.06	88	_:	38	# TO	£ 2	ترم در در در	5	500	0.42	}	0.53	225	0.42	0.45 0.37	282	8 6	503	0.29	0.2 0.48	0.57	25	523	0.42	0.87	10.65	27.	22	264 264	0.13 2.15	2	8.5	122	3.6	9.5	591 591
																												٠																				
	3.5	3	3.	- 2	0.0	33	53	£. 5	25	8.	- 65 E	180	3 5	55	22:	3.5									95	9.0	1.51	22	0.65	987	5.7 091	25. 25.	22 23 28	1.16	885					6.60	2.14	8 _ 8 _	0.5	- 8	5.0	0.0	0.85	-
	EST.	ESTs	7.30g11.a1 Source fold fiver spiece	ESTs; Moderately similar to IIII ALU SUB	ESTs: Highly similar to KIAA0886 protein			irthblor of DNA binding 4; dominant nag ESTs		ESTe cer.		_	***HUM145B08B Clonboch huma ESTs	ESTs: Westly similar to pil.2 hypothetica ESTs	E81s	E57s	ESTs	ESTs; Highty shriter to Rep2 interacting	COW52 antgon (CAMPATH-1 antgen) KIAA1102 antleh	Interfeutin 7 receptor	yezhgul al sommagene kung (#50/210) vasoective intastinal peotida receptor 1	Homo septions mRNA; cDNA DNFZp686L0120 (f	KIAA0439 protein; homolog of yeast ubiqu	ESTs	MAD (mothers against decapentaplagic; Or	Cysome-ten protein 1 (mesting) ESTs	ESTs: Moderately similar to HYPOTHETICAL ESTs	regulator of G-protein signature 5 ecitivetial membrane crotein 2	Gh2-associated binder 2	E81	Homo sapiens clone TUAS CH-du-chal regi sili (Orosophila) homotog 3	tetranecth (plasminogen-binding protein adpose specific 2	ESTs directorydrations of the 2	ESTs; Highly similar to RGC-32 (R.noveg transminiton factor 21	plateleterdotheltal cell achesion molec	endothellal PAS domain protein (	Homo appens mRNA; cONA DRFZp664M0763 transforming growth factor, beta recepto	solute center family 35 (CNP-static ad adenosine deaminese; RNA-specific; B1 (h	deteted in ther cancer 1	cerbonic enhydrase IV	TEK tyrostne kingset; andomelial (venous ESTs; Moderately similar to III ALU SUB	phosphospase A2 group (8 (pancreas) Orromosome condensation 1	Homo sepiens mRNA for ostsoblest specifi KNAM095 own product	plateist-activating factor acetyfflydrota	MAA0175 geve product	"collages, type VII, apha I"	TIGR CD4 (epican, al. banscript 12	TIGR: placental protein 14, endometrial
113	Hs.42768	Hs.39288	1000		Hs. 125019	Hs. 187628	Hs. 193787 Hs. 110288	Ha. 34853 Ha. 170278	Hs.151323	Hs. 102560	Ht. 231082	H.22878	Hs.24979	Hs. 126712 Hs. 150318	H. 124282	Hs.102647	Ha.105895	H. 107361	H-214742	Hs. 237868	Ha. 198726	Hs.98314	Hr.12017	Ha. 13256	Ha.152863	H.201591	Hs.22567 Hs.22588	Ha.24950 Ha.29191	Ha.30687	Hs.258675	Hs.49476 Hs.67929	Ha.5424 Ha.74120	Hs. 204831 Hs. 173381	Hs.76640	Hs.78146	Ha. 166082	Hs.82028	Hs.82921 Hs.85302	Hs.8700	Hs.89485	H3.89540 H3.90421	Hs.84746	Hs. 136348 Hs. 155314	Hs.6783	18439			
WO 02/086443	117209 H99959 118901 N90719	118981 - N93839	119221 F38105	119861 WB0715	120132 23839		121643 AA417078 121690 AA418074		124214 H58508 124357 N72401		125174 W51835								29057 X62468 29210 AA401654									131263 R38334 131589 US2100				133120 X64559 133488 DAS370 .				134300 U81984						135346 MZ1056 100113 D00591					100668 HG2981-HT3938	
			S		5		_	15	-		20		_	3		-	ર્	-		35	-		<del>2</del>			45			2			2		9			9			2			۲ ۲		80			85

0.63 1.68 1.18 2.4.7 2.4.1 0.89	25.5 25.5 25.5 25.5 25.5 25.5 25.5 25.5	258	25.4.2.5.0 1.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	98.5 <u>3</u>	355_5	2885	3 <u>1</u> 8	-5	233 <u>3</u> 5	222	25_23	<b>2</b> 22	358	\$25_39	28252752
25.1.0 25	ARS 0.8 1.13 0.74	- 85-	9255	8 5.	555 E	32533	292	-8	20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0	1535-	5		885	255 - 653 259 - 653	25.00 20.00
	TEIN PREC		DANA1		ZE C .		ī			. 6	5	2		<b>4</b> 4	8 48 F E
tial cds* Inhig 5 (sur f fing prote finacrophag	UCED PRO		(LOWLZ), o plor-relate Se biNBH MA RAT WI	e (actival lahase dom dymerase B a protein LS	UNO ZDSBAT until (excen 2 roboln (EBBF se inhibit	a page	mone mone setilyelr,	A A cancer,	M 250	Nationa M2B. 5 SALCIUM-DI	mily B (MDR c emitro	yptophen 5- zin Interso ase domain	n C) RNA RNA poln) 258 e.	member C3 e deficient (8 psin) subuni	micher Az emesan i., o tir (teq office become see-related port office become see-related port occome micherance defortent (8, gebra miCku for equateme econe- jehosphale symbolise 2; esperi dep potes, 2 coordise; homo coorne micherance dechemi (mi rese (DWA) il briding protein
Confittle, per epost-conta enchoming th factor bing chainese 12,	MANAA IND teln 1 (DNA) II elph ssencephely	product h protein 1A tiler to protei cosphete syn	protein rece ha) protein rece index to WO	or AP-2 abb	FOUR CORA belle A sub- sive B box p ine) proteins	XI, etphs I*	ingen (NY E- Ione-like hor IAT I Izahinse 7 (n	lly, member molog 2 (col	to dehydroge kinase 4 kinase na; neuronal	RNA for for totlon factor y similar to C	selle; sub-fa dly 7 (calon)	aygenessift neuron prole metaloprola	activated kir stromograni Srbosomal stase some; macro	e synthase se family 1; maintenanc ome; macro	innover or seneran is, out it is in move or seneran is, out it is out of the control of the cont
Alph-Artisochen  Farman DNA-PK mPNU, partist con  Baschhind Lovo escharking 5 terr  Plategie mon-dermatering 6 terr  Martin medityrprintess 2 (mon-dyna)  ESTE, Wesshy sinils to barierin p0 texto  ESTE, Wesshy sinils to barierin p0 texto	INTERFERON-CAMMA INDUCED PROTEIN PRECURS ANY Induity protein 1 Topoleamerase (DVA) II sipis (170KD) 'Doublecorter_Lisemospheity, X-Erbad ( ESTs	KAA0188 gene product Britist protein-rich protein 1A ESTs, Harity similar to protein regulast guestine-monophospitals synthetisse	inntering (permitted to than golds).  **Low density flooprotein receptor-retain  **Serine (or optische) proteints british  **ESTs, Weachy seritair ib WOMM RAT WOMM!  **Staff profesior-protein 20  **No. John John John J. S. W. WOMM!  **No. John J. W.	Locative toppt Locative Transcription hertor A-2 athra (actival A dishapina and metaboproteinase dom SRB7 (suppressor of RNA polymerase B. y Na siRNA-essecuated Rule protein LSm.	Homo aspens mrove, cards, tox 2,554/1922 Haspien artifin bela-A subutil (axon 2 estrogen-responsive 8 box probin (E887) Sertra (or cytains) prodense inhbit Homo services (NN) = 11 thyrop s.	Pm.2 occapesa "colleges, type XI, ethile !"  STY (sex determining region Y)-box 4  COCCE protein foliase 2.	Lencerress amogen Parathyrod hormone 3 antigen 6 GFX control: STAT1 natrix melathoproteins	HZA Nstane tarriy, member A mut3 (E. coli) homolog 2 (colon cancer, RAP-retated orphen receptor A LIM domain only 4	tosphopluconsis detydrogenaso rdin-dependent kinase 4 corgouenostie kinase tolase 2; (gamma; neuronal) ablinina, IRNA emitalese	Horno expless mRNA for for histone AZB, o exchrating transcription factor 5 ESTs, Moderately similar to CAL CIUM-DEPE ESTs	1511e N.Pbinding cesselte; sub-family B (MDR) 2511e Robile center (amily 7 (callonic amino QUADSS protein	radios 3-monocrygeness/hyptophen 5-mo arvival of motor neuron protein intereo 57 is Gabriegin and metaloprotesse domain richaad box E I	o2VCtc4ZRac1-echnied kinese i fydail sereidgrawh II (dromograwh C) 2819 YC Corbut, 259 (besonal RWA Ymfolytas symbetas xolessome (prosome; macropsin), 269 subu	MADITY gans product Assignatelyberine synthase 1 Archaromedulase samely 1; member C3 Archaromosome maintenance defacter (8 Archaromos	Future mickot for manner to out it per proper consisting (CP): submid (B) and relationscene martination dictivilities of althorizonscene martination dictivilities of the supplies of personal personal personal relationscene martinations of super- postumentes martinations of decident in problemerses (DNA) il brindry projekt
			25 6 7 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		1687	88333 88333	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					2 = w = 2	5 # 2 5 E E	2684281	OFFI OFFR
5443	4444 4444 4444 4444	Hs.211 Hs.510 Hs.538		1111	5.444 5.254 5.255 5.355	Hs 80205 Hs 80484 Hs 80484	H-19626 H-27248 H-2256	Hs.78934 Hs.2156	Hs. 75888 Hs. 77494 Hs. 146580	45.24 4.554 3.654	2	Hs.75103 Hs.102458 Hs.106985 Hs.172028 Hs.159224	Hs.635 Hs.635 Hs.635 Hs.628	Hr.7329 Hr.7324 Hr.7324 Hr.7324 Hr.737101 Hr.89545	Hs. 1620 Hs. 16229 Hs. 77152 Hs. 153468 Hs. 153462 Hs. 153462
WO 02/086443 WO 02/086443 WO 02/086443 WO 02/086443 WO 07/08/0 WO 07/08/08/08/08/08/08/08/08/08/08/08/08/08/	X02530 X38076 X94068 X8461549	D80008 L05187 NA417152 NS9764	MS2432 MS2432 MS2432	63611 52960 VA216299	C57579 C57579 C57579 C57579 C51326 C51326 C51326	44227480 367275 370583 54942	119147 119147 22524	A60752 J03911 J04838 J24576	1370255 137022 141668 (51958	W281599 W282228 W234722 W262491	4436818 49048 430539 4482505	A805754 A234365 (37753 48579 89895	22152 22768 227630 627630 111094	14534 14534 11793 21063 28500	04357 04350 073518 07358 07358 07358 084557
WC 13041 13041 13042 13043 13042 13057 13057 13050 130			13276 13276 13276 13276		133391				62239 62239 62309 62309 62393						100287 100287 10038 10038 10038 10038
· <b>v</b>	10	15	70	25	30	35	40	45	20	, ,	?	8 8	8 8	75	88
														•	
				•											
											• ,				
9.4								•							
PCT/US02/12476													•		
PCT/U															
							•								
855 855 555 555 555 555 555 555 555 555	-8 <sub>7-3</sub>	- 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	52525	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2522	25288	£ 2 8 8	38	2525	2	2555	19885	122222 122222	2.59 2.99 2.99 2.09	152 123 128 138 138
0000 0000 0000 0000 0000 0000 0000 0000 0000	-8,8+8	0.06	252 T.	8	82:188	# 8 4 8 E	0.21 1.21 1.21 1.21	86	<u> </u>		8255	8-26 <b>3</b>	25	0.51 1.8 1.3 0.84	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
f en -	d E	7	A	<u>e</u> =	,	# Je 18		0 7	o pe	2	g 2	ngra Cr	ih GOATO E1	15 a	t fee
dehese dor ublqulin-cogenh (N.s. 540 Ashre p150	OVANCTION (TONKO)*	id transports	5 (cornectin to bor densi 335	brane serine		0238 fis, clo estorase L1 te lung & nz	- 2	pothetical pr 87 o pS3 naguta	strong home osophila) ho 292	r A27 (H.espie	zho finger p csome 20 20109 Purk	uza)-like uzdase M.P.	ne) ramb nemed prote 873 AC clone R	schmid meta reston motes rotein 2 Tasted gi	-family C (C modylo pals modylo pals hibblior 2A (
d metabors th similar to divide to as character to as	de fa, cone theste, rets oleh FLII	djougesyde in	roteln, beta sh n to LRP1 J dain KAA1	type II mem pressed in I	- <u>u</u>	oblivation of the control of the con	d hansoft)	tinilar to hy ed neceptor lety similar	3 kDa with complex (Dr oteln FLJ10	n I precurso almilar to Ji	homa 11A   E9 on chrom similar to P	om) è enog ene addoner	ansmembra imlar to un oteh FL12 o saptens B	C sipha 1 (3 th cyle cell ad cyche-rich p byche-rich p	assella, sud o sapiers la al non-epide ent lánase i .3 arrily, menta
A dishtopt and metalogradatuse doma (1870:150 pacitis strate to subquistacen (1870:150 pacitis strate to subquistacen (1870:150 pacitis strate to bushon (1840) hypothesia prosis is 1850 (1840:120 pacitis (1840:170 pacitis	CONA FULLING IN, cone UV/ **Discriptional hinate, rate (10 ESTs ESTs **Prodicted protein FU 11038	ESTs ATFrass, aminophospholipid transporter-I SSTs STS bronolog GAA1350 proein	"Gap junction protein, bota 5 (comean NAMOSES protein "ESTs, High aim to LRP1_Inu tow density 1 ESTs Hypothelical protein NAMA1335	ESTs ESTs Homo saplens type II membrane serine pro ESTs strand by forcessed by Forceral areas	Noredoxinities STe 23-04 protein typothetical pr	Hypodza-Indocible protein 2 **Termo septems CDNA FLJ 19238 (ig., clone H **Termo septems CDNA FLJ 19238 (ig., clone H **Unital certocyt-learning esterses L1 **LUNX protein PLUNCIpitate Iung & nexal **Dathoutilen**	PTD007 protein Butyrate-Induced transcript 1 ESTs Hypothodical protein FLI10718	Novi i 33 see CVAI.000 ESTs: Weaky sinilar to hypothetical pro G proteth-coupled receptor 87 "ESTs, Moderately similar to pS3 regulal ESTs.	Tumor protein 63 kDa with atrong homolog Achaele ecute complex (Drosophila) homol EST Hypotheficel protein FLJ10292	EST Chandromodulin I precursor CG-09 protoin 'ESTa, Weadly similar to JMZ7 (Kuapiens ESTa.	Solutions 11A (zho finger pro ESTs done RP6-8SIE9 on chromosome 20 TESTs, Wealty striler to POO109 Purkinje	X/GE-1 probeh ESTs ESTs Seture related gons 6 (mouse)-like MADHAUkhune ordonenshare sell/RQ subu	Gyopotein Prasmentown) min Gyopotein Prasmentown) min ESTS, Hgity similar to umarmed probin ESTS, Hgity similar to umarmed probin Hypothetics protein FL13929 RGC done RGCAID11	codigent, typs X, eighs I (Schmid melaph NAA1055 protein achtered leutocyle cell acheston molecu Cystein and dylche-rich protein 2 Belappillan 3 'Soute center famely 2 (scallated gl	VIP-bathong cassesta, sub-lamby C (CFT EST) and the company of the
13 Ha.7164 Ha.7164 Ha.31606 Ha.19539 Ha.292246 Ha.709245	Hs. 19981 11 Hs. 7549 14 Hs. 126733 14 Hs. 16740 14		H-18623 H-23684 H-12579 H-6327		9220	Ha. 87013 H. Ha. 78118 U. Ha. 78118 U. Ha. 78118 U. Ha. 78120 U. Ha. 78130 U. Ha. 78130 U. Ha. 48532 U. U. A. 48532 U. U. A. 48532 U. U. Ha. 48532 U. U. U. U. Ha. 48532 U.	112110 250622 48956 42824					112208 108977 194768 194768	H. 25.06 H. 27.079 H. 27.079 H. 57.056 H. 61635	HL10247 HL10247 HL10286 HL26557 HL26557	Hs.11128 Hs.11128 Hs.111247 Hs.112947 Hs.1239600 CHs.1474 Hs.1239600 CHs.1453223 s
24444444444444444444444444444444444444															
WO 02/086443			AA25214 AA25900 AA276943 AA276943 AA276943											A204248 L18608 UM6008 AA234962 H58873	
H10015 H1	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	115060 115091 115121 115291 115508	115522 115536 115697 115909	116107 116114 116134	1615 1615 1615 1615 1615 1615 1615 1615	117693 117831 118358 118565	119780 17845 120102	120859 120859 120948	121362 121362 121363 121731	2357	12408 12408 12408 12408 125218	125759 125972 125994 126395 126445	128192 128192 128510 128517 128924 129924	129099 129464 129466 129605 130023 130020 130030

S

<b>₹</b>	38222	<u> </u>	<u> </u>	202 222 23 23 23 23 23 23 23 23 23 23 23 2	22 23 28 28 28 28	27.1.1.28 2.1.1.1.28	55558 <u>9</u>	4.1.1.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	25.55.55.55.55.55.55.55.55.55.55.55.55.5	3, 28, 21	8-2553	282856	925 925 925 925 925 925 925 925 925 925	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2.1.1.2.2.2.1.2.2.1.2.2.2.2.2.2.2.2.2.2
	24488		2-228	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	88	9_5_8	35555 3555 3555 3555 3555 3555 3555 35	555 <u>-</u> 55	60.00 78.00 71.1.1	7,220	F 888 9	77 - 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2.1.0.1.2.2.1.0.1.2.2.2.2.2.2.2.2.2.2.2.	15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0	0.78 0.88 0.63
E87a	ESTS  ESTS  Horno septems mRNA; c.ONA DATZ0584/0222 ()  ESTS; Weadly stritar to objected droptile  Horno septems mRNA; c.DNA DATZ6438102 ()	ESTS, WRADG SENIOR DE LINGE FRICER PROJECTS  ESTS  ESTS, Moderately similar to COLLAGEN ALP  ESTS, Weekly similar to tumor morrosis (		ESTs ESTs, Moderatally striker to metargidin p ESTs pre-mPNA cleavage factor in (25kD)	ESTs, Moderstaby strutar to pil 2 hypothe ESTs  Hono septers mRNA; cDNA DKF2p54COS3 (to KF4-In mSAA-barding potent 2 KF4-In MAA-barding potent 2 ESTs; Moderstaby strutar to non-forction		Solary research for Around 1922 pooling recommended from the professional from the professional from the formal from the forma	ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	Groupe organization between the Control of the Cont	ESTs, Highly sindler to Myosia heavy cha ESTs. ESTs, Weathy sindler to F2595.3 (C.deqa EST EST Core-attols congenits it dyskurin exts.			ESTI, Weedy sindle to BACISTSCI Id (D.m. ESTI, Weedy sindle to BACISTSCI Id (D.m. ESTI, Weedy sindle to Wack sindlerly ESTI, Kighty sindle to amal the dinge ESTI, ENTRY sindle to pradre floring estimates pradre floring	ESTS FESTS ROAMSS protein CHAMSS protein CHAMS spales mRN4-CDNA DKCZpS8EB0ZZZ (I GLPCuppel family ment-ber GUZ FESTS	ESTS MACP-1 like protein byrosine phosphatore ESTs
16443 Hs.14800	HA 16272 HA 16273 HA 101282		Hs. 28899 Hs. 12094 Hs. 14912 Hs. 256301						H. 20659 H. 209473 H. 209473 H. 20891				Ha. 525.1 Ha. 5246 Ha. 52946 Ha. 66086 Ha. 66655 Ha. 67778		
	10551 AZBONS 10553 AZBONS 10553 AZBONS 10570 AZBONS		105536 AA404338 106069 AA417741 106103 AA421104 106140 AA424881 106149 AA424881	~~~~				107801 AA018433 107857 AA031948 108585 AA085342 108780 AA128561 108828 AA131584					15239 AAC19520 16527 AAC5039 16675 AAC3343 16004 AAC9122 16121 AAC5926 16100 AACC956		
50.5	<b>ふ</b> 3 最 表 語 語	5 \$\$\$\$\$	15 5 5 5 5 5 5 5 5 5	2 2 2 2 2 2 2 2	52 53 53 53 53 53 53 53 53 53 53 53 54 54 54 54 54 54 54 54 54 54 54 54 54	30 144488	35	4 252223		55 55		65	7 70		85 120
															-
PCT/US02/12476						·									
8.1.	£ 5 <b>5</b> 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	25 E E E E	2822	12828:	58 <u>5</u> 58	1.45 1.45 1.35 1.35	25 2 2 2 2 3 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3	2232 223 223 223 223 223 223 223 223 22	1.92 1.31 1.6 2.17 2.28 1.63	2, 2, 2, 2, 3, 3, 4, 2, 3, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4,	25.0 2.0 2.0 2.0 2.0 2.1 2.1 2.1 2.1	2 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 3 4 5 5 3 4 5 5 5 5	25. 1. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	55 55 55 55 55 55 55 55 55 55 55 55 55	2.7.3 2.67
. 12.00 . 12.00	25.00 25.00	22325 22325	128821	258 - E	800000		20 - 20 20 - 20	55555 555555	22 22 24 25 26 21 22 21 22 21	0.58 0.58 1.25 1.25 1.00	6.55 6.75 6.75 6.98 6.99 6.99	1,12	200 200 200 200 200 200 200 200 200 200		
N-myc downstream regulated Nuchroside Otghosphate Kinese Mm.23.H72s	Desmodath I "Nedr, Gla-Derhod"  "Roceomal Protch L'39 Hermog "Extran, Alt. Spibe 11"  Rad?	phoose phosphate bonnerses spilicing lactor, expainerbanine-rich 3 souhe carrier lamit 1 (pubarrischmetr macrophage migraden leibilbory factor ( 173 kinner famire macrier (	oydh-dependeni kitasa hitibibu 3 (CDK chaporarin containing TCP1; subuni 64 ( sorbita dehydrogeniasa giftogen eyilitsa khasa 3 beta	Annua agains (cer marte) apra ( hinfutbh-1 recoput-sasod sed thrase profite offic cell nucker antipen EphA1 amal nucker fibranteoprotch polypept	suggraphe opinitaties estaryold tend soft netter carein furses 2 beta polypeptibe CD9 enigen (p24) suggest of congent py pane, 3 suggest of pane, 4 suggest of pane, 5 suggest of pane,	Industrial Control of the Control of	singed (Drasophila)-Base (see enthin fee abothefor reductions family 1; member C1 controverse provision A (1740) entail muches modernate properties D3 polyp. AUI. Hussed gene from chromosome to	entaryolic trassian in ladon lactor hyd oxidasa itta 1 (PAG cohort 1; impor chromotor homoto 1 (Drosuphia HP1 bela amali nuclea it RNA activading complex, po Geochili opmali recentor family, rimmiter	Affirms, (1947k's trasporting, beta 3 poly aouto carrier temp? I (instruit arrivo a "Youno stocker entrucyte differential puddhe grotte entrucyte differential behagen carrier protein E.2-C BRQAI excellent (SRQA) excellent	Numen (New New House)  Characterion factor Ac-2 gurrant (exhet)  charpements containing 1021; suburil 2 (b  small nuclear stronuchactrotein polypept  annears Ac  non-neissidic sells 1; proben (NAC2A)	multipructions) polypopide straits to 8. COCCS potch likes a 1. Diocuscoldus entatase MI polypopide plutalinine peructiase MI polypopide plutalinine peructiase 3. (pestrolinetin transmenteme proble (BOI); entrolinetin plutapinoritiase lihitese, aphi 1. (mescal) phosphorytese lihitese, aphi 1. (mescal) phosphorytese lihitese, aphi 1. (mescal)	castety giths  Nexata service (leaseth C. cyclateth)  Insula service inchescoprotein polypet)  SULTIC suffor eraiferese she coult harmedon (totoophila) hambo promittee-Gearborklas neribatas (fat	probe some (proteoring, macropacit) should.  Hereas prostoporation 24/2)  cachen I; Ecacheni (pothelia)  incrop addapotic and addapotic addapotic or cacheni (pothelia)  incrop addapotic and addapotic addapotic (pp I; phin a 1  EST; Westy parks by NOTOSA (Caspa EST; Westy parks by NOTOSA (Caspa	RNA popraess is studied EST, Weady strake to RZ7000_2 [H.aspi NAA/0556 protein Ordager; the VVI acthos I (spedemotys system SN rectors to Ray and an experience to KRYCRO. EST, Weady similar to KRYCRO.	adence ha Alb receptor pseudopene HBV essociated lockyr ESTs
76789	123 BS2 1	Hs.944 Hs.167460 Hs.174203 Hs.73788 Hs.795	Hs.84113 Hs.82916 Hs.878 Hs.78802	Hs. 182018 Hs. 78398 Hs. 89629 Hs. 1068	HA.12163 HA.251669 HA.1244	Hs.7604. Hs.77597 Hs.77597	H-118400 H-201967 H-1594 H-1575	UZXZZ H12447 UZXZS H165436 UZXZS H165637 UXXSI H17724 U4754 H177324 U4705 H178312	Hs. 183558 Hs. 183568 Hs. 12346 Hs. 54089	Hs. 61796 Hs. 6456 Hs. 86506 Hs. 7268	Hr.17550 Hr.2834 Hr.2704 Hr.2365 Hr.2365 Hr.2365	Hs.204133 Hs.77496 Hs.75554 Hs.54416 Hs.14366	H.7858 H.20478 H.19457 H.2340 H.172928	Hs. 5409 Hs. 65222 Hs. 75478 Hs. 123114 Hs. 125845 Hs. 7010	Hs.247280 Hs.247280 Hs.34744
WO 02/086443 55 087933 Hs 91 HG1153-H71163	HG1828-HT1 HG2874-HT3 HG2874-HT3 HG2881-HT3 HG4074-HT4	L10238 L10238 L14596 L19688	125876 17708 123001	M15796 M16391 M16391	MZ9538 MZ9538 MZ9690 MZ9690	MEDODS M9/362 S8/364 UDIGSB UDESB	U03057 U14518 U14509 U16954	U23028 U24389 U35451 U44754 U48705	US1478 US2347 UF2514 U72514 U73379 U76638				X98280 X98280 X99133 Z35402 Z88228 Z74615 AA092838		
V 100455	100518 100528 100581 100567	10105 101182 101182 101181	101218 101228 101247	2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	01525 01525 01607 01607	101833 101833 101832 102003	210201 210201 221201 241201 241201	10220 10220 10230 10243	102522 102522 102520 10250 102687 102704	102821 102821 102831 278201 278201	103023 103036 103076 103168 103183 103223	100260 100360 100364 100375 100375	103404 103437 103638 103638 103638	10426 10426 10437 10453 10451 10451	165132 165132 165132

WAY O D 10 10 16 14 13   PCT/US 0 2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1/2 1	
5 20 20 11 10 20 20 12 20 20 20 20 20 20 20 20 20 20 20 20 20	77 . 80 . 88
PCT/US02/12476	
58655588888885555555555555555555555555	682252555555555555555555555555555555555
	20 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
escoluta intélibra ( ( unn'hi)  ESTI, Wicatry Infate to Sichar to phin  ESTI, Wicatry Infate to Sichar to phin  ESTI, Wicatry Infate to Sichar to phin  ESTI, Sichar to Sichar to phin  ESTI, ES	EST's Abodevately shrifter to putative Rob Organie IIII Thoughas III Thoughas II
1.1778 1.	H 200 H 200
WO 02/08/413  WO 02/08/413  A AA2294  A AA2295  A AA42295  A AA42217  A AA422	AKI 1593)  WAZDA AM4172  AM4173  AM417
0 V V V V V V V V V V V V V V V V V V V	
5 20 10 25 3.30 3.00 25 25 25 25 25 25 25 25 25 25 25 25 25	70 77 75 80 80 85

PCT/US92/12476 WO 02/086443

WO 02/086443

10 10 10 10 10 10 10 10 10 10 10 10 10 1	000000 000000 000000 000000 000000 00000	002/1086443 488_1177 488_1177 488_1177 488_1178	1864 44 14 18 AND CONTRICATION OF THE STATE
--	---	---	---

12912 (1921) WITER EAGURD WITES METTIN MISTIN MANETED ALTSON TEXTS ALTSON TEXTS ALTSON TEXTS AND THE TEXTS ALTSON THE TEXTS ALTSON TEXTS ALTSON TEXTS ALTSON MISTING WITER TO ALTSON THE TEXTS ALTSON TEXTS ALTSON THE TEXTS ALTSON AMTTERS ALIGESTS AWTIGES BEGITDI AWGIRLA AWLIDSS AWGITICS AISSAG AATABKI ARTICHT AND THE AWGIST AAATTER AWGIST AWAITED AWGIST AW HESSES TESSEN ALASOSSIS MENTERS. HATRATZ NAZZITTI ANNOZIGES ALASTIELI 1498.44 TEMIZA MERZESA MEDEZZI TAPIZA 1703.44

MESZES STERSIN ALASZES ELINES RENZZA MERZENIE ALGESKIE TREGE AAZZESZA MODYGE TETITA ALASIELI SAASIIIS 157112

AAGASSA ALTOSIO FAZZES ELINES RENZZA MALTZAZI ELINES ANNOZIGA TESSES RENZZA ALTOSIO MESZESZA MALTZASIA MARZESZA MALTZASIA MESZESZA MESZESZA MESZESZA MESZESZA MALTZASIA MALTZASZA MALTZAZZA MALTZASZA MALTZAS 102947\_1 238266\_1 12973 128192 113195 ಜ 

	22	MALL OF
	<b>T/US</b>	100000
	۲	C. Property
		76560
		700 007
		4 444.47
		3000
		1
		W. 2 2 2 1 1 1 1
		2000
	•	COT C
		WETER
		A MALAN
		1470 AA
		CSN GCG
,	<u></u>	T CHANK
	798	
:	070	
	<b>9</b>	

PCT/US02/12476

WO 02/086443 Tables 2A-8C were previously filed on November 9, 2001 in USBN 60339,245 (18501-004100US)

WO 02/086443	ANTOTED BEDIEVA ALOSALO ANTITOTH HETCH ALCOSEIS ANTITOTO ALCOSEIS ANTITOTOS BEDIEVA BE	AAGGEZ MAT (19 ASPATZ MAS) TEN MISTER DATES MATERIAL MATERIAL MATERIAL AND TEN ASSET MATERIAL	ASSPORT ASSPORT MANAGER SECURITION AND THE SECURITION ASSESSMENT ASSESSMENT OF SECURITION SECURITION AND THE SECURITIES AND THE SECURITION AND THE SECURITIES AND THE SECURITION AND THE	RS 1726 ALCHSENT A MESTICAT A MESSEA PROSEN PROTEIN BESCRIZE BESCRICE BECARDS! BECLIGAS HAVINGS HAVINGS TO SECURIS BECLIGAS HAVINGS HAVINGS TO SECURIS BECLIGAS HAVINGS HAVINGS ANN SECURIS BESCRIZE AND SECURIS BECLIA MESTICA AND SECURIS BECLIA MESTICA AND SECURIS BECLIA MESTICA AND SECURIS WRIGHT AND SECURIS	AUST TO TO THE SEA DASHITA ABTITAL ANN LODG MASTERS AUSTROITS AUSTROITS AUGUST AAGESTOT ASST GRADE AT 200156 MA, COTTAL MASTERS AUGUST AAT 1855 AVESSTOT AND 1855T DAT 1855T ATST GRADE AT 200156 MA, COTTAL MASTERS AUGUST AUGUST AND 1855T DAT 1855T ATSTALL AT 200156 MA, COTTAL MASTER AUGUST
	80		š v	8	86628
		=	∺	×	73

Fabe 2A shows 604 genes down-reputable bung binnon refere to committing and chrost-table deseated way. Chrostoph dates and lung semples represent chrostophers and promoting. These genes were selected from 5050 probesses on the EquilAhmeth Hudi Genechip erray. Gene mentage may and date such probesses obtained from the scalptal was expressed as everage bleastly (A), a normalized rabs enfecting then steller level of mRNA expression. 3. S. 5.5 6.65 8 2 2,73 Ş ormal lung, chronically diseased lung and lumor semples divided by the 90th ormal lung, chronically diseased lung and lumor samptes. sed lung and tumor samples divided by the 90th aly diseased tung and tumor samples. 38 278 52 aride of AI for normal lung samples divided by the 80th percentile of AI for edenocardnoms and equamous cell cardnoms lang lunor 5 30 22 divided by everage Al for equamous cell carcinoms and adenocarcinoma lung tumors. 25 86 13.00 00.01 34.50 193.20 64.88 88 22 ន្ត 3 23 28.5 8 8 8 39.40 30.20 37.40 42.40 2 64.60 9.49 23 And differentiation factor (0 acrytion elongation factor A (511); A0276 gene product UnigenelD Unigene Title 2 23 3 45 23 9. 2 23 8 83 13 ಜ 35 <del>성</del> 20 ଓ

12476											4.16				3,42											85				3.83			8.9				3.42
PCT/US02/12476	21	2.	2.82				275	72						83,				2.74	<b>4.</b>											2.68							
PC		8							3.48		8			<b>=</b>				5	8		8	5	162		2			228			8.8		2		;		: ·
		10.00		8.5		23.40 E.00		107.00		32.00	20.00	66.80	08:14	17.14		33.20 51.00			13.00		14.00		29.60		12.00		10.00				38.20		13.00	8:3	48.80	10.00	35.40
Į.	•		2.40				8					3.13							;	5,7	249	3		ង្គ	İ							ភ		2.31			
	. 8	8		6.0	9.40		90.0					5	3				16.00			8.0		8			9,50	8	14.00		9.00					200	8	14.00	
					31.20				44,20	28.40			\$				8												8 8	8		30.40					33,00
	ESTs CET	EST ESTS, Wealdy shriter to PROSPIATION LETHA	637a	20 E			ESTa ESTa ESTa	ESTs ESTs: Moderately skrider to SYNTAXIN 18	ESTa ESTa	ESTa .	· ESTs polassium vallage-gated charnet, shater-				KOAA0870 protein ESTs; Moderately shrifar to HYA22 (H.sep					_	Institic system-associated membrane protein ESTs; Wealdy struttur to CD20 receptor (H			ESTS	ESTs	EST4 EST4; Wealdy skrifer to III ALU SUBFAM DICZP434C171 grotein			E618	EST:		oxidative 3 styla hydroxysterdid deliydro Homo sapions mRNA; cDNA DKFZp58880220 (1	EST:	ESTs Human hymothoid nuclear grotefn (LAF-4)			"zm97 e.s.e.f. Strategene oden HT29 (#53722 "zm250.s.e.f. Strategene neurospiltzeltum NT Homo aspiens RNF-Jbela mRNA for hepatocy ESTe
443	F 71625	Hs.252739 Hs.62113	Hs. 139202 Hs.87191	H-27714 H-311662 H-27116	Hs 23540	Hs.127842 Hs.14945	Hs.28889 Hs.28792 Hs.282982	Hs. 10299 Hs. 31581	Hs.31330 Hs.32468	Hs. 184261 Hs. 11038	Hs.35992 Hs.24379	H. 108920 H. 28401	Ha.21411	Ha.1629	Ha. 18168 Ha. 283724	Hs.181003 Hs.9218	Hs. 23666 Hs. 18827	Hs.21559 Hs.8022	Hs.22945 Hs.167398	F.748	H-28479	Ha.321677	H. 28694	Hs.29040	HL 167393 HL 3770	Hs.6655 Hs.7369 Hs.209100	Hs.176967 Hs.11392	Hs. 177894 Hs. 177894	Hs. 16168	Ha. 16028 Ha. 333181	Hs. 17832 Hs. 269192	Hs.11958 Hs.170056	Hs. 269181	Hs. 25425 Hs. 125019	Hs. 306117 Hs. 173091	Hs.25332 Hs.253010	Hs.155651 Hs.288464
					R31770 H18017	59899 B020644	00656 00656 64183	1798320	C28985 WB74263	62507	\$8505 W961818	103109	U76098	79639 W068350	E247767	W449573	1741471	G7472 L372588	U3713 W148652	WZ06093	W300887	A324898	51620	80552 W373104	08168	AA928953 AW081710 AA346839	50405 IM 004469	B1473	J022166	654223 95358	98935 A004693	189281 E178285		H05785 W57554		VA020736 VA020736 V369276	AA079505 AA101058 BE094291 AA146979
OW tomos				109578 109601	109682	109724 C	109833 109837 1	10148	110201	110578	110634 8	110875 110875	116971	11057	111330 111374 B	1142 11737	111807 A									112054 A											114609 A 114648 A 114731 B 114762 A
		S		9	2	:	2		70		25		30	3	;	33		40		,			20		55		09		77	3	ç	2		75		08	85
2476	-					87					an	3.20	4.57			e de							4.33										138		295		
PCT/US02/12476			2.28																												25	292			97	į	
PCT/	72	2:	Į	82	2. 20		342									4.48			3.60	•				:	38		3.73	316	3.65			308					
			:	8					60.40		8	3				5	;	8	12.00	36.40	9		:	10.45		8	,	3 9		888	8			12.00 12.00			8
	240		:	40.00		2.47			8	3,8	8	į		355	<del>-</del>	07 Y	3.63	42.60		88.5	X X	2.38		2.57		2.32	-	51.40	-	2, 22, 5 6, 69, 5	Ri E	3	34.00	;	F3		. 67.80
	7	~				~	89	11.00					16.00	~~~	•		2.00	1			~	~		~	88				83		•	4			~	8.38 8.38	
					8.80	5		8	26.80	R 1	0.1	34.20			33.60			74 80	Š			39.29				:	97.0									2	32.80
Barkn contabiling monoccygenese 2	"Masplens DAT1 gene, partial, VATR" contactin 1	gycoprolein A repetitions predominant "A sepiens lociorm 1 gene for L-type cal	H sapers ALS mixAA (Done PCPS) CG-100 protein	rypomenca protein Mass (Jean to S.K. ESTs ESTs	dual-epeditaty tyrosine (M) phosphory ESTs; Weakly similar to putative p150 [H	ESTs; Moderately similar to TGF-BETA REC	ESTs: ESTs: Weakly similar to SSI-1 protein (	ESTs	ESTs; Bela-1-adranergic receptor ESTs	ESTs	Momo Explans CUNA: PLUZIU42 hs, done C ESTs	ESTs	EST8 EST8	ESTs trustmentions 4 superfamily member (later per per per per per per per per per p	homeodomath-Interacting protein kinase 3	erresum, pous 4 synaptopodin FRTs.	catdionin receptor-like receptor activities	ESTS .	AVAULUS PORTIN	ESTR	Homo saplens mRNA; cDNA DNFZp5548078 (fr novel SH2-contaching protein 3	sperm essocieted enfigen 6 serum deprivation response (phosphalidy)	EST\$	EST8	EST ·	south carrel tamy 17 (south prospin lattert transforming growth factor beta b	EST	UM-ZM-44KIDI protein ESTs ESTs		ESTe Human DNA sequence from done 141K5 on o		2m34b1.s1 Strategere colon HT29 (#937.22 ***********************************	ESTs. *zn1bi2s1 Strategene hVT neuron (#53723	Homo sepiens clone 24881 mRNA sequence 2n116.s1 Shategens hNT neuron (#83723	ESTS ESTS *m24c8 est Stratonana commandibution NT	2m55c5.s1 Strategere Shrobtast (#33721 Home sepiens mRNA; cDNA DKF2p564N1164 (f	EST 5 EST 6
2821	1b.143434	Hs.151641	1b.298156	Hs.303276 Hs.303276	19.38790	4.79059	4. 27 (568 4s. 93967	4. 105201 4. 18912	Hs.37744 Ns.278585	4.141883	4.10236	4.36529 4.38163	4s.8364 4s.19800	4s.26608 4s.16529	5,30148	18.70142 16.37741	4.25691	4,25930	4.24106 15.154162	4.23804 1.23804	4.21103 1.26054	4s.158213 4s.26530	4s.9973 4s.204038	4s.27018	15.30077	18.85087 18.60536	9/267-8	4.60781 4.225290	Hs. 143811 4s. 63869	Hs. 48469 15.82223	Hs.1651957		Hs. 68055	Hs.226440	4.283022	b.117037	A118272 15.02713 A118272 15.02713 A156801 16.71721
WO 02/086443	10141 -(-001843 !	W_005612 8256 ·	244567	VACZBO1	123930	V960427	799603	010539	208243	4 CLESCO	(_016348 )	W854365	6780	430650	808	397825	769788	045290	450040	329648	124251	485055 I	128847	233588	3362	7822 V082221	015967	017291	025000	049176	787341	078399	133092	084867	W972330	127221	138272 138272 1428891 142889
OW ov sexest	TOTSON Y	103576 103576 22	103767	104078 A	104352 Bt	1045 4 4 5 4 5	104595 AI	104659 A	104691 U.	104776 AL	26.00	105062 AV	1051 105 105 105 105 105 105 105 105 105	105256 Rs	10567	105817 A 105817 A	106894 All	106075 AA	106381 AE	106636 AV	106805 AF	106844 AA 106870 AK	106951 AF	10710 10710 10710	10720 10720 10 823	107530 107688 Av	2 22 22	2 5 5 2 5 5 2 5 5 3 5 3	107873 A) 107899 BE	107994 A.	103048 AF	10843	108499 AA	108535 A	108625 AV	108655 AV	10895 AL 108921 AL 108921 AN

S

≥

PCT/US02/12476		2,23	:	B:		3.14		237		2.53	3.95				. 124		:	·	83		. 212	2.78						94	<b>!</b>	. 2.58	:		4.02	3.76	3.10		E
		9	31.40		39.60				41.8	60	62.80		3240	70.60	13.00	29.60		08.00	3	94	10.00 10.00	34.20		33.60	29.60	34.40	:	37.20	38.40		34.40	93	00.78	808	8		
	234	-	ř		25		263	•	· ·		25		7 7 7	E		2 22 23	3.07	2.48	, 280	•	•	•		•	~		2.38	N 69	•	88		-			927		
					9.00		15.00	9.67									8.2			8.9				87			8.0		111		10.00						
			37.40	49.40		30.60			5	6.9		35.40	8	28.40					;	69.20		8	32.20	\$	2 S	88						31.20					34.60
							-		EST8	EST:		E8T Homo sapiens done 24760 mRNA sequence	ESTs offsctory receptor, family 7; subfamily	ESTS; Weakly striffer to GLUCOSE TRANSPOR ESTS; Weakly striffer to PTB-ASSOCIATED 5		ш ш .	ESTs  "yw35g11.s1 Morton Fotal Cochina Horno sa	u ← u	սնա		ESTA ESTA	ω		KAA0022 gens product HUMS25A058 Human placents polyA+ (TFull		ESTs; Weakly similar to pl.2 hypothetica aa58b04.s! NCL_CGAP_GCB1 Homo septens o	шш.	651a 651a 657	EST.	mannosyl (apha-1:3-)-glycoprotein beta- gutathone percodese 3 (plasma)	ESTs; Weakly similar to LRS [H.soplers] ESTs; Weakly similar to ZNC FINGER PROT	ESTs potassium inventity-rectifying channel; s ESTs: Nonderstalv almiter to IIII ALU SUB			eukaryollo translation etongation focior ESTs millo 2 (mischs)		documel protein LA1
. 143	Hs. 104864	H. 98467	Ha.98724	Ha. 96849	Hs. 98890 Hs. 104938	Hs.121602 Hs.121602 Hs.59081	Hr.160318 Hr.98321	Hs.99489 Hs.5120	Hs. 211869	Hs. 194024	Ha.112497	Hs.112795	Hs. 120017	HS 24 15 19 HS 95497 HS 107149	Hs.124585 Hs.108135	Hs. 270962	Hs. 10299 Hs. 102415	Hs.285825	Hs. 127436 Hs. 137274			Hs. 102726	Hs. 128797	Hs.2441	Hs.23964	Ha 126712 Ha 293977	Hs. 105468 Hs. 191788	Hs.292388 Hs.292388			Hs.12126 Hs.269152		Hs.23767 Hs.104476	Ha. 1051 Ha. 194581	Hs. 10683 Hs. 10683	Ht. 107761 Ht. 107767	Hs.330468
WO 02/086443	AB033030 AA427794	AA534863 AA426429	AA/29516 AA/31310	AA431725 AA300900	AA436676 AA436703	AA436840 AA436981 AA446830	AA524547 AA420683	AW117452 AI857570	BEDAT680	AW451999	AA353113 AA606570	AA609971 AA620448	A1807243 AA938905	NW_004673 C21171 AL521938	R40290 H77570	AA618527 H87680	AI796320 AW070211	AW683832	AB011130 AI670058	NM_004657 A1768289	AW576389 AW206468	AW836591 T32982	AL 110151 HD0083	D78841	AU040137	AW962712 AA760776	AW002846 AA594027	X80031 AW976035	AW340720	NM_012214 WZ7411	W68800 N76462	Al265784 AA305407 AA464918	AW271273 AU311238	W26687	H39537 R25513 AF134801	WD4245 AA744902	AW156903 AW580945
×	121835		121950 122030	200 200 200 200 200 200 200 200 200 200	1225		122485			1213				2002						124711	125097	125200	125810	126303	126507	127307	127488	127609	128073	128149	128333				128870 128878 178884	128998	129038 129098
		•	,	5	2	15	}	ć	3		25		30		35		Ş	ř	;	<del>.</del>	;	20		55		9		39	3	;	9		75		80		85
PCT/US02/12476			332	-			3.57									3.74				e S		100			3.21		3.60			87		5.08	ar				. 197
		3.	•			2			_		8.		8	ì	12.00	3						;	_	_					8		00	12.00	••		_		
			48.00	88 X		2 C C C C C C C C C C C C C C C C C C C			30.00	. 27	93.00	32.60	30.60				8	i	0,		*	33.00	5	8.20		33.80		36.60			38.60 38.00		ş	8. 8.	34.80		
		6.00					3.06	3.85		i		į	90		16.00	8	38	900	240	3	3.94		14.00		2.76		8	. 200						228	3	2,00	
	34.40	3260		31,40			i	8.8		47.20		49.40		67				31.40	32.80	30.80				31.40			83.00		39.40	20.00	;	9.			34.80	38.80	R. 25.
	EST <sub>2</sub> EST <sub>2</sub>	ESTs, Wealty similar to hypothetical L1 ESTs ESTs		ESTs. ESTs. Weatby shrifter to (define not eva ESTs: Henby similar to (J117845.3 Diss		EST8	EST. 6ST.	Houche rich repeat (in FLII) Interaction ESTs; Weathy similar to futfolin (M.muso	ESTs; Weakly similar to testicular takil	tanasch R (restrictin; janusin) ESTs .		EST	ESI:	EST .	ESTs							MAAGES protein		EKG-ZERG-1; V-sts swan erytrabistics EST - Accepted to Contact	edvenced phosylation and product-oped DKFZPS881,2024 protein	ESTs; Moderately similar to IIII ALU SUB ESTs		ES 18 Human lymphoid nuclear protein (LAF-4) ESTs.		ESTs microtubule-associated protein; RP/EB is				EST8			Homo saplens mRNA for arpha integrits the ESTs
413	38	Hs. 290825	H.207413	H-63977 H-54650	No. 41135 No. 43125	Ha. 184684 Ha. 41644	Hs.55278 Hs.59729	Ns. 328740	H.47152	Hs.301281	Hs. 9059 Hs. 102415	Hs.130093 Hs.41192	Hs.306881	Hs. 44055	15.42722 15.44565	Hs.44676	H. 83956	Ha.47385	Hr. 124154	Hs.269121 Hs.49193	Hs.322854 Hs.60813	Ha.247043	Hs.323058	Hs.279477 Hs.65325		Hs.49943 Hs.58671	7s.58815 Fs.40111	Ha. 125019	Ha.96427	Ha.194718 Ha.78335	F. 1003	Hs.97827	Hs.25274	Hs.88132	Hs.98234 Hs.98234	Hs.98328 Hs.98334	Hs.3346
WO 02/086443	W151719 W251561	(W564897	AW976252 N. 268391 AL079707 N. 207443	U142338 U7255910	AA486620 Alatba27			AA292105 AJ767947											N62518 AL109567																A441659 A441659 A338247		ALSS0770 ALCM0235
WO	114776 A 115009 A	115272	1555	115568 11568 11568 11574	115819 A 614831	16005		16213 A 8238													118549														121665		

		'n		•	2		15	:		20	3			3		6	30			35			40	}		,	4		;	. 20			\$\$	3		9	3		8	;											
/12476	8	88							Ş		:	8			386	3	1.87	i		34								5	P.	3.67											5.49					3.35			3.45 50.5		
PCT/US02/12476																							10	3							3.48																			32	ì
کِ		}		3 3				:	2	Ę.	35				_	3.1	8			:	<b>9</b>				22		8										1	7 7				8		_	1.0		;	g			
٠.			160.80	ž	92.80	3	Q.23.	91.60						8. K	8.				32.20						₹ 5 8 8				40.60				34.20				30.60		1.43				31.40	86			90.80				40.80
	22		283			27.	7.							.,				2.88								2.47		278	_		797			268	8	2.66	• 7		2.0	22	3	623	-,					. 283		9	•
				٤	8					8		8									8	10.00														\$	3														
													41.20									:	28.80	30.00			45.80					51.80			34.20									52	20.20						
		¥	<b>2</b>	_	E	2	4	ă						z.	_ 3	T.				5HZ	<b>&gt;</b>		159 401767 (F	2 2 2				2		<b>z</b>		84			B			_	18491		=			7		_			_	8K1220.II	_
•		18 (NIBC) m	protein dele e receptor 1	etche nedel	ж сапфете	redated sequ	1.3-getacto	spentacleg	rd (adpsin)		H De	٠		KVAA0Z73	offinger pro	ame; sub		dracelluler		dass ); gan	potative s		(EGF-respo	aphorts Vi	al specificily			spendent, b		CeM-Kil h		eracting mo			Cfducha		Coodpastur	Cardesin PC	NA EST ya	And and				ad gene far	oteh 1	no integral	i e		eston molec	A DXFZ05	2-69 protes
	apper septor	ome PASO4 miller to CG	membrane that peptid	inflar to co	Ing factor k	1; myelolo	loNAc beta	against dec	la protetta Completta		obposta co	.e.e		ey cirilar k	inite to ch	ge-gated c	24 protein	mutasa 3; eo		C esame	ely similar t 8 orotein		ne factor 2	milar to see	similar to du			t vollage-d		aly similar to	s	sh Max2 int		44	ctone TUAB	rain 2	V. alpha 3 (		da alim	7	o-undousing	eptor-like		vision) relati	d-related pri	arme form	se B2 (plass	10r 21	shaloetladh a protein 1	MRNA. cft	Imilar to C
	KIAA1102 probbin Interfeukth 7 moeptor ESTs	Human cytochrome P450418 (NIBS) mRNA; ESTs; Hghly similar to CG3-38 protein	udin 6 (trans loacitya inta	Tr. Weatly	acay accelerating factor for complement	innecon As Infensin; alpha	UDP-GalbelaCleNAc beta 1:3-gateclosyltr	AD (mothers against de	component of complement (adjush)	ESTs ESTs	anomations p	ICAA0758 protein	quaportn 4	ESTS; Moderat ESTs	ESTs; Weathy similar to the finger prof.	assam volt	FZP586006 Te	suporoxida d'amutaso 3; extracellular	12.5 13.1	chol deliyon	ESTe; Moderataly similar to putative sev DIYEZPS64D208 orotein	STs	bulyrate response factor 2 (EGF-response Homo semiens mRNA: cONA DKF7::554011763 /f	Ta: Highly at	ESTS ESTS: Weathy similar to dual specificity		EST8	caldum channel; vollage-dependent; beta	ST&	STs; Moderatory similar to CaM-Kil Inhi	.5T& JAAG633 prote	QAAQB29 protein Max2 Interacting nucles	<u>.</u>	8T8	Located prouve from protest Homo saplens done TUAB Cri-du-chal red	LIM binding dor	collagan; type IV; sipha 3 (Goodpasture	IS; MOCOTEL	ESTS; Weakly similar to cONA EST yA484g1	ST8	estanacan (per ESTs	Interheddin 1 receptor-like 1 ESTs	: ,= ,	78 C24 (5. com	secreted intitled-related protein 1	queports 1 (channel-forming in	arboxypeptidase B2 (plasma)	618 Inscription factor 21	pittelothindotholisi celi adhesion molec selonium bindina protein 1	USA protech	ESTs; Weakly similar to CG+69 protein [
	Hs.202949 FQ Hs.237859 Hs Hs 109843 FS	386	6736 6736 6 16 16	2847 ES	3.5	4463 es	00 9894 1844	200	90		912 ad	2 2 2 2 2 2	-	874 886 58	6218 6218 6218	1 E	25 E	8			Ha.25274 ES Ha.25956 DX									ш,	Ha.184377 E.S Ha.33010 KU	_	34 EST				Hs.530 on										• • •			Hs.8022 TU	
WO 02/086443	222 222 222	## ##	# # # # # #	::::::::::::::::::::::::::::::::::::::	2	¥ 5.7	27.55 27.55	# 12 22	28 AS.	2.5 2.5 2.5	23 F	2 E	1 25	# # 75 14 15 14 15 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16 1	1 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	#	7 1	02 Ht. 24	2 E	Ŧ	# # #	81 Hs.2	# # # #	2.3	2.5. 3.5.2	至	# # # #	£.	7 F 19	# # # # #	2 E	¥:	E E	7. E. E.	i i	20 Fs.40		£ £	£ £	7 Hs.64	E E	25. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	4	8 E E	1. E	#	12.5	18.25 18.78	7. Ks.7	2.2	#
0.02/0	AL039940 AA381258 RF277148		XTTTX	AW9785	F0778	AL03655	AA30588	AW9724	8 X	AA99970 APR7764	N 005	AL03929	N 80	N64328	A614770	AFOCO	A17138	NW OO3	A2517	XOXOX	A56794	AWORST	A499284	A80377	AL13743 AKD0038	AA35981	A12505	550415	A4435	AA74480	A801724	ALDSEBS	AM18000	A33269	AL11984	NA 801	X8003	M 525	N52298 R51604	BE38493	W 285	AAOZESS	A903/2	AM9784	AF01798	Wista	NA SO	AF0057	L34657 AW1757	AL272588	AIBTAZ
*	0.582 0.582	200	2000	200	888	2882	30160	525	300	2062	130885	131002	131031	131061	131082	1316	515	3120	131281	131282	131285	131391	131461	13151	31545	131647	131678	131708	131756	131762	183	131881	1200	1320	132478	132/80		132652	13726	1300	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1305			133407	7357	133689	133978	133985	13411	134204
		S		5	2		7	:		20	2		č	3		ç	₹		į	33			40	?		76	<del>5</del>		5	ဂ္ဂ			55			9	3		65	:		20	2		75	:		80			82

	"Accession" column.		and the second research and the characters are consistent to the constant of t
0	Pkey: CAT numbe Accession:	Pley: Unique Eos probesel Identifier number CAT number: Gene cluster number Nozession: Genbenk eccession numbers	Identitie number number
	2	CAT number Acc	Accessions
S	108560	43452-7 AA0 120073_1 AA0	AUOTOT 28 AUOTOT STATE AUOTOT AUOTOT STATE AUOTOT STATE AUOTOT STATE AUOTOT AUOTOT STATE AUOTOT
_	126303 126303 125810		14/1688 177784 D19820 17780 S1052
•	12136		MITASIS ALAGEST AVEZTETUS MITASIS AVEZTETUS ALAGEST MITASIS AVEZTETUS MITASI
Ś	108424 123802 123802 123802 123802	112189_1 A070773 A 114012_1 A078899 A genbank_AA620448 /	MUTUSSY AUTOTAL AUTOTA
0	102638 104776 120504 113502 106499	ontex_U67092_U67092 penbent_AA026349 penbent_AA256837 penbent_T89130T89130 cenbent_AA083103	W025349 W256837
ς,	101308 103098 103241	2	25
0	121002 121002 128634 105817	entrat_czo.cos _ czo.co NOT_FOUND_entrat_W37931 W37931 genbant_A4398722	ZZLIKEW. ZZLIKEW. SIGN
8	121518 114448 114648 121950 107723	genbank, AA412155 genbank, AA020735 genbank, AA4101056 genbank, AA429515 genbank, AAA19515	MATZISS MODITS MATSISSIS MATSISSIS

PCT/US02/12476 3.78

**5**8

7

28.60

3.62

85.

52 52

39,23 3.28 25.28

Unipene Titte

Unigeneil

2

2

23

ဓ္က

35

츙.

45

2

25.23

25.25 26.45

8

12.80

8

CETI, Weaky dinflar to 138022 hypotheri crankolacia development protein 1 KIAA1020 protein Cade, sesociatica, germ ESTa, Weaky eindas to TRAY, LIQUAN TRUCH sarvind of make neuron protein interes spord/inspibytes dysplank lies Ent. Water genter in 1883 serketh inferients in respice Any Any Carlo and Any Carlo and Any Carlo and Manuaria 2 and Any Carlo and Any sapiens cDNA FLJ12568 Is, done NT sapiens mRNA; cDNA DKFZp588LD120 (I che intestnal peptide moreptar 1 by bensmentarare epthelial entique of by bensmentarare epthelial entique of bons spheme cDNA: FL72783 III, chone Knembrane-especialed nucleic acid binding by ES128707 Censbellum II Homo septema o CorreseAutZ protein
E81\*a, Weady similar to 139022 hypothei
Daul Mapuli homning, publiming B, membe
ESTs, Weady similar to 21991. HQBANN ZINC
ESTs, Weady similar to AF191020 1 ESTGS
cablepach B hypothedical protein F1,22511 ESTs, Whady similer to ALU4 JHUMAN ALU 8 ESTs, Whady similar to 130022 hypotheli ESTs, Moderately similer to ALU7 JHUMAN A add transporter 2 human gene mapping to chomosome 13 Homo saplens cDNV. FLJ23123 fts, done L 8-etencopherbibohne docarbonylase 1 mitogen-ectivated protein timase kinase E81a omo saplens cDNA FLJ20780 fs, clone CO issnoliphi bzu68c01.rf Soarse\_lests\_NHT Homo sap btcsg2228.soq.F Human felal heart\_Lamb ucterr factor VA 45c01 r1 Source placenta Nb2HP Homo ESTs NDRG tanify, member 4 collagen, type IV, athra 3 (Goodpasture ESTs TP-binding cessette, sub-tamily G (WHI) obsished investigated themes, s odium channel, voltage-gated, type XII, hypothetical protein FL/21901 38Ts ypothelical protein FLJ10546 Hs.173933 Hs.151999 Hs.61635 Hs.6093 Hs.11227 Ha.13849 Ha.13849 Ha.230771 Ha.129750 AUSTREE ALITORA ALITORA RESTOR Y13163
AP018526
ANG6578
ANG6578
ANG6778
ANG0732
BE15776
ANG0618
ANG0618
ANG0618
ANG0618
ANG0618
ANG0618
ANG0618
ANG0618 10 72 13 2 25 2 33 8 50 8 2 8 S 23 65 Table 34 shows 452 genes up-regulated in chronically diseased lung mindle by Chronically diseased lung samples represent chronic conventional transfer in the Second lung diseases such as larged, emphysicials, these genes were seased from SSSQ process on the Eaulithmetic Hold Generich error. Ones copression date for associated from the australia was expressed as everage intentity (M), a normatized rate effecting the ritizes band of mitNA expression. Unique number Depos passe de la constant desseed lang sambles divided by the 6th percentile of AI for named lang samples. Stop percentile of AI or chrotically diseased lang samples divided by the 6th percentile of AI or chronical states and sedebocarchicans. Stop percentile of AI or chronically diseased lang samples mitten to the 5th percentile of AI for all normed lang, chronically diseased bug samples mitten to Be 15th percentile of AII for all normed lang, chronically diseased bug and turnor samples of bothed by the 9th percentile of normed languages, equations cell carchomas and althocarchomas minus the 15th percentile of AI for all normed language chronically diseased lang and turnor samples. 35 22 2 8 3 584 364 8 8 3.8 33 22.60 22.60 22.60 22.60 22.60 22.60 21.40 12.40 29.80 25.83 25.83 25.83 52 212 15.20 5.00 8.5 8.8 uman BRCA2 region, mRNA sequence CG030 UAZ oroteh Monte of the control saplens clone TUAB Crick-chat regi nor of actin mutations 2, similar to T33458 hypotheti ESTs, Moderately stratus to A45010 X-8 MHC class it transactivator SPB2-associated binding protein 2 tolipase A2, group IB (pancreas) rebral cavemous mailtornations 1 pothetical protein Unique Ece probeset identifier number Exempliar Accession number, Genbank accession number A40781 protein dnase (PRKA) anchor protein 2 epithellal membrane protein 2 ESTs Metical prolein FLJ 10210

MALESTON HE LEADS HE

S

25

ප

8

2

73

21.28 21.28

2

17.13 17.13

103

82

v	-
ř	ξ
-	2
•	٠
-	•
ì	3
ũ	ň
Ξ	-
S	2
SILVE	
ř	i
>	•
ē	٠

23 23	1.78	1.76		702 700	1.02		£.	£3.	1.88 2.16 1.75 2.31 2.68
3.51	23.00	88	388 8	82.72	11.40 6.04 3.60	<b>2</b> 5	8.00 12.20		999
20.20 16.20 19.40	16.20 16.20 18.50	11.62 10.60 25.20 25.20 25.20 25.20	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	20.40		12.40	2	22 22 22 22 22 22 22 22 22 22 22 22 22	18.40 24.77 24.77 12.20 13.00
NSTPCH) protch  Norman page menty CDN DIG 2,588 (1) 1 ()  Norman field from speen  Norman field from field  Norman field from field  SEST, Westly when field from A Marrian  effects on morea Anti / Dimit protein  SEST, Westly from from A Marrian  Marrian field from field from the Marrian  Marrian field from field from the Marrian  Marrian field from field from field from the Marrian  Marrian field from field fro	thin three purchs 105 ECCS, enclockering refroatm transfoon production of control FL07003 hypothetia prothe FL10970 interedular mentures executed cache interedular mentures executed cache interedular mentures executed cache interedular mentures executed cache interedular mentures executed cache		ESTI ESTI ESTI ESTI ESTI Phytological protein FL L 22333 ESTI, Moderately shifter to ALLU J. H. IMAN A optochrone 0.	ESTR. Watch present of the present o	Person explens mRNA: GDNA DNG-Zp-4346033 (th ESTs Home stapken cDNA FLJ 13510 fts, done PL ESTs, Westy strifer to ALUB_JAUAAN III MAGG-Tprobeh ESTs, Westy strifer to ALUI_JAUAAN ALU 8	ESTs hypothesis protein FLZZ191 ESTs ESTs ESTs ESTs ESTs	EST 18 Weekly similar to S4 (1044 chromosom EST). Weekly similar to S4 (1044 chromosom EST). Weekly similar to T17248 hypothold EST, weekly similar to A45(10) V4 (EST), weekly millar to A45(10) V4 (EST), weekly millar to A45(10) V4 (EST). EST 18 (EST) to S4 (EST) to S4 (EST) to S4 (EST) to S5	Form supplies cone 2,103 introvalequees  Home supplies cone 2,103 introvalequees  Home supplies cone cone cone cone cone cone cone cone	Hono supplies mRNA, GDVA DICTE/37524177 fth CG-55 propiles Hono supplies mRNA, GDVA DICTE/35462052 (7 EST FOR CAPACITY AND
14.3 Ha.306881 Ha.301281 Ha.301281 Ha.80697 Ha.8050 Ha.20509 Ha.20509 Ha.20509	H.15220 H.17577 H.173230 H.4198 H.332338 H.54650	Hs.289908 Hs.73251 Hs.184411 Hs.290825 Hs.124292 Hs.11387	H.188717 H.188717 H.18886 H.296100 H.128290 H.169248	H-271616 H-271616 H-283021 H-6107	Ha.155019 Ha.37898 Ha.77898 Ha.77898 Ha.77898	Hs.15026 Hs.15026 Hs.15967 Hs.12967 Hs.1392 Hs.189813	Hs. 10305 Hs. 10305 Hs. 270862 Hs. 270863 Hs. 220847 Hs. 2030647 Hs. 2030647 Hs. 2030647	Ha. 7004 Ha. 138283 Ha. 138283 Ha. 5783 Ha. 52823 Ha. 194178 Ha. 194178	He. 22483 He. 18385 He. 18782 He. 16922 He. 16929 He. 28419 He. 28419 He. 2842 He. 10927 He. 107872 He. 107872 He. 107872 He. 107872 He. 107872 He. 107872 He. 107872
WO 02/086443 www.wx.mx.mx.mx.mx.mx.mx.mx.mx.mx.mx.mx.mx.mx	4,040521 16613410 14,132916 14,001732 17,503613 14,73062	AA406341 AUB9110 A142336 AA608001 AA0064897 AA001671 AC01671	A237022 A235872 E244930 A149781 A143781 A310162	77908 1369278 14677 11677	W384793 IS7554 W083893 96965 M_013343				ALI 57484 AA373527 AA983536 AA47763 AA983536 AA77763 R65503 AA77763 AB002417 AB002417 AF000768 R44557 AA001268 AA884208
WO 11729 V 11729 V 11671 H 11671 H 11671 H 11671 H 11671 H									111341 A 111280 A 111280 A 11032 A 11032 A 11032 A 11039 B 11039 A 11039 A 11039 A 11039 A
\$ 10	. 15	20 20	3 %	35	<b>\$</b>	5	55	65	75 80 85
PCT/US02/12476		·							
06.1 188.1 18.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19	77.20	. 623 . 623 . 623 . 623 . 623 . 623		12.10		1.83	1.79 3.	10.00 10.00 10.00	1.50
			85 8 8 87 7 87 88 88 88		8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8			•
	menthan e-panning 4-domains, subternity A foryw17907 at Merina Felal Cocites Hemo ESTs ESTs ESTs ESTs	minicolous insperient, mention i endocabella prema endocabella promise de control giuseldo a i Statopene lung cardroma ESI ESI ESI ESI ESI ESI ESI ESI	poptorytoth bornerso A (sychoptin ESTs ESTs Wally einder to reverse traviol KUAN 1255 potein KUAN 1255 potein to treverse traviol KUAN 1255 potein to the ALUS, JULIANA ALU S				Verzelloff a NGC (CAPP, PFH Harm registers Horns was presented to NGC (CAPP, PFH Harm registers HAC (CAPP, CAPP) Harm registers have been registered to the new properties of the new properti	SET, Wasky juniar to SERST drive (C.  All neared glocas/daton and product-upoid producting produce ground and any profuse to the programment of programment of programment of programment of programment of programment of SERs in section of CREM in least to expert or	To the state NYO-SP15  ESTI, Washed printing 1858224 werens I 10.40  Myophadra proded the 185224 werens I 10.40  ESTIS—secondand proded The 1852 shall be 18.50  ESTIS—secondand proded Lackmody 18.50  ESTIS—secondand proded Lackmody 18.50  ESTIS—secondand proded Lackmody 18.50  ESTIS—secondand proded Lackmody 18.50  Myodhadra product To Carbon transfer (18.00  Myodhadra product 10.50  ESTIS—secondand Lackmody 18.50  I Lackmody product 10.50  I Lackmody prod
163717 16137 16137 16254 178 178 178 178 178 178 178 178 178 178			Hs. 182937 Hs. 195228 Hs. 195624 Hs. 105522 Hs. 195102 Hs. 192837 Hs. 34853		Hs.98506 Hs.193784 Hs.300670 Hs.178096 Hs.110286	Hs.9750 Hs.126095 Hs.87201 Hs.12533 Hs.97509	Hs.190745 Hs.181165 Hs.205442 Hs.20548 Hs.50368 Hs.50368 Hs.50368	H. 184 H. 21068 H. 25328 H. 253700 H. 17183 H. 27347 H. 243589	Ha. 48927 Ha. 48927 Ha. 48930 Ha. 48930 Ha. 48930 Ha. 47788 Ha. 47788 Ha. 47788 Ha. 47788 Ha. 47788 Ha. 47788 Ha. 47788 Ha. 47788
WO 02/086443 22 A80228 ht. A27589 ht. A27589 ht. A27589 ht. A27560	N3.231/ BE178538 N72401 AW973078 H58608 AW298735 T89332	ALGEO184 NIA_004673 AA62048 AA609861 AA609861 AA609861 AA609861 WAS02964	AASO4284 AA489212 AW451899 AA48505 AA48505 AA485130 AA811286 NW 001546	AA451884 AA973253 AA524547 AA300900 AW207176	AMA31082 Al860775 W36487 AE003030 AF241254 AV660305	AA417011 AA412031 AA412031 AW708227 W07343 AA400857	AA226180 AA312834 AA811804 AA811804 AA83170 AA830882 AA830882 AA830882 AA830882	W78816 W74536 W74536 AW021407 A001118 C14322 C14322 R45175 BE245360 A4312799	AND 2017 AND 2017 AND 2018 AND 2018 MEGOZE M
W(125422) 125333 125333 125339 125139									11866 11866 11846 11879 11832 11832 11833 11833 11833 11833 11803 11740 11740
\$ 01	15	20 20	30	35	40 ×40 ×40	2 %	55	59	. 75 . 80 85

<u></u>
9
_

PCT/US02/12476	of the gene chitain rambar from witch the requesters were destrond bested on sequence ces comprising each cluster are based in the		-
812 812 813 814 814 814 814 814 814 814 814 814 814	1.51 1.79 1.79 RMAs. The		
3.60	4.00 4.24 21.20 21.20 6.40 6.40 is gradest v		
11.00 10.00	11.20 14.80 33.00 18.20 18.20 11.29 11.29 11.29		
	ean-B If it Table of Carlos from Table it.		
WO 02/086443         Ha 2773         ei-Ha mockée omderkée, mach-Bas, Ha 2760         ei-Ha mockée omderkée, mach-Bas, Ha 2760         ei-Ha mockée, Machana, Ma	BENTO N. R. 6221   BENTO N. B. 6221   BENTO N. B. 6221   BANTON N. B. 1725   BANTON N.		11831 genbent, MOSCH49 11832 genbent, AUGRSCH49 11832 genbent, AUGRSCH49 11832 genbent, AUGRSCH49 11833 genbent, AUGRSCH49 11834 ge
\$ 110 mm 1	35 44 45 45 45 45 45 45 45 45 45 45 45 45	55 69 55	
		•	
PCT/US02/11476			·
881 XIII	2.05 2.05 1.78 1.78 1.78 2.19	1.02 1.75 1.92 1.92	181 181 .
17.29 4.75 4.75	7.13	3.70 3.70 8.30 5.40 7.60	10.20 5.69 3.82 2.82 3.82
22 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	21.40 35.80 13.80	10.44 77.20 13.80	27.20 11.20 12.00 11.20 11.20 11.20 11.20
NA A WIT	F 4 500 F		46H A clone (4229 (if
	mychility protein mychility protein mychility polyd or maxility and mychility polyd or maxility mychility protein protein PLI2011 in blood beginning by Amarilly mandense assum deprhalan response (becapitally hills) ESTI as mychility protein prote		
44.3  **********************************	H. 153978 H. 153971 H. 153971 H. 153971 H. 153973 H. 153		
	MITAGS AF7575 AF7575 AF7575 AF7575 AF7575 AF7575 AF7575 AF7575 AF7575 AF77725	E38368 A42240 300772 304740 304740 45812 229139 229139 229139 229139 229139 2207 229139 2207 229139 2207 2207 2201 2201 2301 2301 2301 2301 2301 2301	402590 402590 402590 407690 116209 116209 116209 116209 116209 117809 18782 18
WO WORLD WITH MINISTRA WAS A WARRY WARRY WAS A WARRY WARRY WAS A WARRY WARRY WAS A WARRY WARRY WAS A WARRY WAS A WARRY WARRY WAS A WARRY WARRY WAS A WARRY W	1007064 AR 1007064 AR 1007064 AR 1007069 AR 1007099 AR 1007099 AR 1007099 AR 1007099 AR 1007099 AR 100709		
30 25 20 25	35 40 50	55 60 55	5

romodorinals adjacent to this finger dome onno expless mRNA; cDNA DXFZpA34E062 (tr

1231 Domes Ace A 10 Domes Ace A 10 Expression of the expension of the e

bansmembrane protesse, serine 4 ESTs, Westly similar to DAP1\_HUMAN DEATH 3STs

nucleosoms assembly protein 1-2ke 1 ESTs

pothetical protein FLJ10618 pothatical protein FLJ10461

2018.
B-cat CLAymphoma 118 (zinc Briger pro
DKCZP6660318 protein
ESTs, Westy similar in T34038 hypothesi
gbcz56916.4 Soerse JahNuke, 35 Herro sap
eschosts-ecula complex (Crosophile) fornol

CG4-09 protein chords channel, calcium activated, fam E816 gbzsi 682.s 1 Strategene lung (9372.fg) H E816

thmost cozat NCI\_CGAP\_Pr2 Homo saplens

ate resistance protein ARS2

increagnath III and Albert Cataly and Albert Cataly Alberto septem cDNA. FLZ1631 83, cone C Homo septem mRNA tall length Insert cDN

sedical protein FLJ21901

histocompatibility complex, class

no saplens, clone IMACE.3867243, mRNA Area of modor neuron proteith latera shapen and madioproteinuss doma shapen and madioproteinuss doma prosoome 14 open neufarg frame 2

s i b vodev tocky UA Id/ILH-813-48-6-12-0-Ulls 1 NCI\_CGAP\_Su CSTs, Moderately similar to PC4259 families to PC4259 families ESTs
ESTs
ESTs

iln, actin-binding protein, 10

UMP-CAP khase Namo seplens CDVA FLJ12598 fis, done NT ESTs Chromosome 12 open reading frame 4

		2	
12/12476	ets on the	ted value reflect	
PCT/US0	m 59580 probes	y Mil, a normality	
	rere selected fro	everage intensi	
	. These penes v	ss expressed as	
	or radiotherapy	n lits analysis w	
	D chemotherap	set obtained from	
	efents treated w	a for each probe	
	samples from p	expression day	
43	up-regulated in	Chip array. Con	terrestion.
02/0864	tows 202 penes	utx Hu03 Gener	have of mRNA .
≩	120 C.S.	EcelAthma	the refative

	SA Homo		MS ESTS 1578 hypoth 1411 eburte 155 tensm	781 E87s, 1 732 E87s 2572 hypothe 637 homes 657 bomes 657 bomes		1531 DACEP 1442 ESTB, 1 19 achiett 187 EST 187 CG-09					956 hypothe gb:EST 50 ESTs 77 consist, 999 ESTs 933 nuclear		347 ESTs 511 ESTs 014 Homo ti 456 survival 25 cystales 0 a dishta 052 chomos	664 ESTs 847 delta-br 63 UMP-CL 66 Namos 780 ESTs 188 chroma
086443 H: 86: H: 26:			43 Ha.88045 48 Ha.42484 77 Ha.122578 91 Ha.184411 Ha.63325							27 Ha.16849 20 Ha.295378 185 Ha.249034* 25 Ha.22646 Ha.210336 65 Ha.295278			11 Hs.124347 12 Hs.124511 Hs.286014 616 Hs.102456 8 Hs.10526 17 Hs.8850 17 Hs.8850	
		14518 AW1633 14824 AAGOO 14837 BE2449 14974 AW9684	15076 AA814043 15084 BE33368 15291 BE545072 15313 AA808001 15697 031382			19940 ALDSDOY 2025 ABSTSA 20516 AASSB3S 2053 AASSB434 20054 AWSTGTO 21054 AWSTGTO					26133 AA1266 26133 AA1256 26509 R47400 26538 AB0306 26668 AA64888 26812 AB03768 26812 AW4509		7768 AASQZO1 2781 AQ22103 28618 H07103 28609 NM_003616 2877 AIBTB918 28168 A132888	
. 22	2 2 2 2 2	1111 2	15 188	20	25	35 30	4 333333	45 22 22 22 22 22 22 22 22 22 22 22 22 22	20 20 20 20 20 20 20 20 20 20 20 20 20 2	55 18888888	69	70 1271		80 128521 128521 128574 128598 128785 85 128970
			-	~	7	e1 e1		4	ν,	δ.	9 9	,	,	o oo
											•			
ecting														
.02/12476 sets on the stred value ref														
PCT/US m 59580 prob y Wil, a nomu		samples.												
re selected fro verage intensi		or normal lang	٠											
hesa genes w expressed as a		everage of Al f								•				
adotherapy. T		y divided by the Ri	28999	256 256 256 256 256	38.40 198.80 78.60 162.20 26.00 37.20	12.00 13.90 110.60 110.60	250 250 250 250 250 250 250	2588555 258855 2588 25885 2588	3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22.22.23.23.23.23.23.23.23.23.23.23.23.2	22.20 21.00 21.00 21.00 21.00	222222	72.50 77.20 77.20 77.80 77.80 77.80 77.80 77.80	22.00 22.00 22.00 23.40 24.00
notherapy or n		r radiotherapy R	•											
sated with cher h probaset obt	ž,	етотняту о	chronosome condensation 1 dob-tato roductase family 1, member C3 IGAA0042 gene product giftiamide reception, metabodropic 5 C2 Enecopolise (cape 3)	Ang protein origion facto d satisfile 3	or tinding pr 1 (230/240h0) ulgaris entigen 2840 (com 5 protein (his entigen 1	ents (E. col) homotog 2 (coton caroor, RAVestation option readors (S.1 in miscrotion host, I.Whomosodma denorgations be hase Homo applies cOW, E.12(800 Bz, chen H perferentially expressed antigen in mela	of) Interstited ted kinase yeoprotein A DIG-Zp564D	2018 VIAAL(18) proteh Nycochette (1904eh FL 12028) Nycochette (1904eh FL 12028) Phron supiers PROZ751 InRNA, complete cds patrical box gave 6 (Peval lineage apool Governation and pright or 6 (20) instead FR 1000 InrnA   1000 I	co it, versory servar to soucze rypotuse Heros septers mRNA; cDNA, DK72;781(50212) ESTs Prophoserine amhobarsfesse	gonzulozia i Nul-Cukiv-Lukiv romo saperas MANDSZ protein OKSZPOSORFZIŻ krotein Homo saptera mRNU-CMA DKFZp782GZIT (k ty superfamily menjor UNR hypothetze protein	or (rabbines 93 ng 9	hypotherical probain MGCA487 ESTs Lineati family mamber 13A ESTs HMT1 (mRNP methytransferera, 8, cereni atmospherer and binnothomes 1 ESTs ESTS ESTS ESTS ESTS ESTS ESTS ESTS	hypothetia proteh EST  LISTAIR gradeh NUDE1, rat hono AAAQS4 proteh COC14 (est division orde 14, 8, cerent studio carrier tentify 6 (esterotrampilia	ESTI, Weady shallow be ESTI 4 eafway ESTI Pypolohera prober EJ1020 Pypolohera Pypolohera Pypolohera Pypolohera
om petlents tr an data for eac	accession num	treated with of	condensation uclase family ne product reptor, metabo	Lord resolution states of the control of the contro	ng growth fact hygid safgen i (pemphgus v protein, bets 2 srigenio spem rien carchome Leinha, D. onta	homolog 2 (compan recept after factor, Lil he khase s couv. FLJ2 expressed an	arma, neuron optoblesso 1 ortoold reguta I trophoblest g a mRNA; cDN	orden FLI202 s PR02751 m me 5 (8-cell lit neighbor of SC	s mPNA; cDN	Xeh Xeh 1124 proteh a mRN4, cON receptor LNII roteh	RABB interacting, threat-hate (rabbees MCBB) protein interacting threat interacting threat interacting threat interacting threat interacting threat interaction repeat containing 9 thrushootide repeat containing 9 ESTs.	potietical protein MGCS487 31s nesh family member 13A 51s VTT (mRNP methyltansilent ochogens and homodoxes	noteh ng protein NU Xish Shishan cyde tarnfy 6 (neun	y similar to 155 motein FLJ 102 s mRNA; cDN ssociated proj
d in eamples it Sene expressit	titler number ber, Gentbank	from patients Unigene Title	chromosome aldo-kato red RAAQOA2 ge ghtlamate red	topoloomera NAA0874 pn S164 protein POU domain gb:Human af	hepath-bind bullous perm desmoglain 1 gap jandbon nuclear auto oytoaollo ova	mutS (E. col) RAR-related ISL1 transcrit decoypusion Homo saplem preferentially	enolose 2, (g matrix melati serum/glucoc 574 oncotata Homo sepien	KUA1488 pn Nypothetical Homo esplen petred box gr downstream	Homo saplen ESTs ESTs phosphaserin	gondoegus xx no KOA0922 protein OKE2PS86F2124 Homo saptena mi ig superfamily noc hypothetical protein collagen, type XXV	RABB interacting, KIAA0883 protein hypothetical protein KIAA1702 protein ESTs thruckeddle repea	hypothetical personal family ESTs ESTs HATT (hard) HATT (hard) American are also family and also family are also family and also family and also family are also family and also family are al	hypothetical prot ESTs US1-intaracting IGAA0942 protei CDC14 (cell divisional solute carrier ten	ESTs, Wazde ESTs hypothetical homo saplen microtribute-
143 sup-regulate echts array. C	corression. probesel ider coession num	A for samples UnigenelD	Hs. 78183 Hs. 78183 Hs. 3104 Hs. 167165	H-91417 H-27973 H-180789 H-182505	Hr. 1630 Hr. 1925 Hr. 1925 Hr. 223733 Hr. 155185 Hr. 155185	H. 78934 H. 2166 H. 77494 H. 1427 H. 80743	Hs.146580 Hs.83169 Hs.296323 Hs.82129 Hs.14846	H-283978 H-283978 H-283978 H-17834	Hs.234074 Hs.145958 Hs.105421 Hs.286049	Ha. 17892 Ha. 173684 Ha. 61460 Ha. 61450 Ha. 617938	Ha.73825 Ha.131915 Ha.139610 Ha.18862 Ha.18869 Ha.10826 Ha.10826	Hs. 211556 Hs. 170287 Hs. 146728 Hs. 133521 Hs. 12940 Hs. 12940	H. 5223 H. 110555 H. 6763 H. 6763 H. 22003	Hs.1226 Hs.722 Hs.18127 Hs.103042
WO 02/086443  Tabk 44 shows 22 person superiabilio earropia from politicit brands with chemoderapy or radioterapy. These person were selected from 5550 probases to the East-Myrmatch Hold Genecity erray. Gene expression data for each probased dobained from this analysis was expressed as servings intensity My, a normalized value indicating	The restries level of mistrick karptesson.  E. Worter. Unique East proberest fourther number E. Worter. Exercised Accessed number, Gentants accession number Integrants. Uniques earnings.	EvAcon	MA_001269 017783 026361 028539 04 001646	AA013031 K00821 3E245294 211933	AWS5908 111690 MM_001844 W86549 W176374 VFZ07881	UO4698 UO4698 NIV_002202 AA296874 U44060 U85011	MA_001975 M13509 M00512 SEZ70268 SEZ8665	WS03733 8E387790 142047 W767528 NLIST441	AL137311 AL137311 AW970502 AW075465	AH38843 AB023139 AA43473 AA43473 BE153858 BE409857 AU07842	AA219891 AW978518 AW01355 AV975746 AA219172 U80738 AA232103	AW967069 AW03785 AW989482 AW001268 447224 AW98863	AB037807 AA837396 NN_016310 AA383343 W39609	ALTIDZIB AW206453 AB033023 LLISTA25 439342
W( Table 4A si EnstMyrme	Pray: Evicor: Uniperation	Rt:	100113 100210 100220 100223		101549 101724 101878 101878 101916 101916			105238 105310 105310 105073		106998 107302 107302 107902 108509 10876		109502 109538 109788 110920 110924	2511122 11224 12361 1236	

9
2
፷
Š
F
2

130149 AW067803 Hs. 172653 methylenetestarkydroddata dchydrogensse 130199 Z48579 Hs. 172028 a distingth and metaltoprobeinase dome

WO 02/086443

					d by the 90s		normal and of	MAI for norm	SOUTH OF SOUTH OF	De 150 per	and fund and				2	•																								_			
					min dyda		JOAM	percentle o	od Alfore	coles minus	Cally disea.				2					8	Š																87.						
מלונים של המו או המינו לומינים מינו					non humor sam		90th percentile	d by the Soth	BOTh percentile	and famor sam	mal and chrom				æ	Ē						7.4	2				2.55				5.07								3.70			18	
personal runs cooper processes on the court, present rucks consisting and a constitution of the constituti		Unique Eos probeset identifier rumber	Exemplar Accession number, Genbank accession number		Outpeas going and At the solutions and continuous and adoptocations a luca funct soundes dolded by the SOS		80th percentile of All adenocardinans hare lamor earnabs divided by the 90th percentile of All for normal and or	guerrous cell carcinoma luro tumor Ramohas Grido	denocardroma luno tumor sambles divided by the	or sentamous cel cardinoma and adentocardnoma la	diseased turn and burns samples divided by 90th percentils of AI for normal and chronically diseased tung age	normal hard, chronically diseased ture and turnor earnoles			Ilelmene Titte		AEE's control CapPill	ACT CAMP CADA	ACTV COMPA CADOM	Marco Cable seconds ships I subsul	Surply of the su	MARKET STATE	ablackets reductors family 1 member C3	ministromenome maintenance deficient (9.	chozohośnichostasa, olatelat	protessome (presome, macrobaln) subunit.	E2F transcription (actor 3	chaperonin containing TCP1, subunit 5 (e	protein disultde isomerase-related prot	minichromosome maintanence deficient (S.	clatefel-activating factor acetyfindrals	uridine monochosohata kinasa	KOAA0175 name needing	emitse, eith 2A: nancreatio	RAN member RAS occusene fertily	non-metastate cells 2, protein (NM238)	cardinoembryonic antigen-related cell ad	protectin-induced protein	collagen, type VII, state 1 (epidemotys	calclioninteactionin-related polypeptid	mangen-activated protein kinase kinase	Homo saplens ribosomat protein L38 mRVA,	
d value reflect	-21	Eos probeset	ar Accession o	Ingina rumon	mention of All 6	diseased lung samples.	rcentlle of Alle	centle of Also	reartifie of All a	centre of Alk	d lune and bu	and opposite			Clemental						Us 83063	7067070	H- 78183	10101	Hs.99910	Ha.139	£ 133	₩.1600	Hs.182429	Hs.77152	Hs.6793	Hs.76539	H (843.70	Ha 2007.80	He 10842	Hs 275163	= <b>£</b>	Hs 99949	Hs.1640	Hs.37058	Hs.21291	Hs.132748	
A. B normalize		Chque				disease	800 000	800 000	BIR DR	700 007	disease	Bullon			EvAnne	3			•	4704013	20107	705300	200	AW2477SD	HF294407	AA489908	NN 001949	AU076657	AU077258	AW410976	AW247629	W70171	NW 014791	NA 000699	TIGOR	D56165	090278	X51601	NM 000094	X00358	AA015693	BE623001	
Intensity (A		Picey:	Extoor	Dipered Title	ż	į	ఓ	Ħ	R.	8	į				P.		\$5,000	2000	2000				5 2				100269					100050					_				100829		
		n		•		9					15	:				5	ì				25	3				30	:			,	35	:				40	:			;	45		
	,																																										
									•																																		
																											-																
	-							•																																			
																																										And the Party of t	
	•				_																																						
22,36	2 2	2 2 2	2 9	2	110.00	<b>R</b> .X	\$0.65 \$0.60	37.50	8.2	33.40	60.80	29.62	<b>9</b>	32.40	27.40	8	31.38	22	23.40	61.20	22.33	23.50	30.00	23.80	51.68	88	8		69.33	33.20	31.60	8	23	<b>\$</b> .2	8	2	24.5	S :	3.5	28.60		1	
at a fact	la chore KA	ne) o	Total		, polype	(CEBP)	_			e factor (	20	fis, clone H	the 4			steogenic		95	(GED)	Proofes		se doma		cephalos	erase B. ye			•		400		raciling pro	010 X-En	fransfor	ted, acti ·	phony		openase	atory su				
A-echreted, c	W FL220653	Ser contamus	- Proception	Creat Chear	ferase 1 (amily	binding protein	ecretogranin 1	900d ii		adds exchang	(activator 1) 4	W: FL122373	3 (Importin alp			to protein ? (o	P.	chata syntheis	chance factor	far to 133468	paphalase	petallocotene		hamolog (scro	of RNA polym	FU10074	on factor (IIA	homograph C	phila) homoto	) proteinase in	oduci	ETB 19kD-inte	chrilar to A46	cinamide form	math associa	szhe-(Y)-phos		r beta cahyd	dnase 5, regul.				
protein Idnasa, DNA-activated, catalytic	tomo saplena cDNA FL/20653 fts, ctone KA	peculonial IAP repeat-containing 5 (sta	grutamens-fractions-5-proceptions from antiti Esta	catherin 13. Hoseberin (heart)	DP gircosytramierase i territy, polype	CCAT/enhancer binding protein (CEBP),	chromogranin B (secretogranin	E1A binding protein p300	KIAAOSKIB protein	The greatine nucleation exchange factor (	replication factor C (activator 1) 4 (37	fomo saplena cDtAr. FLJ22373 fa, done H	caryopherin alpha 3 (Importin alpha 4)		Cyclin Landa-Ga	cone morphogenetis protein 7 (ostaogenic	parbonic entrydress XII	suamine montphosothate synthelese	Sted 2 coarring exchange factor (GEF) 9	STs. Weath strate to T33468 Imported	thosohoserine phosohatase	distriction and metallicorate has a doma	HSKM-B protein	wist (Drosophila) homolog (scrocephalos	SRB7 (suppressor of RNA polymerase B. ye	hypothetical protein FLJ 10074	peneral transcription factor (IIA	ecroporate 11 (chamograph C)	Isca, large (Drosophita) homolog	Lerine (or cysteine) proteinase inhibito	KIAA0203 gene product	3CL2/adenovirus E1B 19kD-interacting pro	STs, Moderately strellar to A45010 X-tin	hosphorbosylgycinemide formytransfor	SWIVSNF related, matter associated, acti	dual specificity tyrosine-(Y)-phosphory	Gardgen 78	hydroxysteroid (17-bets) dehydrogensse	cyclin-dependent kinase 5, regulatory su	eurotrophin 3			
_	Hs. 1800559 Hor	_		_	_	Hs.2277 CC	_	_	_	_	-	-	_	_	_	_	_	_	••	-	_	Hs.64311 ad	_	_	Ha.286145 SRI	_	-	Hs.75428 sec	_	_	_	Fa.79428 BQ	_	•	_	-	•	_		48.99171 neu			
		_		2		AIBT9165 Hs.		_			_	_	c									U92849 Hs.								NA_005025 Hs.		UIS174 Ha.				~	AAMBS42 Hs.	_		_			
	_		130617 MS0516	30732 AWR		131028 AIB79			-		131945 NM_(					132550 AWS			137577 WZT721			133070 1926			133282 AA44				133865 AB01			DATES UIST			_	_	35002 AA44		_	35045 X53655			
: 2	# :		25	: #		10 12	=	2	₽		5 5	₩.	₽	#		20	₹ <u></u>	#	•		25		<b>.</b>	₩.		30 3	₽	₩.	₽.		S.	#	2	<b>t</b>		40 €	<b>₽</b>	<b>.</b>	=	E 46	3	i	
																										,				•	•										•		

WO 02/086443
Table 54 more 600 perse spread to equations of carcinoms or admixestation to form the product of chrotically described by These spread with sead of the 5000 persecution for the carcinomers of the carcinomers o and chrorkesty dissessed turp samption, recruit and chrorkesty dissessed turp samption, as delicerbones turb turb are averybes. She percentilla of Al for all recruit a transport and a samption of Al for all recruit a first, percentilla of Al for all percentilla of Al for all or all security. 80th percentile of Al for normal and chronically 573 £ 85 ŝ 83 7 8 2 4 8 14.20 20.50 20.50 15,85 5. 8. 2.69 12.89 38.80 8 24.80 8 7.60 10.20 8.00 12.94 8 8 888 22 23 10.50 8 the other containments by 1 co Actualing with UR2 strooms what oncogene hespetiv-bading provels tear bading per HZB hathers along, remove 0. HZA hathers family, member 4. HZA hathers family, member 4. growth erest and DNA-damage-hotoche, Hs.121686 Hs.121686 Hs.100469 Hs.295112 Hs.4756 Hs.287270 Hs.6398 Hs.117729 HR.180532 HB.5524 HB.55290 HB.55390 HB.5233 HB.5231 HB.6233 HB.6203 HB ALTISSES ALT 2 55 9 65 2 75 8 82

¢	•	1
•		3
•		

PCT/US02/12476	38		18.79 17.40 8.65	. 477	2,501		10.00 9.20		4.14	39.85 29.85		5.04	10.84 45.60		4,27	24,80		889		23.40 (2.80 12.80	11.60 11.80	23.do 23.do 23.do	00:01
	_	- 83				8 ≑ ₽	\$	8 25	23.52 23.63 34.03		13.20	13.80		11.40 6.00				<b>5</b> .	. 8				8:1
	8	10.29		~ 7 8	41.0	15.00		~~		00	89		. 9		8		8	Ş			88	8. 8. 8. 83	_
		Ş		3282		56		344		88				3,0	4.71	280	2,71		. 0.6 0.40	25.			3,00
				Outwo responsive general modulariza NPD002 powith hypothogizal provide RJ 12691 mittade spride-ball mittade prot dhomescane 20 open reading farme 1				Author agreem, Come wave, at 1990s, more, paired box gene 5 (B-cell fineage specif asms domein (Ig), B-cell CLL/hynghoma 118 (zivo finger process).			ESTS, Weady similar to ALUI_HUMAN ALU 8 http://www.ncbing.goop/nonhibroe-dromoso ESTs, Weady strilar to putative p150 [		GESTS Home sacional succession of the procession of the phone parties and the phone procession and parties of the phone procession and procession and parties of the phone procession and procession and parties of the phone procession and parties of the phone procession and proces		Erytes prosproproses s Erytes prosproproses selected to a NAA 1272 protein RADS1 (S. corevisios) homotog (E cot Re			Homo sapiena clone 24416 mRNA sequenco Bibiliarin mudedar protein (AOE/D repeat) Homo contesso since (1467-1401)		hypothetical profesh FL21620 protos knasa MCG-SP15 ESTs ESTs hypothetical protesh FL316372		hryothalical protein CMCZQ434(0428) gizzn13b02a i Breitageae NMT neuron (337 goz384QA4 si Breitageae colon (3372A4) Horno septens cDAA Full (1446 fa, chore HE frontielleriol nordah El (2013)	KAA077 protein ESTs ESTs, Moderathy similar to 2109280A B c collegen, type XVII, styhe 1
5	# 9222 # 5409	Hs. 258730 Hs. 258730 Hs. 66969	H. 23823 H. 14846 H. 14846 H. 292911	Ha. 16244 Ha. 16244 Ha. 16244	H. 24780	H.2546 H.25740 H.2641	Hs.26389 Hs.301855	H- 57830	H2 269088 H2 26999	H. 22372 H. 3467 H. 37166	16.5250 14.19114 14.37751	Hs. 5243 Hs. 161383	H-57787 H-21103	Ha. 20149 Ha. 181022 Ha. 25245	Hs. 21768 Hs. 15978 Hs. 23044	Ha. 75688 Ha. 15243 Ha. 4756 Ha. 9948	18.41639 18.35861 19.187958	4.5957 4.99853 4.296585	4.81172 4.335952 4.81460	Ha. 18878 Ha. 49927 Ha. 139709	4.77842 4.161523	Hs. 68055 Hs. 120905 Hs. 778737	Hs.70823 Hs.70832 Hs.193540 Hs.117838
2/0864	248364	240450 110992 878	104590 AW373062 Hs.8. 104858 AA360964 Hs.2. 104850 BE288855 Hs.1. 104889 AA420450 Hs.2.	5311926 5311926 5311926 531926				AA787628 BE246502 H09748												AW392655 H AW798357 H AM943676 H AM943770 H		AL133092 H AA084948 AA086005 AA086328 H AXD07297 H	7 C + C C
MO	\$ 19 5 19 5 19 5 19 5 19 5 19 5 19 5 19 5	M415 A8 M558 R5	4658 AX	04759 BEE 04971 BEE 05011 BEC		05175 AKS 05175 AKS 05200 AKS														107832 AW7 108015 AW7 108056 AA0		08554 AADI 08554 AADI 08573 AADI 08584 AADI	
•	555		2	12 22 22 23 24 25 25 26 26 26 26 26 26 26 26 26 26 26 26 26	2225	20	25	, p = 2		35 55 5 5	6 5 5 5	5553		50									
			1	_		7		"	)	t.	4		4	Ñ	3	ń	9	59		2	75	80	85
PCT/US02/12476	_	4.10	83.8	4.38 6.12		5.80 5.80	5.15 4.17		3.98		9.24	E. E.	<b>3</b>		7.28	878 4.77	29'5	4.70		5.15 3.88		26. 4. 84.	}
		18.57	12.80	12.00			9.33	¥.5	8	5	8			5	2			8.	11.00	21.40			15.60
			:	97.4				19.20		22.00			14.40	6.70				100.00			6.40		83
	5.23 5.23 5.23	3 o	140.00 2.68	e.	222			- E	8	12.00		6.60	_		-8	8.	 9:	_		, 0,t1	~8_	8	10.40
					6.20 2.82 5.83	8,5		18.83	7.50		8 8 8		. 600	4.2 8.2	3.01		36		25.00		5.02 10.50 6.41	78.50 8.51 3.50	
	chymase i, masi cell bufous pemphipoid entigen 1 (230/24040) desmodelsy 3 (nemphinis vultarits autions	control carrier family 7 (caforic arrivo myking carrier family 7 (caforic arrivo myking cell mydear differentiation en TTK protein kinasa	gap junction protein, beta 2, 28kD (corn collegen, type XVII, eigha 1 mannose receptor, C type 1 middine (neurita growth-promoting factor	increases along protein 1 (LLCM Nan ado-kato reductos family 1, member C1 zho finger protein 131 (clane pit Z-10) interretain enhancer loding factor 2, 4 subbloenterase family, cytosob; 2, 4	centromere protein A (17kD) tarrient, beta 3 (nicein (125kD), kathon secreted phosphoprotein 1 (asteopontin,	JTVI gene protessome (prosoms, macropsin) 26S subu- heterochiometin-Rive protein 1 DEADH (Asp-GSJ-Alfin-AspHas) box oolyoep	chronosome segregation i (vessi homolog) chronotox homolog i (brosophia IP1 bets macrophage stirutiang i (hepatocyte gro	Bloom syndromes of arms, married Bloom syndrome of the Shringshi and metaboproteinse doma vaccular endotherial grown factor C pages 25.0	enhancer of zerta (Onzophila) homolog 2 ubiquith fusion degredation t-like preferantially regressed entitles in meta	melaroma antigen, family A, 9 G protein-coupled receptor Human hbz547 receptor CHS telula recent RNA lacquesoc CHS telula recent RNA lacquesoc	eyes absert (Dosophila) homotog 2 rethold attorne-bliding protein 8 ubquilin carter protein E2-C	boforead box MI go-Homo explens clone 14,99 mRNA sequenc chaperorin containing TCP1, subunit 7 (e					gutalibre perodes 2 (partotherin Faromentorae potein (CAD), endoplasmi Farotoming growth factor, sphe					polymerzes (RNA) II (DNA directed) potyp 614 orozelesi bropodessi glycopyminh 6RY (pex determining region Y-box 2 POU domesh, class 2, essociating is-tor ni Henro, services 64 is-mili brest - (NMA	hypothetae protein FL12468 butory super-family protein ESTs
€	19.00 10.00 10.00	H. 183837 H. 163840	Hs.323733 Hs.117938 Hs.75182 Hs.82045	Ha.205098 Ha.76117 Ha.76117	H-1554 H-75517	18.148495 19.278554 19.41706	15.77254 15.77254 15.278857	H. 36820 H. 79142 H. 79145	15.7728 16.181369 16.30743	45.23016 45.24385 45.24385	4s.29279 4s.29287 4s.01002	Hs. 239	45.82845 45.80952 45.76118	15.20372 15.20372 15.20372 15.20506	Ha. 116638 Ha. 117850 Ha. 83169	Ha. 334883 Ha. 155324 Ha. 8248	4.74368 4.170003	4s.359 4s.324728	4, 37,3378 4, 37,189	Hs.78536 Hs.20716 Hs.79971 Hs.293007	46.119018 46.28991 46.2785	Hs. 48405 Hs. 82128 Hs. 816 Hs. 2407	Hs.38178 Hs.102237 Hs.133543 Hs.330515
WO 02/086413	3	. g	. F . F .		96 25 	2000	22	# 82 A	.88.	2562	7019	E P		258	28	885	- 5892	200	266	 85.	 22 5		
9	888	3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	至6232	3 X X X X	8553	8888	258 25	5883	F 20 =	5 B R R	2 2 2 3	528	8888	882	588	8888	382	经货货户	2 8 V	8330	富芸品商	95 25 25 25 25	5 5 5 5
WO	1695 ME9136 1724 L11690 1748 NM 001	1771 NM_00244 1771 NM_002	101809 M8684 101833 AU076 101842 M3322 101851 BE260	102072 ALT34; 102072 U0941; 102083 T3530; 102111 L36188	2123 NM_00 7154 U17760 7193 ALD383	221 NA 003 224 NA 003 234 AW183	2305 ALDA320 2330 BE29806 2340 US7055	102384 NW 002 102384 NW 002 102404 NW 002	581 AU077 565 AI4351 510 U6501	2023 AW249 2842 AA2054 2654 AV6492 659 BF245	2569 UT 200 1572 UT 200 1587 NW 00	2008 BES402 2760 UB2321 1781 BE2567	2824 UB0516 1829 NW 00	102892 BE4400 102913 NM 002 102825 BE5618	7883 BE3872 7023 AW500 1036 M13508	XXXX AA9263 3060 HM_00 1099 A16932	103168 X53463 103185 NN_00 103192 NZ244	2242 X7634; 2242 X7634; 316 X8330; 318 X8330	385 AL036	430 BE364 430 BE364 146 X9837 177 Y0770	M77 AJ0118 W78 BE5146 E15 Y10275 558 BE8169	103580 AA328046 103587 BE270266 103594 AUX6680 103636 NW_006235 103768 AEPROM	103841 AA3148 103847 AF2199 103913 AW9675 104094 AA41811

~
~7
~
-
₹
~
0
Ō
_
2
٤
_
O
۵.

PCT/US02/1	823	5.62 4.06			4.01	4.1			•		842	
11.60 0.71	<b>8</b> 7		1260	5	9.1.6 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	8.05	5.25	10.60 14.80 15.80		13.80	970	12.20 10.40 10.40
27.40		8.3	32.00			28.9	6.14		_	<b>6</b> 23 67	23.58 23.58 3.88	& <b>₹</b>
		<b>3</b> .	8.7	8		2.8		<b>9</b> .	12.60	9.40		
	2	S 50	3.67	•	1.7	٠	3.14	22	13.50	22 E73	ğ	18.50 7.00 6.00 13.50 4.00
				phosphelotyfnostid ghran, otes F ESTs ghystsSDS.s1 Scares retne NZAHRI Hamo ESTs Hamo sepiens mRNA for KIAA1785 protein, ESTs	ESTs thresh family member 13A mbchondrial rhosonnal protein 142 EST EST butyrata-induced transcript 1			hypothesia pruhe FLJ1180 ebychalicia pruhe FLJ1180 ebychalicia pruhe FLJ1180 ebychalicia pruhe FLJ2333 pychalicia pruhe FLJ2333 pychelicia Chornazane 9 excil i Hono sa ESTi, Modurally Jamie no S31987 i pych		NACAZI FORMIN FLAZI 16 Horos aptien NV-RENAZ mitga mRN, par Horos aptien NV-RENAZ mitga mRN, par Horos petien NV-RENAZ mitga mRN, par Horos petien SKIDA se transportation ESTI, Advented y fruits to EXXX flox ph.259678 s NVC COAVE GX28 i from a speins states (Chrosophia Chrosophia) from datable scrite complex (Proceptible) formed attable scrite complex (Proceptible) formed		TATA haz thading patein (TBP)-earsochel ESTs. ESTs. ESTs. Highly staff is to ASSES (DNA ears). ESTs. Highly staff is to ASSES (DNA ears). Psycholetical probib PS/8022. ESTs. ESTs. ESTs. ESTs. ESTs. ESTs. ESTs. ESTs. Weekly staff is to EST/73 floque pr
H.28178 H.0325 H.7333 H.28768 H.60031	Ha. 177233 Ha. 177233 Ha. 269517 Ha. 268115			Ha.166382 Ha.40478 Ha.241420 Ha.241420	H. 16285 H. 146286 H. 112110 H. 250622						Hs.18793 Hs.18793 Hs.18793 Hs.18793 Hs.18793 Hs.18793 Hs.18793	H. 4820 H. 20518 H. 20558 H. 20558 H. 20529 H. 20529 H. 20539 H. 20539 H. 20539 H. 20539 H. 20539
WO 02/08/6443 22 BERRIGO HLS 22 BERRIGO HLS 23 AAC4820 HLS 24 AAC4820 HLS 24 AAC4820 HLS 25 AAC4820 HLS 26 AAC4820 HLS 27 AAC4	M872527 M01732 M47709	A682382 F126743 F439095 L949095	AW450694 AW450694 AF26316 AT768015 AA586922	ALTO2054 ALA17023 H92225 - AL263517 N23629 WZ0128	N32536 N32528 AW173019 N45100	016709 016709 674126 81344 22886	M269 M339 M329 M222970 M222970	F086161 10839 F221993 979147 12803 A195276	918306 45552 M_016525 779123 A699485 A692402	M67.353 A0000123 A0000059 A000048 A1883243 AA292700 Y19062 AA226434	AA396209 AL38951 AA396371 AA402713 AA448103 AA448103	AA41238 AA42889 BE387162 AA43058 AA43070 AA43702 AA4373 AA4373 AA4373
WO 116652 81 11670 A 11570 A 115816 81			4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4				18708 18708 1870 1870 1870 1870 1870 187					121653 A 121753 A 121857 B 121857 B 122163 A 122163 A 122318 A 122318 A 122318 A 122318 A
2	9	15	20	23	e 8	35.	<b>6</b>	ν, (	S &		8 8	75 80 85
	<del>-</del>	-	6	7	m	n	4	\$	o v	•		<i>C</i> 80 80
PCT/US02/12476	(3)			<b>72</b>							F7 FF	£17
•	8	10.40	12.60		16.80 04.00 04.00	14.67	62.0	14.50	41.20	13.91 13.20 10.00		25.20 27.40 24.40
		17.60 17.60 33.20	11.00		8	15.40	7.10		15.31	. 73	8	8
97	9.00	12.67	82		89	6.80			007	87.7		8:
8 8888	10.58		8	308	72		300	273	8 8	3	32	25.00 3.25 10.50 4.17
			pt+85C354039 normalized Infant brain cDN ESTs ptypollalisal Soores Infant brain IND H 90 hypothetical protein FL20272 tensorbilen factor NYD-ep10						The profit of th			
6443 #.7331 #.27631 #.62180 #.128911	14.497 14.838 14.108	15.285 16.211 16.7154 15.4893	Hs.12878 Hs.26090 Hs.21273	H-219 H-363( H-1451) H-279	Hs. 24349 Hs. 24349 Hs. 253925 Hs. 14776 Hs. 14776	Ha. 978 Ha. 1891 Ha. 1272 Ha. 1123	Ha.7004 Ha.70223 Ha.193274 Hb.285681	Hs.28737 Hs.747 Hs.288760 Hs.6932 Hs.318127	H-1682 H-1682 H-1883 H-2003	H-24300 H-2538 H-2238 H-2738 H-2734 H-2734 H-2734	Hs. 165221 Hs. 165221 Hs. 15443 Hs. 22916 Hs. 22916 Hs. 198249	H.72010 H.23659 H.19431 H.334624 H.334624 H.334624 H.33563 H.65260 H.65260 H.23478
WO 02/086443 togeth with the control of the control	109121 BE389387 109168 AA219691 109227 AA76699 109415 UB0736	109454 AA232255 109507 AW967069 109543 AA564994 109648 H17800 109680 AB037734	109700 F09609 109792 R49625 109381 BES46208 109998 AL042201	110039 H11838 110158 AAS81322 110550 AA907723 110551 AW450381 110854 BE812922	110916 BE178102 111003 NS2880 111337 AA837386 111434 RD1608	111557 R11499 111597 R11499 111895 TB0581 111929 AF027208 112054 R43590	112210 R48845 112244 A8029000 112382 R59804 112392 R60763 112442 AAZ80174	112539 K70318 112772 A1952283 112659 BE261750 112933 R71449 112970 AAGS4010 112970 AAGS4010	113053 W15573 113073 W15573 113078 T4044 113291 R4567 113291 T81801	11384 A39273 11384 R9588 114073 R4933 11408 AF5588 11428 R4338 11428 R4338 11478 H15281	114407 BES39978 114550 A157469 11479 A158285 11479 A158245 114331 A158245 115047 BEZ70330 115060 AF052833	11913 AA2840 11913 AA2840 11913 AA2840 11914 AA8807 11914 AA8807 11924 AA2870 11624 AA870 11624 AA870 11624 AA870 11624 AA870 11624 AA870

Ξ			,	
	8	۰		
				-

	PCT/US02/12476																												•						
	PC 1/0					4.30	<b>4</b> .56	4.48	297		603		80.		8	£ 2	4.02 6.71	4.21	<b>4</b> ,03	4.65	3.91		909			5.7 5.23	4.92								£.
	14.18	24.60 16.83	37.40	9.50	10.40		10.00								1,00	12.00						9.60			15.20		96		88.2			14.67		:	89.59
	•					_		18.80		_	5	Ď.							7.00		7.40	9	25.55	2.00						8.80			19.20	88	
	-		7.08	:	5.00 5.00 5.00 5.00 5.00 5.00 5.00 5.00	12.60		=	25	1260		8.0		6.50	5			o =		8		_		<b>4</b>		:	z	12.40			<b>2</b> ~ ~	~	16.00	*0	
	957		<del>-</del>	,	2						. 259	8			•		_	8 8		2	<b>i</b> :	4.0		3			16.84	10.21			300	ង	# ₽	, 12 26	
	E87a	ESTs Homo septens CDVA: FL/23123 ls, cone L phosphatido ecit phosphatase typo 2A	Hamo sapena curia FLJ 145/6 ila, done i hypothedical protein MGC14139 ESTs	ESTe Inferteron regulatory factor 6	GNZ ganglosida activator protein mafrit Gla protein ESTs	transcription factor 3 (E2A immumoglobul ESTs	aderylate kinase 3 Interlaubin enhancer binding factor 3, 9	cystaine and glycine-rich protein 2 small mudear ribonucleoprotein polypept	orisisti, ceta c programmed cell death 5 nistrochtin 3	EST:	soluto comter family 2 (faciliated glu dilydrotokida reductase Monte seriese helio hence secretidad ned	KIAA0962 protein unto eseccasion pro- KIAA0962 protein onlike Historica protein-Interaction	hemstdodical and neurological expressed ribosomal protein L26 hamdog	ESTe sspart/glucosaminidase	ESTs terraln 16 (tecal non-exidemolytic palm	ESTs NOEL (Lys-Asp-Glu-Lou) endoplesmic relik	Homo sopiens, done WAGE:3457003, mRNA APMOFT protein	Historia, family 2 hypothetical protein FL/22704	PAL1 mRNA-binding protein nucleotar phosphoprotein Nopp34	EST H2A Nations family, member X	mouppersonaire polorare despungates ubjeuth specific polorare 14 (IRNA-que polein kinase, DNA-activated, catalytic	bacaborital IAP rapeat-containing 6 (sur IGAAQ444 protein	neurollament, light potypeptide (60kD) phulter tunor-t-enstoming 1	replication protein A3 (14kb) hautin-fixe growth factor thirding prote	matrix metacoproteinasa 12 (matropraga hypothetical protein MGC2376 major histocomealbility comotex, class	POP7 (processing of precursor, 8, carer) hypothetical protein MGCS469	UDP grycosytransterase 1 famey, potype undine monophosphate synthetase (orotal multiple PDZ domein protein	ESTs CCAT/entrancer binding protein (CEBP),	aquaponn 4 Homo sapiens mRNA for KIAA1737 protein, hypotheticel protein FLJ10342	vishin-tite 1 Home appleas mRNA; cDNA DXFZp566A1045 (1	p53-induced prolata PIGPC1 cycla B1 hypotherical protein MGC3195	amail inducible cytokine subfamily B (Cy ESTs	ESTs RNA 3-terminal phosphato cyclose hypothetical protein FLJ (1998	hypothetical protein FLJ11210 MRS2 (S. cerevizies)-Re, magnesium hom Novel luman gene mapping to chomosome 22	putative RebS-Interacting protein
9	Hs.120189 Hs.20189	Hs. 163065 Hs. 124262 Hs. 41569	Hs. 334659 Hs. 164153	Ha. 128720 Ha. 11801	H-278062	Hs.101047 Hs.258618	Ha.274691 Ha.256583	Hs. 10526 Hs. 105465	Hs. 169468	Hs.107510 Hs.301088	Hs.169902 Hs.83765 Hs. 43766	H-9059	Hs.109708 Hs.110165	Hs.217584 Hs.207776	Hs. 112062 Hs. 115947	Hs. 11805	Ha.179999 Ha.12162	14.123053 14.282804	Ha.165998 Ha.142838	Ha.147097	Hs.75981 Hs.155637	Hs.1578 Hs.158291 Hs.158291	Hs.211584 Hs.252587	Fs.1608	H. 17296	Hs. 19574	Hs.2057 Hs.169378	Hs 2227	Hs.22452	Hs. 2289 Hs. 168950	# 200128 # 20060 # 201732	Hs.24395 Hs.24908	H-27076 H-3364	Hs.20067 Hs.305605	Hs.184062
		AA836841 AL302471 AU513226	Z21189 AM33721		A7284940 A1954968	12857 ASMS83 128538 R48163		A1876918 N71826				AB023179 AF013758	AMPRES7 W94197	129404 AL267700 129457 X81969				M16707 AlBEAST2	BE514376 AA301116		AA063546 U63630		X05608 AF062649	AA383092 M69241		H59698 Al187292	AF093418	W17044 A1879165	T15767 W28545	A143139 H15302		W25005 AW339037	AWZSOIGS NW_COCT729 AISZ1660	BE245374 BE302464 BE300971	
•		S		10		15		. 5	3	ý	3		က္က		35		40		45		20		55		9		65		2	!	75		80		82
		•																																	
																٠	•																		
221 511 503111 40	011030411410																•			•										•					
			6.35									. 80.9			~ 8			£.			138	3	4.38			53		Ω <b>Ω</b>				8	8-		50
201 th to share		ta.to		08) 80	001	10.50		12.80	-	. 35.80	11.00		1080	09:3	9.67			11.20	15,50	-	4.23 3.58	70001	10.60	14.80	11.60	14.50		22.83 11.80	11.50 20.80	27.80 21.60 1.33		16.50		13.80 28.50 19.80	11.20
24 FILENSING OF	8.80	6,00 6,00 13 cs		12.40		8.2	202		-	27.50	11.00	21.00	0.40	7.60 9.00 6.53		83	71.40	11.20			68 65	11.80 8.67	10.60	•		14,00	11.50	22.83 11.89	11.60 20.80	27.50	 07: 1	28.55 52.53	11.20	13.80 · 28.00 · 19.80 · 19.80	11.20
THE FREE CHANGE	8.80	6.80	999	96	12.20	82.2	7.00	8	. 82	27.80	11.00	27.00	9.40	7.80	:	83	71.40 8.6396 	11.20	15.60	2.65 2.40	68 65		10.60	14.80	7.80	280	8	3.50			278	14,00	11.20	2	11.20
THE THEOSINA DO	budding untirtibited by benutrihidazolos 1 8.80 8.40 ESTs	ESTs 9.20 ESTs 6.80 History bans 9.20 1.550	Bend CLAymythoms 11A (zinc finger pro ESTs, Whealty timilar to 139/22 hypotheri	ptcr0701010,s Soares prany tumor NbNOT H errell student RNN activation complex, po errell student RNN activation complex, po	Notes treast enter the control potent	hypothelical protein 1,80 Homo supleme cDNA: EL223503 fs. come L	ESTS, Wearty similar to 12XX, HUMAN TRANS 23.00 hypothetical protein FLJ13490 7.00	gramadulas belangene Ang cercanona 3.50 s.cu KJAA0129 gene product EST	ESTs 87.00 ESTs, Weathy similar to 664054 hypotheti 3.02	claudin 1 ESTs, Roderistoly shrikar to 565657 alpha ESTs, Roderistoly shrikar to 565657 alpha Farmedomin adjusted to shis flower down 7 10	Outstanding lighter to the upper come (1.00 gb:E81372594 MAGH Horno gb:E81372594 MAGH Horno (1.00 gb:E81372594 MAGE resequences, MAGH Horno	phosphoghreatele mutase 1 (brain) Ref.GEF-like protein 3, mouse homalog 21.00	KOAN1622 protein 9.40	ESTs, Weathy striller to T33298 hypothef ESTs, Weathy striller to LCT2 HUMAN LEUKO 6.59	ESTS ESTS, Westby similar to 2195_HUMAN ZINC	Homo sepiens, Similar to KIAA0052 gens p 8.20 ESTs	hypothetical protein DKF2g78ZD035 ESTs	procepting/mostra great, cass Procepting/post Act (120 phyothetical protein that (1420 colony) are as a colony are a secure transmitted transmitted to the colony are a secure transmitted	ESTs, Halihy similar to 1814/80A p.53-ass . 15.50	ESTs ESTs gbym(8009.1 Somes intent brain INIB H	99	University of the second and seco	CGI-18 protein 10.50 solution ambio solution carder lamily 7 (cataoria ambio	ESTs 6.50 ESTs 6.50 14.80 cOM, and a different state of the company of the compan	ESTs, Weatby sinitar to KOAA0758 protein 7.60 (1.50 physics) of the Spares letter free sphere.	hypothetise protein FL 10,332 hypothetise protein MSC10946 hypothetise protein MSC10946 hypothetise protein MSC10946 hypothetise protein RC10946 hypothetise protein RC109	nuchear phosphoprotein similar to B. cer 7.50 hypothetical protein FL/21634	soffing much 6 Listo Consistent of the first memory (937	101	ptrystactive formers infant brain 1NIB H got.Egy54026 Fettal heart II Homo sapiens ers	SEC24 (3; care-states) related gene famil 3.10 choride channet, carchan activated, fam 2.78	EST87. Homo legations CDNA FLJ11458 fts, close HE 14,00 Homo sealess mBNA for KIAA1729 metals	ESTI 11.20 ESTI Moderately strater to TOUO94 A-kin 2.80 ESTI Moderately strater to TOUO94 A-kin 2.80	Forms suppress, Contra mouse, Limitory, Contra Calaboratory, March 19, Suppress, type 1V, stoppe 3 (Goodpesture NAAU) 86 serie protection.	E81a
	8.80 building unhibited by benzhridszobes 1 8.80 8.40 8.40	6.80	Bend CLAymythoms 11A (zinc finger pro ESTs, Whealty timilar to 139/22 hypotheri	ptcr0701010,s Soares prany tumor NbNOT H errell student RNN activation complex, po errell student RNN activation complex, po	Notes treast enter the control potent	82.2	ESTS, Wearty similar to 12XX, HUMAN TRANS 23.00 hypothetical protein FLJ13490 7.00	gramadulas belangene Ang cercanona 3.50 s.cu KJAA0129 gene product EST	ESTs 87.00 ESTs, Weathy similar to 664054 hypotheti 3.02	27.80	Outstanding layer in the way of the control of the	phosphoghreatele mutase 1 (brain) Ref.GEF-like protein 3, mouse homalog 21.00	KOAN1622 protein 9.40	ESTs, Weathy striller to T33298 hypothef ESTs, Weathy striller to LCT2 HUMAN LEUKO 6.59	ESTS ESTS, Westby similar to 2195_HUMAN ZINC	Homo sepiens, Similar to KIAA0052 gens p 8.20 ESTs	hypothetical protein DKF2g78ZD035 ESTs	procepting/mostra great, cass Procepting/post Act (120 phyothetical protein that (1420 colony) are as a colony are a secure transmitted transmitted to the colony are a secure transmitted	3.20	ESTs ESTs gbym(8009.1 Somes intent brain INIB H	89	University of the second and seco	990)	ESTs 6.50 ESTs 6.50 14.80 cOM, and a different state of the company of the compan	ESTs, Weatby sinitar to KOAA0758 protein 7.60 (1.50 physics) of the Spares letter free sphere.	hypothetise protein FL 10,332 hypothetise protein MSC10946 hypothetise protein MSC10946 hypothetise protein MSC10946 hypothetise protein RC10946 hypothetise protein RC109	8	soffing much 6 Listo Consistent of the first memory (937		ptrystactive formers infant brain 1NIB H got.Egy54026 Fettal heard II Homo sapiens ers	SEC24 (3; care-states) related gene famil 3.10 choride channet, carchan activated, fam 2.78	EST87. Homo legations CDNA FLJ11458 fts, close HE 14,00 Homo sealess mBNA for KIAA1729 metals	ESTI 11.20 ESTI Moderately strater to TOUO94 A-kin 2.80 ESTI Moderately strater to TOUO94 A-kin 2.80	Q;	E81a
	8.80 building unhibited by benzhridszobes 1 8.80 8.40 8.40	Hassaco Estra 9.20 Hassaco Estra 9.20 Hassaco Estra 6.80 Hassaco Estra 6.80 Hassaco Hassaco Hassaco 10.50	Ha. 130831 Best CL. Amerikana 11A (that finger po Ha. 284235 ESTa, Whathy shrift to USAC22 hipsubali 6.06	dozyjiddio i Soare overy tamor NbHOT H Hs. (1931)	Hs. 21057 For the Forting to the service of the ser	Hs. 98906 hypothelical protein 7.80 Hs. 109363 Homo appliers cDNA: FL125503 Rs. ctore L	Pt. 1555-9 E61s, Westry smiler to 1223, HUMAN 1KANS 23.00 Hs. 282877 hypothelizal protein FLJ13490 7.00	Gurandu is branging and carbona 3.50 Hi 17770 MAKO129 gene product Hi 17233 EST EST	Hs.281713 ESTs, Whatch similar to 864054 hypothed 3.02	Hs.7327 claudin 1  Hs.7327 claudin 1  Hs.7327 claudin 1  Hs.7327 claudin 1  Hs.7329 ESTs, Moderately strikar to 665657 alpha  Hs.7329 ESTs, Moderately strikar to 665657 alpha  7.50	Hs. 102201 Horn scales FRIAN, CASALUZO (F 11.00 pb.ES/1772594 MAGE reacqueures, MAGH Homo (16.00 pb.ES/1772594 MAGE reacqueures, MAGH Homo	xmpHz, 181013 phosphoghycarde mulase I (brain) Hz, 127826 RafGEF-lae protein 3, mouse homolog 21.00	Hs. 93972 KOAA1622 protein 9.40 Hs. 100258 E8Ts :	HS.110540 ESTs, Weathy strillar to T33298 htps://doi.org/10.100/ Hs.100105 ESTs, Weathy strillar to LC12 HUMAN LEUKO 6.59	Hs. 1027.20 ESTs Hs. 133554 ESTs, Weathy similar to 2195_JHJMAN ZINC	Hs. 134159 Home supjerns, Similar to KIAA0092 gens p 8.20 Hs. 188501 ESTs	Hs. 140197 ESTs.	PLS-100-92 PROSPILIDO/UTBACH BJP-81, CR89 - C.BU PLS-5677 - Physchiedus Placed R-5 PLS-255 - C.BU PLS-2577 - COVA, Drawnia Breakfu Famenda 5	Ha. 168833	Hs.9904 ESTs 2.65 Hs.9904 CD.yml (9009.ff Scares infant brain 1/13 H	Hs.82109 emdecan i Hs.35408 ESTs, Helpfy further to unnamed protein Hs.35408 ESTs, Helpfy further to unnamed protein	Ha.44648 ESTs formes fortal forme spleen 6.67	Hs.285847 CQL 18 protein 1050 Hs.184601 solute center tenthy 7 (reticnic embro	18.20333 E819 6.50 p.cz/5602.1 Percentific bitel Homo sepi 6.50 H-65617 c404. for differentiative moments and CO16 6	Hs. 57887 ESTs, Weadly dintar to KOAA0758 protein 7.80 11.80 pht/fish07.s1 Sozers_feld_feer_splean_	Hs. 2003 hypothetical protein FL 10.032 Hs. 17094 hypothetical protein MCC 10946 8.00 Hs. 707707 Hp. non-resident SONA FL 12134. B. done C. 297	Hs. 172589 muchan phosphoprotein similar to B. cer 7.50 Hs. 97056 hypothesized protein FL/21634	Ha.284291 sorting meth 6 Ha.137401 ESTE Ha.137401 ESTE Obc.meth.Ha.137401 (237	Hs. 46801 sorting neath 14 gares_NFL_T_GBC_61 Nome s	Gryg-2-CUT, I Sources infant brain 1918 H GDES(3540)26 Fetal heard II Homo aspiens 14 Portees.	Ha.81894 SEC.24 (S. caravitias) related gave land 3.10 Ha.241551 Chords channel, calclum achirated, fam 2.78	HI 170819 EST8*: HI 17566 Homo expires CDNA FLJ 11458 fts, clone HE 14,00 HI 17571 Homo expires nPINA for KIAR 1779 mnteh	11.20 14.5.150	Has 100328 Selfie appears, Louise mouse, vices, instructor, continues, table 1859 Selfie appears, Louise mouse, vices, instructor, continues, table 1859 March 20 (Coodpastures Ha. 539 NAMIOSS Genes percent appears and table 18534 NAMIOSS Genes percent and table 18534 NAMIOSS GENES	Ha.133993 E8Ta
STITUTE OF THE STITUT	8.80 building unhibited by benzhridszobes 1 8.80 8.40 8.40	AZZOOS HASSOZ ESTI . 9.20 AVZOOS HASSOZ ESTI . 9.20 AVZOOS HASSOZ ESTI . 6.00	Ha. 130831 Best CL. Amerikana 11A (that finger po Ha. 284235 ESTa, Whathy shrift to USAC22 hipsubali 6.06	AMERISES GENERAL SCARRE PREVIOUR HAND TH 24752 Hs. 178312 small souther RNA activating complete, po LATESTAC Hs. 1981 OF EST, Washing Industry Incomment review 1970	AUXIA14 Pa.11274 ESTs 12.004, reteary serious to sementary protection of the control of the cont	AVXXXV452 Hs.89806 hypothaltesi protein 7.80 AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	EE-50112 PLS 1565-99 ESTS, Yearry enter to 1200, HUMAN TRANS 23,00 AR083088 PLS_282877 hypotheta protein FLJ13490 AR083088 PLS_282877 hypotheta protein FLJ13490 AR083088 PLS_282877 hypotheta protein FLJ13490	Gurandu is branging and carbona 3.50 Hi 17770 MAKO129 gene product Hi 17233 EST EST	AI/47155 Hs.270016 ESTs 87.00 BE387335 Hs.283713 ESTs, Whatdry similar to 884054 hypothed 3.02	AF134160 Hs,7327 cleadin 1 27.80 1795539 Hs,218549 EST), Rodinately timitar to 865657 aphs 27.80 A487314 Le Bells homodynathy discord to this force from 7 20	Hs. 102201 Horn scales FRIAN, CASALUZO (F 11.00 pb.ES/1772594 MAGE reacqueures, MAGH Homo (16.00 pb.ES/1772594 MAGE reacqueures, MAGH Homo	AUSGU 19.comp14. (B1013 phosphoglycerate mutate 1 (brain) BESSO182 14, 127826 RafGET-Re-protein 3, mouse homidog 21.00	AKGOO423 Hs,83872 KOAN,682 protein 840 AKSOUSD Hs,107258 ESTs :	HS.110540 ESTs, Weathy strillar to T33298 htps://doi.org/10.100/ Hs.100105 ESTs, Weathy strillar to LC12 HUMAN LEUKO 6.59	132962 Hs. 103720 ESTs A057052 Hs. 133534 ESTs, Westby striker in 2195 JUMAN 2NC	AA236743 Hz. 134159 Homo septem, Similar to KIAA0092 gens p 8.20 AA771590 Hz. 186501 ESTs	Hs. 140197 ESTs.	42.15987 14.160842 prosprincytroster prest, cass - a.co. AA515800 14.5677 hypothekein protein AF40225 (11.20 BE174587 14.259773. promy armst stoeffit transcriet 5	Ha. 168833	M868.9 Hs.89804 ESTs	BE272506 Ns. 82100 syndroan i AUST/11 bis 35400 syndroan i AUST/11 bis 354	Ha.44648 ESTs formes fortal forme spleen 6.67	AW614529 Hb.283847 CGH-18 protein 10.60 AV283809 Hb.184601 soutle center termity 7 (restoring embro	18.20333 E819 6.50 p.cz/5602.1 Percentific bitel Homo sepi 6.50 H-65617 c404. for differentiative percent of 0.516 6.50	ANDSB104 Hs.57887 E.STs, Wheathy similar to KOLAU768 protein 7.80 (1.60 ANDT8910 (bh.278507.41 Source_feld_feld_feld_feld_feld_feld_feld_fel	A443704 Na. 2083 Pripolatica protein LJ 10.032 N49776 Na. 176994 Pripolatica protein MCC1092 AAPTS6118 Pripolatica protein ACC1092 202	AW805510 Hs.97056 hypothetical protein FL/21634	Ha.284291 sorting meth 6 Ha.137401 ESTE Ha.137401 ESTE Obc.meth.Ha.137401 (237	A279592 Hs. 46601 cortionarin 14 A809521 cp. A700003.4 Source AFL, T. GBC, 61 Homo s	R25006 Gray 42:07.1 Source Intent train 11/1B H A2407050 Gray ESES 50.20 Fetal heart II Homo sapions AARTHT 14 TOTTEE EST.	ACUSOS 18, 81994 SEC24 (S. crandita) related gene famil 3.10 BEO02109 Hs.241551 Oblodde channel, catchin achieved, fam 2.78	AA319333 H1,120879 EST8*. A002011 H5,47546 Hno tephon eDNA FLJ11458 fb, clone HE 14,00 A80738274 H7 1540 Hnon septions mBNA fir KIAA1720 metals	ANSTASS National Series and Anstalla Series (120 ANSTASS) Regulate (	Has 100328 Selfie appears, Louise mouse, vices, instructor, continues, table 1859 Selfie appears, Louise mouse, vices, instructor, continues, table 1859 March 20 (Coodpastures Ha. 539 NAMIOSS Genes percent appears and table 18534 NAMIOSS Genes percent and table 18534 NAMIOSS GENES	AISA3257 Hs.139993 E8Ts

O 02/086443 AFW5239 Hz,221576 AAGM1103 Hz,843 AAM34157 Hz,8823 ADM1528 Hz,8718 BE268236 Hz,9718	D2849 14,50017 EST XAUXOTT problem  8,501025 Aux 6,0017 February 2011	13.50 6.46 10.00 10.00 8.00 P	TABLE 68 shows his seconstain numbers of glockscholders were deligned. Gene du emittarity uits Charante and Algoment II. Accession Column. Perry University States CAI common Consultation of Characteristics CAI common Consultation of Characteristics (Second Consultation Con	30 Acesticinic. General acesticin numbers Play CAT number Accession numbers 35 (1701) 1821/17_1 182123.197135 1015/21_18222_46 NASSESS	18724 74694 1 RESEA 1 RESEA PORT 1870 1 RESEARCH PRICE RESEARC	153222 153222 17411_1 180555_1 282419_1 13522_1 150742_1	115353 115111 1 1 1 1 1 1 1 1 1 1 1 1 1	100554   pobbled_AU08548   AU08548   AU08548	ALIBERA DAVILLIS MESCEZ AURIZZO AURIOS ALORGOA ALGORIA DERBORA ALGORIA PAREZZO AURIOS ALORGO PALEGO PER	ACTION OF ACTION
PCT/US02/12476	977.			85.85 5.85	35 84 4	1858 (- 4.23 (- 4.53 (-)	88 85 5 84 5 85 5 86 5 86 5 86 5 86 5 86 5 86 5 86	168 188 188 188		3558 <b>9</b>
		13.20 19.20 19.80	15.83	9.43		10,80	17.80	13.00	14.74	. 67.8
8.40	•							8.20	24.60	
18.00 56.00	23.0 21.00 27.0 27.0 64.0	28 28 27 27 28 27	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	85 8	Secretar		9 ·	r 40 8	9 88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	13.60
topokomense (DNA) il ajma (1704). ESSI E. ESSI			SiMC) (Liverbul antiherance of chronoso proble registra of cytichests 1 (2) Abbare registra of cytichests 1 (2) Abbare registra of cytichests 1 (suboperic bore month-operator proble / (suboperic 2) ( historine Semilyfransitess   hypothesized camples of proble systems (liverbul of cytiches / (suboperic probles) (suboperic pro	guerden considered behanding perinden (15 pr eerbe (or cytished) productions shickly. 4.55 photocontering behandings and 2.17 SACT (suppressed or self nanishens 2, externof transition bildison inexis and	Los Is, Nesdy among to Yach, Exis Introl.  3.0 Gold groten 3.0 Farrance, founder (A. 2 albu jech z. 1.6) chee Hoost (O PROXIV) (A. 1.6) 2.0 2.0 Chapter, Carlon and Carlon and Carlon 3.1 2.0 Chapter, Carlon and Carlon and Carlon 3.1 Chapter, Carlon and Carlon 3.1 Chapter, Carlon and Carlon 3.1 Chapter, Car	high-modally group fourthickne chronoso RMA binding nodil groties it. RMA tondrag nodil groties it. Ambit (Toncalphila) hormolog (simonphales endres i. (gibra) quantes modeolde binding protein (G pr etaudin endeolde binding protein (G pr etaudin.) 255 phylind-cytochrome e reductasa hinge p	profit proficial profits (2014) gradin profits (2014) hypothetical protein MGC1433 ELV (embryothetical protein MGC1433 grych-first profite isnat, anomal vistor, grych-first profitation is and propriates 1, exhibit is and propriates 1, exhibit is profite carter senity 2014 proteins-chi 5 inchibit is profite carter senity 2014 proppiats ten	Act. record presents (now.) py function of the		
3 6,3402 8,3472 8,34720 8,35120 8,35120	Ha. 35978 Ha. 35878 Ha. 40088 Ha. 40202 Ha. 54560 Ha. 41270	1,4801 1,4805 1,4806 1,3048 1,4801	50768 5101 51011 5170195 52756 5338 5338 54451	2,59381 2,5579 2,58407 1,169407 1,57783 1,234698	15153	1,139600 1,65648 1,66744 1,65744 1,73112 1,73112 7,327	173826 174316 174316 175236 175230 175333 1166975	770790 1,72878 1,73878 7,7877 1,7877 1,7875 1,7875 1,7875 1,7875 1,7875 1,7875 1,7875	Ha.79432 Ha.181634 Ha.701914 Ha.77881 Ha.80978 Ha.82720 Ha.82720	8000 80753 80753 84131 84131 250370 250370 8739
O 02/08 JOUGE BESOZAI AMSGOSS NIK_002816 NIK_014062	13200 AWATOTO HI 12200 AWATOTO HI 122109 AWA90302 HI 122114 AMA90302 HI 132184 AMA90303 HI 132184 AMA90303 HI 132184 AMA90303 HI 132184 AMA90303 HI	AMBERS11 NAL 014210 AMBES910 AMD01745 NML 014787 AMD01680	T78738 BE568452 L19778 AW969253 BE621865 AK000631 AF037335 A796870 Z15008	W38566 W74001 Y10276 W73311 U76525 AW634050 BE613337	AA57633 X77343 AA117748 AL04244 X73424	L17131 AF19962D M68583 X91662 BE267696 U41453 AF134180	133433 AESSOOG HA. 13350A HA. 200416 HA. 13350B EESESSOS HA. 13352A HA. (2020A7 HA. 13352A U75545 HA. 133563 NA. (20632 HA.	AD01165 AJ001234 N55540 BE2762528 BE513171 NM, 005629 AW449809 U16174	198162 AA39998 AA295138 L15035 X76040 BE083938 AL139201 AA33949 AU077143	1342 H5497 Hs. 1346 A27961 Hs. 1347 X5647 Hs. 1347 X5647 Hs. 1346 R61653 Hs. 1345 R61653 Hs.
'n	10	15	52		40	45	\$\$ 6		07 27	85

A MASTERS AACTSTTA ANYSOTTA VESSET RECTED AACSSOS AACTSTSS ANYSTSS AACTSTSS AACTSTSS ANYSTSS AACTSTSS AACTSTS AACTST		S	10	15	20		25		30		35	} .		40		45	!	ç	3.		22		09									
PCT/TICS  - ACRESON ACCESTOR AND ACCESTOR AND ACCESTOR AND ACCESTOR ACCESTOR AND ACCESTOR ACC	002/12476 okt nbezke nbazer s amzkeba		nts on the stand vatus reflecting		carchona Ith aquamous ceil																											
AAASTRO AAASTRO AAASTRO AAASTRO AAATSTO AAASTRO AAATSTO AAASTRO AAASTRO AAATSTO AAASTRO AAATSTO AAASTRO AAATSTO AAASTRO AAATSTO AAATSTO AAASTRO AAATSTO AAATST	PCT//IS NOTES AND SES AND 4210 AND SES 14 AND SES 54 AND SES 55		These genes were selected from 53680 probes ras expressed as everage intensity (Af), a norm		ands of AI for samples from smokers with edence Oth percentile of AI for samples from smokers w	. K2		246 1200 268		950 950										929	888						85.25 88.55					
102/086413  AAAGST AAAAST AAAAATT AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAATT AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAATT AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAAATT AAAAST AAAAST AAAAST AAAAST AAAAST AAAAST AAAATT AAAAST AAAAST AAAAATT AAAAST AAAATT AAAATT AAAAST AAAATT AAAATT AAAATT AAAATT AAAAATT AAAATT AAAATT AAAATT AAAATT AAAATT AAAATT AAAATT AAAATT AAAAA	B AAZZETZ AWSGOTR WZGRZ ROCZEZ AAASSCO AASTGGG AA Dysgety a migsy aangelgg awszyst kaasgot aagstet aa 1 aagsggg wigso alibszba anzłost a reissz	AA277834 9 AA88646	onsmotera with larg carcor relative to smokers with larg carcos. I are expression data for each probered obtained from the analysis w	ntiter number ther, Genbank accession number	s form non-unokens with adenocarchoma divided by the ROD perce s from non-emokens with aquemous cell carchoma divided by the K	Unigene Title R:		thyroid hormone receptor thereoper 11 thyroid hormone receptor this recipion 6 E.(10) capet in blanches mare in 12 females											92.th	Ì					netical prototon FLU11362	_	nuchear receptor audiemily 1, group l, m Homo saplens mRNA; cDNA DNFZp584N1063 (		Weathy similer to ALUZ_HUMAN ALU			
9 0 0 2 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 8 0 0 0 8 0 0 0 8 0 0 0 0 8 0	54-43 AA4387 AA2093 A128862	45552 W45552 Bayah Residu Azzara 1102 Azbioz AM983	es up-regulated i mechip array. G tA expression.	Eos probesel ide ar Accession nur i number	t gano tife of Al for sample of Al for sample na	UnipenelD	Hs. 83213 Hs. 280	Ha. 65092 Ha. 6665 Ha. 112404	4 1584AD	Hr.2442	Hs. 161640	Hs.150402 Hs.45033	Hs.21355 Hs.83623	Hs.196701 Hs.296244	Hs.30643 Hs.18282	Hs.32501 Hs.194478	HL.57887	Hs.292633 Hs.892653	Hs.22672 Hs.310764	Hs. 258989	Hs.72249 Hs.14629	Hs. 710457 Hs. 26026	14.7246	Hs.103042 Hp.31137	15.8764 14.8929							
	02/08(	Perbant, Per	ione 89 gen Mx Hu03 Ge level of mRN	Chipus Exempli Unigens	r Unipers everage everage certanon	EvAcm	3E379727	Y12490 4A001024 44586894	582472	NA (00381)	X52509 X98266	LO2911 AIO7679S	AB002367 AW373062	AA055829 BES14788	H47233 T66887	4A156238 243846	A035375 A100796	BE219231	R44607 A1004874	H24458 R94207	AW274992 179639	AF071594 R53972	123699	438342 4001333	(48011 (4958672	M52854 W32854 W33078	W17058 A4235609	ANYBERASS WELESZ	AA481768 H61037	ABV62173 HS0875 AF088019	AF217525	AA923278

ALBLE Before the excission interest for these primarys lacking uppealing in stock. A reduced were that the greatest primary and opportunities and excission interest to the excission interest and excission for a facility of the excission and excission for a facility of the excission and excission for the excission and excission for the excission and excission and excission for the excission and excission for the excission for the excission for the excission and excission for the excission and excission	enterbackets was defined. Gene chaten were compiled units sequences defined from Gethand EGS a not mRNAs. These sequences were chatered based on responsibility using Collecting and Algument Took (Doublet Fink), Coklend California. The Genhard accession numbers to sequences computing each chater are Ishaf In Parksension Codem.  **Accession Codem.**
Pkey: CAT number Accession:	Phay: Unique Era probeat identifier number CAT furmber: Gene datas number Azzestor: Gen'sant azzesson numbers
Phony	CAT rumble Acceptions
108562 100439 123551 123861 102832 101972	38373-1 AN 100786 AFGECKER AND AFGES A

PCT/US02/12476

15.50 15.50 8.50 20.00 11.50 6.10

MAYDESS NESSES (MAYDESS NESSES)

MAYDESS NESSES (MAYDESS NESSES)

MAYDESS NESSES NESSE

TT/US02/12476 6980 protests on the , a normatized value reflecting		In adenocarchoms. tokers with squarrous call					٠.																						
PC hang cancer. These games were selected from bringles was expressed as everage interestly (A),		everage of Al for semples from non-emokers will ed by the everage of Al bor semples from non-sm	₽	164.10 77.40	77.20		103.10		58.80 268.80	212.10			71.00		03.40 03.40 03.40		58.70		78.70 120.20	: 8:6		351.60	83	91.10		_	104.90		
WO 02/086443 Table 74 shows 30 pains connecting the non-amplear with tang cancer nables to ampleas with large cancer nables to ampleas with large cancer nables to ampleas with tangeness were sealched from 5000 probests on the could have done cancers and the such probess to date on the market was expressed as everage intentity (AI), a normatized return minding the address were ampleas of the country of the co	Uniquo Esa prodocal direstina number Esercitya Accession number, Centaint accession number Uniques number	x samples from smokers with adenocarchrome divided by the x samples from smokers with aquamous cell carchroms divide	Uniperse Title R1	edo-kalo reduciase family 1, member C3 namobilations deson fatue) protein cacionintesticimin-relate porpopiel 102.4 fath acid briding norbie 1, addocrina 40.18	(NONE) Charol-Layden crystal protein metanoma entigen, temity A. 2	homeo box 45 62.80 HZB Mittone furth, namber O 78.00 complement component Labrating protein, 198.30 days decimal components Labrating protein, 198.30 hardrowers of 80.00 hardrowers for the further person of 80.00 hardrowers for the 80.00 har	dalytiransterase relindo acid receptor responder (tazaro maznophaga stimulating 1 (hapakocyta gro	hepshocyte nuclear (actor 3, arpha dust specificity phosphates 4 eyes absent (Drosophila) homolog 2			gb:Hastpiens DNA for endogenous retrovir 64.50 KIVAD300 protein 65.80 cell eitheston moteode with homotogy to 63.80	solute carrier family 4, sodium bicarbon ESTs	ESTa, Weatly straign to ALU1_HUNAN ALU S ghulamata-cysteine figuse, catalytic sub ob:50118016E1 ATH ANG. 17 Honor scriens o	Homo septems mRNA; cDNA CNC 2056/19076 (th. 83.90 hypothetical protein AF301222	hypothetal probability 120417 ESTA, Moderately shrifter to 2102260A B c	erith (Dresophia Scraps homolog), act E8Ts	EST	ESTs 75.40 EST 74.60 ESTs. Moderatory similar to A45310 X.9 64.80	Homo seplens mRNA; cONA DKFZp761J1324 (I microtubule-ussociated protein 18	Homo sapiens CDNA: FL/23123 fs, clone L 174.00 hypothesical protein FL/19461	Abosomal protein L13 ESTs, Westry similar to DAP! HUMAN DEATH	rypowacca protein FLJ 109/0 hypothetical protein FLJ 20093 hypothetical protein FLJ 20093	gb3fUMGS0Z848 Human adult lung 3' direct gb3z32g08.s1 Morton Fetal Cochlea Homo	EST 61.60	ESTs 64.40	major histocompatibility complex, class 188.60 gb:ab 1900z.s1 Stratagena lung (937210) H	EST 71.00 ESTS, Weakly similar to JC7728 amino aci ESTS, Modernary similar to ALUT, JULMAN A		
WO 02/086443 Table 74 stons 99 pens down-eguid EcstAffmeth Hud3 Genecity errey. The relative level of mRNA expression.	Play: Unique Eca probessi I Exicori Exemplar Accession in Uniquenilit. Uniques remoter	University to the Congress game and Rt: 800 percentile of Al to RQ: 800 percentile of Al to carchoma.	Phoy ExAcon UnigenelD	D17783 Hs.78183 D82343 Hs.18551 X00356 Hs.37058 BE379727 Hs.83213	KOT160 AW970254 Hs.889 U82671 Hs.36980	101487 WXS150 Ha.37034 101663 NIA_003528 Hs.2178 101577 NIA_000715 Hs.1012 101745 MS9700 Hs.150403 101441 S77541	NM_006456 Hs.288215 U27185 Hs.82547 U37055 Hs.278657	U33840 Hs.293857 NM_001394 Hs.2359 U71207 Hs.29279	ALG79548 NM_006163 X77790	X76342 Hs.389 X78416 Hs.3155	AB002296 Hs.173035 AF002246 Hs.210863	AF007216 Hs.5462 AA126311 Hs.9879	AXA9583 Ht. 151393 8E29210	AW772298 Hs.21103 AA648459 Hs.335951 AW75485 Hs.705640	H 1936	AK001468 Hs.62180 AA989362 Hs.283780	T65568 Al743880	R63503 Hs.28419 R23924 Hs.23596 T03927 Hs.283147	AL157426 Ps.133316 N38342 Ps.103042	H. 124292 H. 122579	AW905329 Hs. 180842 AW872527 Hs. 59761	AL133916 Hs.172572 D20538 Hs.184849	DAS652 N66741	AA398209 Hs.95473 AA398209 Hs.97587		AI716702 AA487200			
	3	2		5	္က	5	•	0	9	,	0				0		S		0		2		0		S		0	S	

1/8EE 78 shows the accession number by those planebys techny uniqued/by to Tebe 7. For each prognocularities were declared. Gene obtains were complete taking sequences downed from Genhan's EST in additional, Time Genhan's EST while yeary Construction and Algorment Tools (Double Finkt, Challand California). The Genhan's accession in Vecesarian's colors.

3

22

Ptay: Unique Ece probesal Identifier number CAT number: Gene chalte number Accession: Genbank accession numbers

PCT/US02/12476

130 S

25.55 52.55 53.55

xoteh ans oDNA FLJ11640 fa, clone HE

ah 36 (KOX 18)

78.90 106.90 59.63

71.00 68.40 69.30 73.53 108.30

133.20

ន

8

88

23

125

4.4.3 ESTs. Practical propertial channel 6 No. 165140 UDP-Cathaelockelve beta 1.4 generatests No. 165140 UDP-Cathaelockelve beta 1.4 generatests No. 165270 Maier call beta-that messages untutates No. 165277 Maier call beta-that messages untutates	20223 ALO4937 He 166361 Home applies mONA, CONA DICTASALF112 pc 168 20220 ALITHOUTH HE 178202 Home applies mONA, CONA DICTASALMINS y 1.00 20220 ALSS408 He.22200 Home applies CONA FILLSON St., Cone pc 202204 ALOSS107 He 184225 Great, cyclopisersh, light harmedide 227 202204 ALOSS107 He 184225 Great, cyclopisersh, light harmedide 227 202204 ALOSS107 He 184225 Great, cyclopisersh, light harmedide 227 202204 ALOSS107 He 184225 much de monitoremide 227 202204 ALOSS107 He 184225 much de monitoremide 227 202304 ALOSS107 He 184225 much de monitoremide 227 202304 ALOSS107 He 1842207 much de monitoremide 2014204 much	Hs.211956 CO3-spetten-essociated protein; entisons Hs.218028 adaptor-related protein complex 4, speti	Ha.225574 KUAA1054 protein Ha.275534 Home speker smRVA; cDNA DIGF2p584U082 (if Ha.272775 also codit homeobax (Drosophila) homeob Ha.272777 UDP-Neceshydpoosemines i Ja-G-marroadi	AA156223 Hs, 340770 nucheer cap binding protein enbenil 2, 2 AA11761 Hs, 5332 F. SMYSTE Hands, marks encodated, seel AF10229 Hs, 241573 US enfitth-seasoriand Smiths protein LSmit 700509 Hs, 230424 Home suplems GDNA FLI3590 fs, done Pt.	AU06565 AU06588 AA085986 AB029488	A445379 Ph 102559 MGT-1 protein A27373 Ph 189273 NGM heinydropense (ukquhone) 1 bela a A273782 Ph 196274 ESTs STS PROTEIN Home seylen, dare IMAGE2223131, m894A, A375020 Ph 277014 Home seylen, dare IMAGE2223131, m894A, A375000 Ph 277014 Home seylen, dare IMAGE2223131, m894A, A37500 Ph 277014 Home seylen, dare IMAGE3223131, m894A, A37500 Ph 277014 Home seylen, dare IMAGE323131, m894A, A37500 Ph 277014 Home seylen, dare IMAGE32314, m894A, A37500 Ph 277014 Home seylen	Microsco, manusco, so fortunamento Officiary Epithel Historia AWY 1923 H. 48.38219 EST AWY 1923 EST	WRS773 Hs.28855 hryshelte grotel F.12520 62-50m apera (chox WRA, 10VH) erich AVX28418 Hs.18272 ASA,1655 probin HB6170 Hs.42522 E.STs	A124506/ A1245313 Hs.772838 Y08250 A4447824 Hs.293811 N31301 Hs.152664 x69400	AL137763 AISB1344 AW263124 AF078950 AF080405	FOTTSS NA. 255555 RABZZA, member RAd sonzopene family. AF161822 NA. 27553 poptifylolybe lommers (cycloplan)- AF163305 S. AF16230 And AF162	M-ZT2055 I NELSUTTO NAZZAH MANDELI HL21880 OZZPONAH ALNZZELI HL22383 myskal, iphi kohipothika, neziakar, n ALNZZELI HL22383 SERIA ALNZZERI HL22385 EBIA		AVAIGOS NE 105 DAT APPLIAGE PAR INCHES POR ING POR INCHES POR INCH	A-MAGNICA HAZERRA PORQUENCE ECO DICEOPINADO DE ACA- A-MAGNICA HAZERRA POR PERE, ((1914/N°+ transporting, bell a po- A-MAGNICA HAZERRA PER PORTA (1914/N°+ transporting, bell a po- A-MAGNICA PAR PORTA (1914/N°+ transporting, beautica)  List (1917) promote de frances (1914/N°+ transporting)  List (1917) promote de frances (1914/N°+ transporting)	ANNETTA 16:171600 polymerase (FAVA) II (DAM devendo polyp ANNITRO 16:2005 (Polypera CDAM LATISOR) a, chone IA ANNISTATIO polymerase (PATA) IN CARP CARPA ANNISTATION IN ANNO PATHER IN LINE JAMAN ALUB ANNISTATION CARP (AND PATHER IN LINE JAMAN ALUB ANNISTATION CARP (AND PATHER IN LINE JAMAN ALUB ANNISTATION CARP (AND PATHER IN LAND PATH	AWS18449 gbx168005x1 NCI_CGAP_UZ Homo septem AWS18811 gbxp70b11x1 NCI_CGAP_DX Homo septem AWS18811 gbx166n02x1 NCI_CGAP_UZ Homo septem
302153 302202 302203 302208	30220 30220 30236 30236	302409	302427 302432 302435	302454 302472 302478	30255 30255 30255 30255	302647	302680	302715	302795 302802 302803 302812	302864 302943 30200 303006	303013 30309 303090 303090	303095 303131 303198 303198 303218	303234 303251 303251 303295	303/87 303/87 303/52 303/52	303658	303907 303978 303978 303981	303998
'n	01		15	70	25	30	35	9	45	20	55	09	. 59	20	75	08	82
WO 02/08/6413  Table M. covers 1720 person sinks or conversable for the conversable of the conversable of the conversable for	· · · · · · · · · · · · · · · · · · ·	82	4.63 0.08 0.44	0.85 2.28 1.00 809	12.78 4.58 5.55 5.50 5.50 5.50 5.50 5.50 5.50 5	0.65 0.65 0.65 0.75 0.75 0.75	588 - 588 - 592 - 593 -	6,545 6,244 7,461 1,561 1,561	5.56 5.56 6.00 1.50 1.50 1.50 1.50 1.50 1.50 1.50 1	1.08 0.37 1.54 14.28 0.08 0.08	7.18 11.56 7.78 7.78 1.78 1.79	0.78 1.61 1.51 1.44 6.02 8.45	0.00 0.00 1.00 0.00 4.70	8,79 6,79 1,38 1,38 1,00 1,00 1,00 1,00 1,00 1,00 1,00 1,0	5.45 13.89 12.00 12.00 12.00 12.00 12.00	56-8 37-7 175-7 103-8 103-8 103-1	1.20 3.87 3.87
ung reladiv A. emphy obtained t	r normal bag		12 FB 12 S	3 FR FR FR			28282	= 00 8 5	*******			wo≈+00	»	00000		mmo-0	~ ~
diseased I the fibrosed in probesed	rormel lang ille of Al K	2	\$ 5 5 5 5 5 5 5 5 5			13558					2 4 8 4 1 2 5 4 4 5 5 5 5 4 4 5 5 5						
or down-regulated in lung temors or struckeds expressed choose non-reductable lung diseases sor IZ Generally serse, Gene expression data by eas- te bred of mRUA expression.	Physic - Unique East probessed Manifers number Esboors - Excryption and the Command accession number Uniquentity - Unique number Uniquentity -	Unigene Tida	EST: EST: EST:		gbt-MSOPB121 normalized Frient brain cON ESTs ESTs ESTs	E.S.I., Mezzy straid to LZXZ_TOUNON LINC. Propodentical protein FLJ12401 hypothetical protein FLJ1191 frypothetical protein FLJ1191 gb:sb37401x1 Stratagene FELa cell a.3 53	EST hypothetiza protein FL72X33 KIAA1542 protein KIAA1527 protein ESTs	ESTa, Weakly similar to T0323 transcrip calclum channel schial Jelbani hypothetical protein FLIZ2023 Homo sopiera GONA FLIZ0428 fts, cone KA ESTa, Wenthe schiate in 11773 homelyal	gh: a003a10.st Strengene fedd reffins 83 ESTs ESTs, Weakly samble to unnamed problem ESTs	ESTs, Weatly similer to AF7/3845 i BH-00 ESTs ESTs, Weatly similar to 55/3990 mitogen   ESTs ESTs	ESTS ESTS ESTS ESTS ESTS	ESTS ESTS ESTS CMPed	zino linge protein 117 (HPF9) EST a spicing factor, ergiulmaterine-tich 1 ESTs, Hoderathy similar to 601251 Rar p i desi dila-crokonation enzome FPE 2 floron	DKFZP414F162 protein D15F37 (pseudogens) andin (prosophie Scrape horndog), eci http://creative.org/les.gens.gens.php.gens.gens.gens.gens.gens.gens.gens.gens	ESTs, Weathy similar to pN sensifine max gb.yc97g09.f1 Scares infant brein 1NIB H ESTs aboves lamp 1, member B11		
6443 pens elber t ng samples n Upmetrix Hut sing the relatif	Eas probess! If Accession in member gene title cardile of Al for strike of	UnipenelD	Ha.147474 Ha.147474 Ha.216286	Hs.197506 Hs.181394 Hs.288241 Hs.202090	Ha.314158 Ha.254516 Ha.146164	Ha.233655 Ha.233655 Ha.21838	Hs.128757 Hs.126280 Hs.130541 Ks.88840 Hs.188270	H-22858 H-192570 H-285901 H-285901	Hs.152454 Hs.312716 Hs.293744 Hs.269439	Ha. 208562 Ha. 208562 Ha. 208516 Ha. 165918 Ha. 201916	H. 247606 H. 128350 H. 128350 H. 128350 H. 128350	H.163369 H.126330 H.126330 H.1254635 H.254635	H-133011 H-134064 H-73737 H-27453 H-106323	Hs.7987 Hs.266132 Hs.62180 Hs.271986 Hs.271986	Hs.13861 Hs.117202 Hs.116724	Hs.27973 Hs.125166 Hs.23495 Hs.129716	Hs. 137508 Hs. 23244
WO 02/08/6443 BAthors 1720 pans electrol describing san sets on the Eosl/Mymetri fized value reflecting the	Unique   Ecompta Ecompta Nicumbers 70th per	EvAcon	AI916973 AW189787 AIS85661	A1989963 AW274682 A1469035 A1707881	242308 AIBS9947 AW270150 AM21541	AU362967 AW135830 AW135830 X85711 W27363	AW118822 AZ16113 AR23332 AAZ35361 AH92471	AIEBB147 244942 AIEB2897 AW449802 AIEB0356	AASO4860 AID41019 AW204069 AAS93373 AAS65209	AW136940 AW136973 AW136973 AA677570 AA728905	AA737694 AB08751 AA758115 AW297762 AA843088	A4812839 A4812839 AW450458 AA975683 AW272467	A1733621 A1077482 A1878939 243570 F05865	F07744 AA384252 AA581004 X17033 R20002	T71508 T78054 A1991127 AA344647	AW070252 T91418 N40834 NM_001501 AJ238381	AIZES 176 AW044300 AW2696 18
VV Tathe BA Chronical probesess normalize	Pagr. Erdon Hipened Ri: Bened Ri:	Play									20 20 20 20 20 20 20 20 20 20 20 20 20 2						
	10		15	70	25	30	35	40	45	20	55	09	65	92	27	80	82

emoglobin, elpha 2 bow/T0h12.s1 Bosres\_(etal\_liver\_spleer\_

Statistics of Somes, Jeal Jeac, Alchirity Statistics of Somes, Jeal Jeac, Alchirity Carrestotta, 1 Servized upon 19-1021 hom say transfectora, 1 Annaton Innia Corete ho transfectora, 1 Annaton Innia Corete ho transfectora (Jeans Joseph Marian Transfectora, Jeans Joseph Marian Transfectora, 1 Somes, Joseph Millery, St. Honos say Transfectora, Innia preparati, Johens, John William Somes, preparati, John William Somes, John William Wil

Hs.119122

Hs.111334 Hs.147333 Hs.246381 Hs.147885 Hs.77039 Hs.170573

Flooring prosess I is a grown process of the proces

HL 284136 Na. 307670 Na. 272572 Hs.249118

Ha.169476 Ha.119500

bop03c08.st Boares\_NFL\_T\_GBC\_8t Homo s bosomel protein L18s bor84607.st NCL\_GGAP\_LeS Homo sapiens

Ha. (62593 Hs.276083

6443	Ha.163593 Ha.276083	Ha.169476	78.1135W	Ha.207670 Ha.272572 Ha.240118		Hs.119122	Ha.111334 Ha.147333 Ha.248381	H17039		Hs.288262	Hs.276672 Hs.83753			Hs.275737	Ha.181165	Hs.283442 Hs.251577	H-169476 H-276877	Hs.181165	Ns.298768 Ns.278572		H-181165 H-105749 H-105749	Hs.96840 Hs.277117	Hb.101774	Hs.259408	Hs.2166 Hs.217493
WO 02/086443	AAS82508 AAS92304 AAS94304 AAS94500	A995686 A996248 1000320	. MOSEGO	U022565 U027359 U032589	A092465 A093987 A125111	U142774 U144243 U167439	A/208309 A/208300 A/214142	AI241715 AI242718 AI242718	AI243364 AI275055 AI281556	290285 290285 306428	333408	A1336092 A1342387 A1342731	47774 (1350558	U351826 U355761	365541 380462 434512	435240	458624	475950 476803 480123	AISCOGOD AISZOG32 AISS7029	55704	USK2963 U613519	650860 672425 716299	A1719893 A1736593 A1745040	U750864 U757143 U807405 U811109	AB11767 AB16289 AB24118 AB32332
WC	306510 A 306510 A 306555 A 306555 A	06582 A 06582 A 06588 A	06658 A 06676 A 06688 A	M 1920 M		307035		307410 A 307416 A 307416 A						307828 307820 307820 4				308101 A 308108 A 308122 A		306216 A 306216 A				308673 A 308697 A 308762 A 308778 A	
	ν. ·	.,.,.,.	2	15	2		X E	300	90		40		45		8	55		99	y		2		27	 	85
			_	_	,		~	67	,	•	4		4		'n	•	•	9	4	9	7			∞	∞
/12476																									
PCT/US02/12476																								•	•
٢																•									
			,																						
					•																				
11,08	2252	3282	2.5.5. 5.5.5.	725	5 5 5 8	8885	2258	25 88 £ 8	3525	និទ្ធិស	25.5	22	. S. S.	898	25.36	32.5	252	858	5253 5253	52.5	288	825	2532	222	25.28
8	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3233	\$ 8 8 E	255	1222	5,12,0 5,13,0 5,13,0 5,0 5,0 5,0 5,0 5,0 5,0 5,0 5,0 5,0 5	5.50 5.50 5.50 5.50 5.50 5.50 5.50 5.50	358	5	828	8 <del>2</del> 2	855	5.8	285	828	3 4 5 5	8 12 8	8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7 <del>2 2 3</del> 3	220	5.21 1.95	8.2.5 8.0.5	5839	258	310 367 367
	:	~*	£ =	Wei	- 95 8	TH I	rappen	aplens aplens						٤.	pjens	Subject	suado S de	apiens eapiens4.4 Eap	nodoma potes, isiga, Po gbot/saf02.1 NCL_CSAP, Nd8 Nome saplens 5.12 gbat/2008.1 Bantead spleen NPLR82 Nom 166 gbat/2008.1 Bantead spleen NPLR82 Nom 2.34	upiems	Homo s1.5	Homo spens			
	eukeryotic trenslation stongation toctor gü:FB2/B) Felta brah. Stratagene Homo s gü:FB2/C) Felta brah. Stratagene Homo s gü:FB7/C) Felta brah. Stratagene Homo sa	1 speen (9 ny (93721) 1 (937210)	NB24P H	and Care	pain) 259 s sclo 93720 etydrogen:	gp:EST6044 Fetal heart II Home statems gb:xx25g02 at Soemes_MN-HAPPu_S1 Home sapi gb:xx62x11 at Soemes oversy turnor MH/OT H gb:xx02x06.s1 Soemes_Lotal_Anta_Hb2HFB	ehydrogeni Inhibito 1.1 Komo s	nbosomus protein 823 gbrim/TB/11.s I NCL CGAP Co9 Homo septems gbrin13g98.s I NCL CGAP Co12 Homo septems		mmunoglobulin heavy constant gamma 3 (G brzu89h0t.s1 Soars. lestis_NHT Homo ssp brzb99c04.s1 Strategene lung (837210) H	24 Homo si	EST, Weath smile to EF10 HUMAN ELONG go: 957412 a1 Gestler Wilms tumor Homo s	w stroma i	t gamma 3	potervices a scarce per entyroc_paracy potervices as NCL CGAP_GC3 Home septem hypothesical protein FLJ11726	281 Homo	25 Homo s	25 Homo a CBO Homo Art Homo	8 Nomo sa N HPL RB2	S Homos	CBC 61	gc:ckGgg3.s i Soars NFL_T_GBC_S i Homo s gc:ck78g02.s i NCL_CGAP_GGA Homo sepiens gb:ck85h1.s i NCL_CGAP_KG3 Homo sepiens	to hamstere to Home to	4562 mbos	puppacata mula, con-una mula sapera popula professa (NC), CGAP, GCA Homo saplena popula popula (NC), CGAP, Kd6 Homo saplena popula NC), CGAP, Kd6 Homo saplena
a	on stongadt rain, Strator, um, Strator, in, Strator	fagene fets fagene ove fagene box	arge, P1 es placents ares brant ?	res John John John John John Po	me, macro degene mu hosphate d	Marting Tes Overy A	hosphate of proteinese CCGAP_Br	200		my constar nas lestis tapene lum	ayes a	ster Wilms	DOME HOLD	my constan	00.00 G	COMP.G	SOAP P	000 P	CCAP XX that sples that sples	8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	B Idnasa, 9	_ 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Action of the control	the to IC	2007 2007 2007 2007 2007 2007 2007 2007
Posomal protein 877a	Properties of Parties	06.s1 Straight of the 18th of	of protein, is 02.s.t Soor a05.s.t Soo Off.s.t Soos	108.st Soa 106.st Soa al protein,	ome (proso 12a1 Stra Jehyde-3-p	4044 Feta 905.st Soe 171.st Soe 06.st Soe	Sehyde-3-pi r cysteine) e08.s 1 NCI chi polyper	protein S NT. # 1 NC 109. # 1 NC	7 protein	office Sea 201.8   Stra	1241 NO.	eath similar	of at Ja	7.e1 Soam	08.51 NC.	obs. apha	02.e1 Soar 9 protein 8 12.e1 NC	12.51 NO 604.51 NO 05.51 Som	02.s1 NC. 06.s1 Ban 06.s1 Ban	al protein, 108 s 1 NCI 102 s 1 NCI	607.a1 Sou	20 E	Contempt of the Contempt of th	terleukin 21 neceptor oseomal protein 818 ST, Moderately stra	Kal proleh MS. st NG 12.st NG
ribosom	94:782 94:782 94:782	Strict St	phyff7g phyff7g phym31	gbrydg gbrddg	protesso gb:rp:39 gb:oersdq	95.25 95.25 95.25 95.25 95.25 95.25	phoenal sorthe (c gb:nh85 ferritin, 8	gbmm75	PRO2047	gh:2489	ESTS.	EST. W	gh:ag37	EST Franco	through the state of the state	gb:rz 12	dbosom dbosom	90.0029 90.0021	ChroCota gb:ak72 gb:ak82	gb:sh63	gb:em08 nbosom EST	20 40 40 20	150 of 15	ribosom EST, M	Problet gb:oq25 gb:oq72
43	1,181166	170	Hs.177662	.73742	Ha.78466 Ha.169476	- 9	Ha.169476 Ha.297681 Ha.111334	Hs.3463	Hs.284138 Hs.297753	7300697	Hs.303405	Hs.275658	Hs.81328	HL 163019 Hs.300697	Hs. 287445		Hs. 275865			Hs.73742	Hs. 130027		Hs. 288038	Hs.275865 Hs.275865 Hs.276018	Hs.191228
WO 02/086443	AW516206 Hs.181165 100036 . T03160 . T02268	- 8858		~			AA682602 H: AA686074 H: AA513322 H: AA524440 H:								AA737858 AA745684 H				A4828288 H8 AA838253 AA845258					A4953072 H A4961382 H A496859 H	
WO 0	22 22 22 23 24 24 25 25 25 25 25 25 25 25 25 25 25 25 25	8 8 8 8 5 8 5 5 5 8 5 5 5	287 R25376 114 R78948 122 H78966 155 H58598																						
96	304024 304024 304024 304024	****	304087 304114 304122 304122	30420	30428	30456					30507	25.55 5.55 5.55 5.55 5.55 5.55 5.55 5.5	305235	30836		305528	305818		305720 305750 305760 505760	305864				306175 306175	
	ς.	;	10	15	70	č	3	30	35		9		45	Ş	3	55		9	65		2	7,	2	80	85

Sillia peccandi preth GM publicitat i demay LL (3GL, Si Horno a 2 cologen kyol Lebra 2 publicitat i demay LL (1.GL, Si Horno a 2 publicitat i demay History (1) intro a 1 publicitat i demay publicit i demay libit i intro a 1 publicitat i demay publicit i demay libit i intro a 1 publicitati i demay publicitati i demay libit i intro a 1 publicitati i demay publicitati i demay libit i intro a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i demay publicitati i demay septema a 1 publicitati i dem

Hs.288262

and golden Line and an analysis of the state 
Ha.181165 Ha.283442 Ha.251577 Ha.169476 Ha.169476 Ha.181165

Hs.309411

photogodia i NG, CGAP, UR Homo sepiena photogodia i NG, CGAP, UR Homo sepiena unapiris hymborate than RA, III. applica I. I. Edu tumoz Homo sepiena cD applica I. I. Edu tumoz Homo sepiena cD applica I. I. Edu tumoz Homo sepiena cD photogodia prode for mora Homo sepiena cD applica I. I. Soft tumoz Homo sepiena cD materiot berustion deception factor

KAN1527 protein (KAN1527 protein (KAN152

Nb.101774

h04011.x1 NOLCGAP\_0X23 Homo sapler kayoto iransiston ebegation factor wk52c01.x1 NCLCGAP\_PY22 Homo saple baid 8g03.x1 Barstead colon HPLR67 Homo

Hs.217493

10

2

15

2

25

ဓ္က

35

6

20

25

ଓ

જ

8

23.

8

85

Soares\_NFL\_T\_GBC\_S1 Homo!

25

Moderately elmiter to ALU4\_HURANN A

2

128

H3Z78390 Human Istal brain 8. Neber. E o Enger problen 148 (pHZ-52) Te mo saptens CDNA FLJ20118 fa, done CO

siute carrier (amily 1 (neuronal/epithe STs 52855307.81 Scares fetal liver spiber

	8	28	7,4	£ 5	3:	2 8	3 5	8	3.34	17.78	282	23	2	75.0	9.6	2 2			466	3 5	2 12	121	9	12.06	1,39	15.20	1.00	9.61	5	8.35	05.0	25	<u> </u>	2	1.13	3.67	13.71	12.70	18.29	3.07	<b>0.4</b>	2	95	38	3	271	15.31	2	10.65 14.65	4 C	619	908	312	5	67.7	3	587	5.19	8	112	3	3.46	3 9	60	F.	690	13.22	36	283	E ;	5 <b>5</b>	2	25.	9.84	
		88															8 5						-	_	_	2.68	_																								2	1.15	£ ;	Ē	88	8	2 5	8	8	À E	2	3.26	55	3.5	8	5.5	4.40	2	3	9	2.84	8	6.37	6.07	
.*	A should be a december of	chistory, used 4, A conditionalist chist76410.x1 Baratased colon NPLR87 Homo	dowided flux I NCI_CGAP_Util Home septens	phosphaldyfinosibl gycen, class H	gowalnot at MC COAP Lott Home sapens	pormodrata i NCI, COM, princo rumo sapan	The state of the Cold State of the state of	SWISNE related matter reservabled, and	ribosomal protein L3	EST <sub>3</sub>	gb-wo95e11.x1 NCI_CGAP_Nd11 Homo septen	nbosomal protein L13	gb:wp84b09.x1 NCI_CGAP_Bm25 Home sapten	gb:rrx63g05.x1 NCI_CGAP_Br18 Homo saplene	ESTS	gowelscourt NC CLAP GOS Homo tapiens	go, was supported in the Color of the Support	Paris of the sales sales	County aprile, confusions	charalthos of the Cost Inditions conjuga	Homo application PP159 unforce mRNA	taminia receptor 1 (67tD, obsernal oro	obxe33e10x1 NCI CGAP Ut1 Home sapiens	sarine (or cysteine) proteinase inhibit	EST, Moderately similar to GNMU to gamm	EST, Moderatery shrifter to ATPN, HUMAN A	laminin receptor 1 (9740, ribosomal prof	mannosidase, upha, class 2A, member 2	lubulm, beta polypeptide	gb.xq36h02.x1 NCI_CCAP_Lu28 Homo septens	goast scient NG CGAP Kid11 Homo sapien	Intributogostas Rappa constant	chamber of NCI CCAP DOS those seniors	obysolective NCI CGAP Kiddl Home series	immunodobula heav constant carma 3 (G	abth605008xt Sogres NFL T GBC S1 Homo a	obhidded 1x1 Spares, NFL, T, GBC, S1 Home a	gb:hd13d01x1 Soares NFL T GBC S1 Homo s	gb:hb73110x1 NCI_CGAP_UZ Homo sapiens	hypothetical protein MGC3265	Homo saplens mRNA; cDNA DKFZp564P116 (P	ESTs, Weatly shaller to B48013 proline-	EST S	ESTE	ESTS	ESTS	ESTs	ESTS	E316	ESIS malallollsimain 15 /functional	FRTs.	ESTs	ESTS	TO THE	EST	ESTS	# 15 H	£67s	ESTe	ESIS	ESTa. Highly similar to AC004835 1 shull	ESTs	ESTS	ch: Human endocenous retrovius H protezs	ESTS	ESTS	Homo Septens means the rength each con	E31s	ESTs	ESTS	EST8	ESTe	ESTs.	EST	
:	443	200		¥.17				He 78202	H-119598	Na. 255884		¥.188942			H. 299426		14. 94.94.44																		Hs.300697					Hs.257111	Hs.323079	Ha.172824	H. 161354	Hs. 147253	H 223796	Hs.148301	Hr.197422	Hr.147562																			He 157757	Hs.157882	Hs. 157289	Hr.158707	H 161296	H. 221703	H. 161332	H.161330	
200	080/70 0	ARTIZA	AUSS8845	AJB65023	A18/0/04	A073111	2001004	A1917366	A/922426	A1925503	A528178	AU328818	AB37761	A1951118	A991525	AM03478	AVECUAL AUTOENA	AWG0ZU	A1400000	40120369	AVMINERACE	AW150807	AW151119	AW192004	AW194230	AW205881	AW237221	AW235011	AW241170	AW284889	AW272348	44776404	AW276064	A1V70001A	AW309071	AW340684	AWAIA18	AW341683	AW341938	AW449111	AJ439096	AW136822	Alegaen	AW197233	AI611317	AW195642	A/206814	A1627653	AW450439	A124046.3	A747102	A7243332	AW013815	ADS: MO	AI263392	AW119018	A175715	A1984074	A1948801	AW2/5603	AW082270	Al302654	AI653007	A341594 FIB. 150102	A1814.37.3	A1347863	AM72124	AMIBANG	A1989603	AI916560	ALEGES	AW291714	A421677	A187 1000	
	À	30888	308898	308374	306363	1007 P		09060	308083	309105	309122	22 22 23 23 24 24 24 24 24 24 24 24 24 24 24 24 24	300	208	309288	667600	3030	2007	200457	2007	30500	309529	309532	309628	309641	309675	309693	309695	309700	309747	309769	203/62	3000	30086	309903	309923	309928	309931	309933	309964	310002	30000	20012	310112	310115	310121	310148	310193	310255	310201	310275	310282	310230	310.00	310385	31043	31046	310468	310477	310612	310524	310647	310684	310624	310836	310648	310694	310714	310722	310758	310764	310851	310854	310858	
																																																						_																_				_	

											•																						
2476																							•										
02/1																								•									
PCT/US02/12476		•																															
2																																	
									-															-									
																٠																	
,	8 12 × 1	5858	987	Egg	<b>- 5</b>	(হুজুই	= 12,5	§ 12, 12	98	8 E	8,5,1	6 25 5	8:	<b>3</b> 8	25	55	82.6	<b>422</b>	223	<b>3</b> = 5	2 S	2 8 2	828	, 18, P.	25	3 2 8	283	<b>48</b>	98F	32	P = 18	ទីកូនុទ	9 25 2
	~ ~ ~	B0	* ಲಗ	~ ~ ~	00r	- 00 10 10	. 40	,	-				-	, vo				.0-0	- en en e	-~-	-	*0.		- 60 1~		co	@ r		<b>6</b> 6 4		6 6 C		4 F- G
	B 8 22 :	1825	P & Ø	<b>12</b>	2==	222	222	2 22 29		<b>►</b> R 1	8 12 t	285	225	2 52 52	88	= 8	22	2822	<b>9</b> 2	225	NR SE S	8 98 52	221	= <b>= =</b>	R XX	2	582	288	8 5 18	c 9	222	8528	388
	នគត	562.5													_	<b>.</b>			22	223	<b>7</b>	333	44	- 2 2	22	227	225		222	9.9	\$55	& <del>4</del> 7 7 7	- 23 23
	8 8	sapten Sens			sapen	aplens		1	E.	E Š		spiens	İ	aplens	9	ě ě	200	4) 911											2	×			

die acki receptor, beta s, Weatdy similar to CKO, HUMAN VOLTA o appiens cDNA FLJ 12881 fs, clone NT

S

55

rpothefical protein FLJ23056

STs, Wealdy similar to KIAA0973 protein

Otherical protein PLJ14054

JI-H-Bit-etg-g-02-0-UI.st NCI\_CGAP\_Eu no saplens done CDABP0036 mRNA seque

8

H. 22579 H. 189679 H. 124733 H. 18690 H. 187203 H. 284450 H. 288594 H. 288594 H. 288594 H. 288594 H. 288594

65

2

73

8

8

n-coupled receptor 39

POM (POM:21 rat homolog) and ZP3 habon interfacilities homolog 1 KAA1292 protein similar to rat myomegafin

<del>2</del>

	1888	8 E E	ភូនិទ	268	និនិនិ	79:5	8282	1367	884	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22 22 12 12	3 <b>3</b> 8	325	322	8434	885	វិតក្ខិត	2822	5893	883	283	26.83	16225	252 252 252 253 253 253 253 253 253 253
	8 E 8 E	2525 2525	2 2 2 2 8 8 2 8 8	2358 2558	9539	24.0 k 88.0 k 80.0 k	2425	525 525 535 535 535 535 535 535 535 535	242	8 2 2 8	222	5 5 8 8	355	3 2 8	8 8 8 8 8 8 8 8	25E	88.05.E	22.53 25.53	25.24.65.25	887	882	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3.78 2.22 1.67
				NA DKFZp547C244 (tr 2_Pr1 Homo suplens			o mRNA sequence o putative p15			4056 Es, ctone HE 976	b KJAA1200 pro	10570 lls, clone NT		equences, MAGP Homo!		867	B 1035 Homo septen	8 and G2 to	protesse, serine 3	21274 lls, clone C		CTACO151 mRNA sequ	493	L_1_68C_81 Home a DVCA1
	687a 687a 687a		QAA1340 protein . ESTs ESTs	ESTs Homo saplens mRNA; cDi phno18612,41 NCLCGA	SS 25 25 25 25 25 25 25 25 25 25 25 25 25	2512 2512 2513 2513	ESTS Home saplers done 24620 mRIVA sequence ESTs, According similar to potative p15 ESTs	1111	ESTs DEAD-box protein ESTs	Homo suppers cDNA FLJ (405 Fbox, brain, 1 2876 mothetical erotein FLJ (2876	51s 551s 781s, Moderately similar lo KUAA1200 pro	ESTS damo septens cDNA FLJ 10570 Bs, clone NT	ESTS Meled in liver cancer 1	ESTS db:EST391378 MAGE resequences, MAGP Homo1.4 ESTs		hypothetical protein FLJ10498 ESTs ribosomal protein LZ7a	557a 557a 557a 557a	cell Christon cycle 2, G1 to 8 and G2 I ESTs ESTs EST	Fransmembrane protesse. SSTs SSTs	ESTs Homo apiens cDNA; FLJ21274 (ls, done C ESTs	.87a .87a	2316 :518 tomo sapiens clone TCCCTA00151 mRNA sequ :51	ESIS hypothetical protein FLJ10493 fotpethika 1 ESIs ESIs	gbty/3672.x1 Scenes JNF.,T_GBC_81 Home a ESTs ESTs Moderately thriter to OYCA1 transcription techn BMAL2 ESTs
53	H.171442 H.135268 H.13957						Hs.95612 Hs.142570 Hs.130679 Hs.193748				116998	153408			Hs. 290989 Hs. 135174 Hs. 184002	Hs. 192855 Hs. 192855 Hs. 76064			298241 116133 177135				Ha. 279010 Ha. 137516 Ha. 137516 Ha. 163924 Ha. 184639	
WO 02/086443	AW473830 Hs. AW457823 Hs. ABT0175 Hs.	64199 Ha 200048 Ha 66970 Ha	28.25.88 28.77 28.173 28.153 28.154 28.155 2																					AZ3973 AW383391 Hs. A681671 Hs. AW512763 Hs. A193048 Hs.
WO	313926 AW 313946 AW 313978 ARE	31.00 31.00	1667 14103 AB 14107 AB	28 88 88 88 88 88	25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1625 AK	8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		1466 AV		14552 AN 14578 AW 14580 AW				14710 AB				15006 AIS: 15033 AIR: 15035 AIR:		15078 AA5 15120 AA5		2	
		'n	2			20	25		8	35		40		54	20		55	9	65		6	75	,,,,,,,, S	88
							•																	
12476																								
PCT/US02/12476											•													
Ž																							٠	
	55.5 2.7.2 59.5 59.5 59.5 59.5 59.5 59.5 59.5 59	25.5	887	8988	1.68 7.70	255 253 253 253 253 253 253 253 253 253	203 13.78 13.78	252	9-8	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	5.55	888	252	1.30 85 7.5	555	2525		25 2 2 2 2 2 2 3	558	26.01 20.01 20.01	38 <del>2</del> 8 8		2 2 2 2 3 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3
	863b	C 8 8	0 6- 90	o w - a		<b></b>	e==0	0.50	2000	2000	w ex **	= \$0 %	, rv en e		. B z G	<b>80 37 40</b> 6	201 12 12 12	~ 5 B F	- 886	000	w <del></del> w 9	9 T E E E	2.1.0 2.7.7 3.1.0 3.1.0	0=800
	2222	862			122	3233 3				3223	222	23.5	1222										12872	
			152 Homo saplen 10 BT0529 Homo	M-26761J13				ESTs, Weathy similar to unnamed protein ESTs ESTs, Weathy similar to T200, HUMAN TRANS	HUMAN ALU S		ned protein			.5	far lebts	ESTS Homo sapiens cONA FLJ (3103 fs, clone NT ESTs, Wealty similer to enry probin (N.s.		6 fts, clone HE		8 fis, ctone HE	on moleo	un sue de la contraction de la	receptur t	ESTs ESTs ESTs gb:nd/601 s NO_CGAP_AN1 Homo saplens Homo saplens GNA FLI11576 ft, done NE
	ordein EBt	z.	COAP Br	GA; CDRA	In PR02121			dar to uman dar to T200	ater to ALU7.		alar to uman			1	ater to Auto	NA FLJ1310 Par to enr pr		NA FLUTOR	h FLJ 1384	NA FL/1015	i cell adhesi	en emagener	hosphatase,	CGAP_AI
	ESTs TERA protein ESTs clucose regulater	ESTs ESTs cell dikibin cycle 27	A3h12x1 NC	E suedes o	ESTs hypothetical protein PRO2121 ESTs			s, Weedty sin s, Weedty sir	ESTS ESTs, Weakly similar to ALU7_HU		ESTs. ESTs, Weakly similar to unnamed ESTs				s, weekly sir	o saplers of a, Wealdy sin		ESTs ESTs Homo saptems cONA FL11646 fts KIAA1345 protein	ESTs ESTs hypothetical protein FLJ 1398( ESTs	Homo suplema cONA FL/10158 ESTs RP42 homolog	pasieletandotheliai call adheston mo ESTs		ESTS ESTS ESTS protein brookine phosphatase, recep	s u76401.a1 N no saplens ct
						141 ESTS 720 ESTS 200 ESTS 007 ESTS							339 877 878 878 878							-				
086443	92 Hs.143981 38 Hs.150780 Hs.155937 15 Hs.259101						2 19,214678 81 19,20365 19,23325 04 19,20373																72 14:13234 79 14:14889 8 14:15887 14:123641	
	AA216598 AA216598 R66210 AA625512																							AW471088 AW471088 A949384 A969390
_	ĒĒĒĀ	222	582	225	N Z Z	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2000	288			888		965	22.5	3882	329	1888	355		28.8	33.8		2000	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

	និទីនិ	88	588	355	25 25 25	85	858	255														55	និនិនិ	385	383	888	52	228	22.5	5225			522	
	ESTs ESTs ESTs							hypothetical protein FLJ 13117 ESTs	Costs decrynbonuclease II beta Homo emplens CONA FL11469 fb. clone HE	ESTs. Weatdy similar to ALUA_HUMAN ALU S	ESTa, Westdy shriber to 712545 hypothali ESTa ESTa	E87s	ESTs ESTs	ESTS, WESSY SERIES O ALUCUADAM III ESTS ESTS	ESTs	EST0	ES10	ESTs	ESTS ESTS Wanth strates a sittle topus at 119	gb:PTH188 HTCDL1 Homo sepiens cDNA 5/3 E81s	Nome septems crone 24001 mirora sequence ESTs	ESTs. Weatdy similar to unnamed protein poly(A) polymerase alpha	Homo saplera cDNA FL/12136 fs, done NA EST	ESTs hypothetest protein	atbumin hypothelical protein EDAG-1 Homo sapiens cDNA: FLJ2587 fb, clone L	ESTs Homo sepiens cDNA: PJ21238 fs, clone C ESTs	ESTs, Weatby shrides to ALU! J-LUMAN ALU 8 oxidised low density impoprotein (leadin	ESTs Froilbration-essociated 2G4, 38hD ESTs	gbym04f10.r1 Soares Infant brain 1NIB H edenyfate khase 5	DCT25648116 protein L-tynurerine/alpha-eninoedipda eminotra ESTa	EST.	ESTS, Highly similar to WAON JHUMAN NADP. ESTS, Weatly similar to weak similarly KDA1313 protein	putative selenocystelne lysse putative Genderin coupled receptor ESTs	
143	Hr.127122 Hr.199828 Hr.192123	ls.132563 ls.127348	6.13728 6.13228	b. 174794 b. 128014	h.272189 h.128119 h.128119	b.47313 b.128909	B. 128899	152822 14.129119	A. 129142	a. 129225 b. 150814	18.201378 18.130980	1.131155 1.232140	B.131574 B.250114	134090 15.134090 15.143610	b.134862 b.271443	B.143768	1.158438 1.14834	ls.146883 ls.265165	14.14.709 1.144.709	13254	8.90431 8.90363	s.107761 s.49007	1.168630 1.172638	Hs.8861	3.176628 3.289254	a.10336 a.101282 a.242990	281289	3.21273 3.21273	8.18268	301528	3.308298	3,169161 3,98365 3,4953	Hs.285306 Hs.16085 Hs.13306	9.14000
WO 02/086443	33361	33310	7294309	07859	20005	43525	58158	2016	7295184	52430	735697	243058	24540	17540	54341	93840	51395	1 22606	13.53	1368	26.00	2102	A07877	243539	393302	H15 H 36475 H 62487 H	002543	355	222	366520	19221	927.	R13678 F07361 F07361	
W <sub>0</sub>	NA 175718 AA 175718 AA 882718	DA 02371	317674 AV	317592 AG	317715	317771 317799	317803 A 317821 A 51 A	317850 12	317869 AN	05ET1	1806 1809 1809 1809 1809 1809 1809 1809 1809	18054 AW	18068 AD	18223 AIC	18255 AK	18330 AIG	18458 A A	18473 AB	18487 A1	18439 72 72	18547 R21		18587 AA 18596 AM	318629 N2	18650 A. 1785	118679 TE 118711 AIS 118725 AIS	18728 18740 NN	318764 HDC	318865 HH 316879 R56	1889 1890 1878 1878 1878 1878 1878 1878 1878 187	18936 AI2 18982 Z44	18986 24 19041 24 19103 HG	319170 319186 719189 703	7.70
		د		2		15		200	,	25	eo eo eo	39 30		35		40	,	. 4	<del>.</del>	Ç	?	, ,	55	9		65	. 65 67	2		75		8	 	
								•											•		•		-•		-			•		,				
																	•																	
176																																		
PCT/US02/12476													•																					
PCT/I				:																														
																			•															
	<b>= 2</b> 22	223	8.5	<u> </u>	353	848	325	56. 56. 56. 56. 56. 56. 56. 56. 56. 56.	3.45	333	10.69	2 <b>2</b> 3	2 8 B	12.1	9.1.	888	25 25 25 25 25 25 25 25 25 25 25 25 25 2	258	288	<u> </u>	5.8	25 E. E.	2 5 8	8,52	323	55	2,53	255	3 72 88	822	2,23	355	2 4 2 8 2 5 8 8	
	5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	885	353	83	2 5 5 5 5 5 5 6 7 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 7 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 7 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 7 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 7 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 5 6 5 6 7 6 5 6 7 6 5 6 7 6 5 6 7 6 5 6 7 6 5 7 6 7 6 7 6 7 6	581	553	25 EE EE	2.00 12.00	2 8 8	382	88	825	<b>9</b> 8	23	85 55 85 br>85 85 85 85 85 85 85 85 85 85 85 8	5. 5. 5. 5.	9 P S	95	2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	85	2.5.5 5.05 5.05 5.05 5.05 5.05 5.05 5.05	30.0	222	883	98 99	2 <u>5</u> 5	35	282	8 8 8	9.1.9	308	9 <b>255</b>	
			3481272 Ø				ę!		MANA	O 000				MAN A				andrea or		NAW A	Ę													
	•	0690	RVA; CONA DISFZPASABI272 (J		202	1	res_rata_inver_spaem		shritar to ALUS_HUMAN A	aplens cDNA: FLJ21326 fs, clone C				similar to ALU1_HUMAN A					000	miler to ALUT_HUMAN ALU S Sy dimitar to ALUT_HUMAN A Seh FLJ12037	F125780 1 n					920	NA: 67 J21197 fe chas C		over and kazal-like d					
	stod entipen 4	roteth FLJ 10690	2		protein FLJ 20202	1	SORIES TRI			CONA: FL								. 95		chiltr to Al Idy dinitar I deh FLU2	similar to A					produtin FLJ 11350	G-MAG		clin, cucy as					
	STa Perm essectates STs	ESIS hypothetical protei ESTs	omo explans	E818	100	ESTO ESTS	goznajousa ESTs ESTs	EST: EST:	ESTs, Moderately ESTs		87s	STS STS		STs, Moderatory	513 513			EST	510 510	STR, Waskly STR, Modera pothefical or	STe, Westly STe			ESTs ESTs	S 5	pothetical p	ESTs ESTs Homo comiens	ESTs ESTs	STe sarchasteone	# # # # # # # # # # # # # # # # # # #	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	355		
	Ha.123159 at Ha.236578 at				-			Hs.189048 El Hs.209452 El Hs.133263 El			_															3707							Hs. 126860 E1 Hs. 126891 E1 Hs. 126865 E1	
																			520 Ha.122082 86 Ha.127955															
WO 02	M AZ00852 11 A1168233 52 AW445034				AWAG	15 AB217	11 AA8277 0 A46320	AMERICA S AMERIS	H AW276				AW518																				A A A A A A A A A A A A A A A A A A A	
	31555 31555 31555 31555 31555 31555 31555 31555 31555 31555 315 31		38.8	3156	322	3157	358	3 3 33	88	988	316048	31612	31618	31623	3695	316346	25 P	31631	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3167	31678	31681	31681	316827 316891 316851	31697	88	31705	31718	3172	31726 31722 31728	555	344	317519 317519 317521 317529	
		\$		0		8		0		2		0		S		0		v	1	0		v	3	0	,	5		0		S		0	\$	

PCT/US02/12476

55	<b>3</b> 3	253	35528	2 2 2 2 2 3	282	955	1852 1852	2 2 3 3 3 5 5 5 5	25.2.2.2 25.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	285		<b>3</b> 8988		2853	######################################	200	828						
Homo sephera cDNA: FLJ21827 fs, clone H E8Ts	ESTs OG+147 protein	ESTs transforming growth factor, bela recepto hypothetical protein FLIZXXXX	CS18 gb4SC2CE041 normalized briant brain cON ESTs, Moderately similar to ALUS_HUMAN A . ESTs	ESTs gb:ye91b04.r1 Scares fetal Iver splesn gb:yd33f07.r1 Scares fetal Iver spleen	ESTs ESTs Weakly similar to Y48ASA 1 (C.eleg ESTs	ESTs Gbyd52a10.s1 Boares fotal liver sploen	ESTs, Moderately shritar to ALUB, HUMAN A ESTs Homo saylens cDNA FL/13307 fs, clore NT	gojnoo 12.1 ootees leta ilva episen ESTe hypobelical protein FLJ12973 divronosoma 8 oosen raadiin tiene 4	winestin hypothetical protein FU21103 gbym 19510.rt Soeres Intent brain 1N19 H purcharacterized hypothatimus protein 4T0	ESTs syntrophin, gamma 1 ESTs, Moderately similar to A Chain A, H	ESTS ESTS ESTS Homo sequess mRNAx CDIAA DAGZGA34N1923 (7	ESTs KAA 1320 protein likey orthoog of mouse polydom N-ecytophogoelne articohydrates (ecid o Arthrod 1-07 of Chalmans (ecid o	ESTa ESTa Homo saplens cDNA FLJ13534 ft, clone Pt. ESTs, Weathy similar to ALU1_HUMAN ALU 8	ESTs Homo septors CDNA FLJ14199 fla, clone NT Human DNA sequence from clone RPS-650E9 ab:EST40843 Endomental Lumor Homo searle	gbryddi)X9.r1 Scarca felai flwa upten ESTe, Weathy sinder to KDAADG38 probih ESTe, Weathy sinder to AAG010 X-finland hypotherical protein FLJ14001	EST FOXI2 forthead factor ESTs	CDC45 (cell division cycla 45, Scarente ESTs SMC2 (blucharil maintenance of chromoso	ESTs Homs expiers cDNA FLJ 12028 &s, clone HE ESTs	Homo sapiera mRNA, cDNA DNFZp564N1116 (f brbuchrters Wal nephritta anligen tertin 2 (testculer)	Stringer, taring b, 1 (prostate assisted ESTE G profein-coupled receptor 63 Homo septers mRNA, cONA DIGT2654P016 (tr	Homo sapians cDNA FLJ10684 fs, chone NT small profine-rich protein 3 caveolin 2	chtorida channel 2 Homo sapiens cDNA FL/14028 fs, ctone HE ESTs	Homo saplens clone FLC0578 PRO2852 mRNA,
Hs.81360	Ha. 290283 Ha. 12677	Hs.12876 Hs.79059 Hs.285243	Hs. 325823 Hs. 13911 Hs. 201743	Hs.191196	Hs.191198 Hs.111991 Hs.116417	Ha.184221	H-191184 H-191184	Hs. 20403 Hs. 250154 Hs. 283683	Hs.297753 Hs.12283 Hs.173515	Hs. 106804 Hs. 167481 Hs. 21398	H-22664 H-23664 H-295664	H,22846 H,117414 H,271350 H,284330	H-1331 H-201352 H-24109 H-271722	Hs.133510 Hs.14479 Hs.135056	Hs.295288 Hs.292664 Hs.67164	Hs. 302256 Hs. 120844 Hs. 117915	Hs.114311 Hs.188469 Hs.119023	Ha 17132 Ha 24321 Ha 29792	Hs.124778 Hs.127011 Hs.127111	Hs. 24683 Hs. 131924 Hs. 132571	Hs.151283 Hs.139322 Hs.139851	Hs.141660 Hs.281434 Hs.31288	Hs.23368
ve .			245481 245481 H54254 R06304 H67130										517 559 450	248 150 120 130	T83283 H63789 A1699772 AA233671					139	919	AF026004 H10807 H16063	ź

218 218		85538	20 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	9535	588525	<b>3558</b>	8 2 2 2 2 8 8 2 2 2 2 8	78888 7888					28958788 8898788	638888	25.12.25 25.12.25 26.
Payes I Yamagush sersons was reduced Why A WG 205040094 (1	bilistsh-Da 1 Homo sapran eUA FL/12028 fs, chos HE RAAQSS goden hypothacid protein FL/20171 ESTs	E81s hypothesized probah FL/22530 peptidaharan anapaga amonoxyo peptidaharan apina emitidaha monoxyo peptidaharan anapaga amanakan anapaga manakan anapaga manakan anapaga manakan anapaga manakan anapaga manakan anapaga ana	hypothetical polein FLJ3382  Kuno sapiens mRNA for KUA1703 protein, ferfüt, ight pohyaptide FLJ1198 FCTs.	EST, Weakly striker to unnamed protein EST, Weakly striker to AS4849 collagen ESTo gbyqQks10x1 Scores lets Net splann	emnicopoculo imposa ocis poty/A-bending protein, mode ar 1 ESTe WMT1 inducible agnating politivery protein ademini diseasin st.	Homo explens mRNU; cDNA DKTZpS47C136 (* ESTs ESTs urozizkh 18 inbbh, bris C	cares edul brain N2bi	racks ar cap briding protein suburit 2.2 ESTs Horno saplers mCNA full length brean CNA Horno saplers cone 2.04 in mCNA sequence phrzekOdOB / Souces refels a NZOAHN Horno phrzekOdOB / Souces refels a NZOAHN Horno	ESTs Physobratical protein MGCS318 physobratical protein MGCS318 physobratical protein Peter aptenn ESTs	pbyy5610.a1 Somes_muliple_scherost_ Homo sepiens cDNA FL12tal1 fat_ctone MA homo sepiens tabNA; cDNA DVF255481462 (if Ser/kg-reited mulear mattr profen) gbiHomo sepiens lexites AN1 instrusoptiou	ptyy/76c06.31 Soerce felai Prer splaen MAA/1515 protein KAA/1215 protein MAA protein (similar be mouse patedin) transcription (actor SMAA/2)	ESTS ESTS ESTS gb/s.septens (DICS) mRNA for immunophbu Home studens CAVE, FLZ1930 ft, down H gb/stursan Za12 mRNA for keppa-framsnophbu		ingonece your red 11st gbystoged 1 Sonse refer RESH RESH Homo Egits thrustode repeat contained a gbyst ReGLA Gones was a REAHR Homo Physbolica estates I LESH Physbolica estates I LESH Fish Mortenia and as A 118 HIMAN A	ESTS ESTS CAND TO THE STREET OF THE STREET O
5443 Ha.60697	Hb.286287 Hb.24327 Hb.24743 Hb.24743 Hb.24743		H-7355 H-11134 H-91251	H-26638 H-171929 H-172790	Hr.194639 Hr.194639 Hr.194639 Hr.26418				Ha.125494 Ha.298351 Ha.89538 Ha.172982		Hs. 6298 Hs. 137507 Hs. 200846 Hs. 222024		Hs. 255436 Hs. 255436 Hs. 255436 Hs. 255748 Hs. 108251 Hs. 159233	Hs.28300 Hs.21838 Hs.86322 Hs.161851	Hs.247084 Hs.24110 Hs.123158 Hs.173737 Hs.167260 Hs.42588
WO 02/086443 18 A240233 Ha.60 31 R26944 Ha.18	AA094436 R32555 AB007978 N31464 AW374205	AA331732 AF054177 AF056209 Z44524 BS4159	AA243258 N48521 AA489268 A1904218	R59231 AA334609 AW135016 AJ445591	AA281993 AA281993 AF120274 AF122445	AA317372 D60031 A473798 AB002165 R94038	AZD5786 AJB78933 H22544 W88483 H27794	AW372884 AW32824 R87955 AF131782 AA016306	H43760 A817933 AA336835 AA700289 N53742	AW385512 H54176 ALDB0073 AW371941 AF068654	R83560 A937060 A8033100 A8127984	R83443 A739161 AD88667 U05890 N50080 X13076	AA514188 H70665 AW285517 W02356 AA703650 H84972	A22013 H84260 AA019964 AA143735 H95531 AA295430 H87064	AW085917 H95404 AA826149 H97846 AA700017 N55160 AW390923
320448 320451	320499 320514 320521 320525	320536 320558 320564 320587	120659 120658 120651	320683 320689 320696	320771 320771 320822 320824	120843 120863 120853 120821	320927 320997 321045 321046	321062 321062 321067 321067	321130 321155 321155 321150	32126 321226 321225 321238	22.02.0 22.03.0 20.03.	221420 221420 221430 221430 221430	221458 221491 221510 221513	221521 221522 221532 221532 221532	321642 321669 321687 321693 321700 321701
	S	10	15	70	25	30	35	9	5	20	55	8 .	8 8	75	85 80

0.33 3.33 10.18	28588	SE 20	253	288	<u> </u>	5885	222	228	252	282	E82	35	5599	5.34 0.06 0.08	222	888 888	8 5 5	855	888	놀림종	858	=855	858	2 <del>2 2</del> 2
	_	y-like domein, family	Cols under eutoanligenic sperm protein (its 100 to				ESTs, Weatdy stretch to NEUROD (N.sapton ( snoon anenta, compennentation group A spothedical protein FL/10392	P.EST382593 MAGE resequences, MAGK Horno.2.2 1815 1942 homolog	ESTs Homo sapiens cOVA: FL/23249 fb, done C Limor differontially expressed 1		MARK Homo expens mRNA, cDNA DKFZp566F1322 () monthelical protein FL110A50		form sapiens BAC clone RP11-335/16 from STs STs			Homo saptens CDNA: FLIZZSZZ Is, clone H Homo saptens CDNA: FLIZZ135 fs, clone H hypothalical profeth FLIZS73	STs formo septens cDNA: FLJZZ141 fts, clone H CSTs	25 ESTs, Wasky sinter to T14742 hypothell ESTs	Z/m	regulator of differentiation (in S. pomb 0 ESTs, Weakly sinder to unnamed protein 1 ESTs	leuxine-ric		Ē.	
ESTs ESTs Homo explens ESTs	Fromo explens i Homo explens i ESTs GA-ÜKF7-ATB-ÜK	pleckstin horrebo ESTs KIAA1573 protein	ESTs	ESTs ESTs res homotog ge	S-phase kinase ESTs ESTs ESTs	EST: EST: EST:	ESTs, Weatly s Fanconi anentla hypothetical pro	de:EST382593 ESTs RP42 homotog	ESTs Homo sapiens tumor differentii		MARK Homo saplens hypothetical pro	EST:	Homo saplens ESTs ESTs	EST 8	dual oxidasa 1 gb:EST94855 A Homo saplens	Homo saplens ( Homo saplens of hypothetical pro	ESTs Homo sepiens o ESTs	ESTA ESTA, Washdy s ESTA	gb:OKFZp761P ESTs ESTs	regulator of diffe ESTs, Wealdy s ESTs	ESTs MFH-emplified in IQAA1349 protein	KIAA1491 protein hypothelical protein FLJ11215 ESTs ESTs, Weekly simise to unner	Homo saplens gb.ng99c08.s1   ESTs, Weatdy s	ESTs, Woderate ESTs
. 1941 5368 5368	Ha. 49359 Ha. 270471 Ha. 163615	Hs.201570 Hs.201570 Hs.24790	Hs 243889 Hs 292839 Hs 292839	Hs.191501 Hs.280176 Hs.7777	Hs.23348 Hs.191518 Hs.24049 Hs.137418	Hr.161719 Hr.115173 Hr.263780 Hr.120219	Ha. 135569 Ha. 284153 Ha. 2087	Hs.256083 Hs.104613	Hs.2724569 Hs.272169	Hs. 20880 Hs. 145599 Hs. 249721	Hs. 12808 Hs. 321056 Hs. 267604	H. 280668 H. 128212	Hs. 128427 Hs. 92550 Hs. 220704	Hs. 208021 Hs. 303662 Hs. 128644		Hs.285333 Hs.285833 Hs.288838		Hs.98523 Hs.124675 Hs.304420	Hs.128173 Hs.300410	Hs.145078 Hs.59807 Hs.293232	Hs.24724 Hs.24724 Hs.127658	Ha.284247 Ha.306206 Ha.152812 Ha.135240	Hs.287426 Hs.132036	Hs.134798 Hs.134798 Hs.157969
WO 02/086443 WO 02/086443 B C1077 Hs.17 B A73859 Hs.14 B A813042 Hs.19 E A119755 Hs.31				AA226310 AL134620 AU306501				AKS2287 AA28274 A1185116		ALDK2121 AA317561 AW297758			A344306 LD43212 A4862973	<del></del>			AA412395 AA295552 ALO47634	AA43088					A148353 AA492588 AA506935	
W 22288 323000 323013 323028 3230000000000							22345					72852		324005 324005 324055				24281						24633 A 324640 A 324675 A
, N	10	1	15	20	3	3	30	35		40		45	20	3	S	09		65	;	2	75	8	⊋ S	88
	-																							
	•		•																			•		
<b>Va</b>	•														-									
PCT/US02/12476					•	-								•								•		
PCT/US																								
	•	•						•																
- 8 - 9 9 4 8 8 8 8 8 8	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	10.78 10.51	222	85 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2 2 2 2 E	0.64 6.69 6.69	3258	3325	125 125 125 135 135 135 135 135 135 135 135 135 13	223	2,2 2,0 2,0	0.0 0.0 0.0 0.0	8758	2225	1225	153	33	222	828	823	¥855	2222	825	75 55 55 55 55 55 55 55 55 55 55 55 55 5
82222	- 255 - 255											£ 8 8	0.25 2.00 2.00 2.00 2.00 2.00 2.00 2.00	252	822	15 <b>2</b> 5								252
AASS3, member RAS oncogana family Hono Lapiena choa M11 MTenZD1 leratica Hono saplesa choa M11 MTenZD1 leratica Hono saplesa choa M11 MTenZD1 leratica Leratica entropolati marka 8			KIVA1457 protein Homo sapilers mRNA; CDNA DIGTZp434K0722 († ESTs	KFZp55401278 XAP_Lu34.1 Homo sapie	tor ICAA1786 protein. b KIAA0535 protein	CSTs  ESTs  Child I Source fetal five spicen  Child Stores fetal five spicen	chied gland N3HPG	ESTs ESTs muchosoons assembly protein 1-like t	Costs Costs (4601.rt Scenes_fatel_heart_NbHH19W ESTs (Trescoktor) homely (	pour l'orespinat inneue, alta_hear_NbHH19W decorn	Ledge Jung NOHL 19W	Har to Osiz (Almuso Luziota	edaptor-related protein complex 3, mu 1 ring finger protein 7 KJAA1321 protein FSTs.	ESTS phosphotetine enhotransferase puldove protein-tyrashe kinase puldove protein-tyrashe kinas	beart of Ma	University appears for the second control of	gb.zriscott, Scares stall iver spiese. E81a	name protein Jotal Ilver spleen felal Ilver cDNA Rom	led channel, shakar-	FLJ12280 fts, clane MA	proladi A2	ESTs Homo sepiens CDNA FLJ14035 fts, done HE phosphorinostrol 3-phosphoto-binding prot	medica Victors A	U13649
RAB33, member RAS o ESTs Homo taplens clons MI Mono septens clons MI ESTs	ESTS ESTS KJAA1462 protein ESTS		S7 protein aplens mRNA	Brown HOLC C	spiens mRNA lighly similar	003.r1 Boares	JOAnt Soams JOAnt Soams JOZat Soams	one essentity	Mirt Scares	d03.rt Sogre	cO7.x5 Soare Ical proteth	toderately sim protein ficel protein F	related protol er protein 7 23 protein	serine enino protein-tyrosi	and young	an appropriate to	MOB, 1 Soares	cumodum-da 107.r1 Soares 14668 Human	om voltage-ga 27 protein 191727	ocal protein P splens cDIM	telem-binding	apiens cDNA sinositol 3-pho	v dataminimus	hypothetical protein FLJI:
			KUA14 Homes	Mypoth Syrids Symbol	Homos ESTs, h		99788 99788 EST	ESTs muchos	_									SURED. SEXED.	PROOT	Homos ESTs	5300cc ESTs ESTs	FSTs Phomps	ESTs	
16443 Hr. 108223 Hr. 202312 Hr. 202312 Hr. 163835 Hr. 163835	Hs. 87902 Hs. 302805 Hs. 29468	Hs.283781 Hs.181634 Hs.195689 Hs.195689	Hs. 272755 Hs. 158923 Hs. 84522	Hs.154579	Hs.226031 Hs.226031 Hs.106243	Ha.117767 Ha.514178		Hs.211516 Hs.134877 Hs.179662						H-25144 H-286049 H-160340		Hs.269587	Hs.256042					Hs.278727 Hs.256149		
WO 02/086443 WO 02/086443 WO 03587 Hz.10 N3582 Hz.25 N AKB4875 Hz.20 N AM7783 Hz.20 N M4778 Hz.80																								
221709 321710 321775 321775 321779 321779																								
~	0		v,	0	Ý	<u> </u>	0	Ś		0	4	Ω	0	٧.	,	0		52	9	>	Š	ç	2	53

12.57	25 25 25 35 5 5 5 5 5 5 5 5 5 5 5 5 5 5	12 4 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6	20.85 20.85	202 14.26 202 203 203 203 203 203 203 203 203 203	85.53 85 85 85 85 85 85 85 85 85 85 85 85 85	8 7 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	6.20 6.91 11.13 10.58	22.22.2 22.22.23.23.23.23.23.23.23.23.23.23.23.2	4.83 7.58 7.83 7.93 7.93	6.58 11.91 5.46 1.19	6.80 14.56 10.22 0.57	6.54 0.78 10.54 16.38	855 85 85 85 85 85 85 85 85 85 85 85 85	8528 8528 8528 8528 853	552 572 178 178 178 178 178 178 178 178 178 178	25.55 25.55	12.2 1.30 1.00
258	87785	258 258 258 258 258 258 258	82888	88888	88588	355 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	27222	=858 <b>8</b>	27.55 27.55	28228	3.48 10.42 2.74 0.15	28282	22,582	8 5 8 7 8 8 5 8 7 8	85 F 88	88887	958 958
						•									•		
· :.			•														
	•	•	. •					·							-		
386443						٠											
WO 02/086443	88828	. 2558		88228	12885 1	######################################	52586	28228	88888	88288	78888 8888	X 2 8 2 8	2222=	2 to 2 to 2	2222	***	<b>2</b> 22
3270			327412 227442 327467 327463 327483										2262 2262 2262 2262 2262 2262 2262 226				3295 3295 32970
	3	10	15	70	25	30	35	40	45	50	55	99	65	70	75	8	82
و																	
PCT/US02/12476																	
CT/US			•														
83	24888	561.95	555 128 108 108 108	35382	25282 2528 25282 25282 25282 25282 25282 25282 25282 25282 25282 25282 2	283238	2222	85.29.25 64.28.25	8 2 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	284 15.98 10.60 10.00	88.7.7.2.88 5.8.7.2.88	8 5 ± 5 8	25.25 27.25 27.25 24.15	<b>33589</b>	-858 <b>8</b>	25 8 2 B	253
80	22328 22328	75588 75888	525 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	82888	255555 25555 2555 2555 2555 2555 2555	38585	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	588888 88888	98385	25.25.25 25.25.35 25.25.35 25.	32,758 36,758 36,758	## ## ## ## ## ## ## ## ## ## ## ## ##	8 5 <b>2</b> 2 5	7255 <u>8</u>	85488 85488	202 202 1.09 1.09	8 8 5 8 5
	se subjeus	. Me K	<b>*</b>														
	cyl-Coenzyn Lu24 Hom	SPRK (huma 22786 fla, clo hal lung Hom	o AUUZ, HUI														
attis FU11	enderse (e	del protein 8 cONA: FLU 17 Human fo	taky similar 1 20 roteln FL 10														
hypothetical protein FLJ11011	ESTs ESTs steel Carytraniense (asyl-Coenzyne gowd/31/2xi NCL, CGAP_LU21 Hono aspiens ESTs	STB Small profine forno septem STB bSHUML1214	ESTa, Moderately similar to ALUZ, HUMANA ESTa proteathorit 20 hypothetical protein FLI 10549 Emmin, eithe 4														
. 22	24434	1020 1020 1020 1020 1020 1020 1020 1020	125428 125428 125428 121028 1672 1672 1673	77178 67648 87812													
WO 02/086443 39 AW504732 16.212	252 252 252 252 253 253 253 253 253 253	2305 PE. 214 PE. 7755 PE.2 0	AW283818 Hs.265459 AZ84628 Hs.125428 AA825078 Hs.123892 106997 Hs.121028 F12554 Hs.781028 Upsigo Hs.18442	82 - 82 E													
WO 0;	324747 AA63 324748 AA63 324804 AB181 324804 AE923 324804 AE923	866 AW19 171 AW28 188 AABOK	946 AW38 953 AZ64 358 AA62: 324 F1325 49346	114 DE134 148 ADSA 149 DE134 149 DE131	14223	22533 22533 325436 325471 375498	560 560 560 560	597 598 588 588 588	55 55 55 55 55 55 55 55 55 55 55 55 55	883 926 332 741	969 025 789	55 55 55 55 55 55 55 55 55 55 55 55 55	230 350 393 505	585 585 585 585 585 585	8593 7720 772 818	39.03 39.03 0.33 0.33	7040 7053 1075
3246			22,948 12,4958 12,498 12,502,4														
	ν.	10	15	70	25	30	35	4	45	20	55	9	99	70	75	80	85

						0.30 0.30 0.30 0.30									0-0	0-088	
CDA14 physisodal Scars multide adensis.	gtroof/404.st NCL_CGAP_Ov2 Home set ESTs PTD007 protein FCT	f homdog gene fanity, member i Ta, Wesdy skriber to rhotekin [ki.muso agen, type ili, etsha i [Elven-Dari	wingest-type MAI V frequence for arm Home explens NY-REN-62 entgen mRN4, par ESTs ESTs Transcription termination (actor, mileo	EST Homo explers mRNA; cDNA DKFZp585L0120 (i hypothelical protein FLJ11011 collagen, type XI, etyte 1	ESTs ESTs Producted protein FL20073 ESTs	EBIS QA.201211 protein gb.zeol 1e1 1.1 Gesster Wilms temor Homo a KAA(100) protein; Colplessociated, garm muches footor IIA EBIS	ESTs claudin 1 ESTs EST Starpard doeses 2 (guitaonia dominari) ESTs Wandry emfer in mutation of 1601	ESTS Secure of possible process grant depth at the secure depth at the secure depth at the secure depth at the secure depth at the secure of the secure	hypothetical protein FLI23045 retinol-binding protein 1, cethiar FETS FETS FETS FETS FETS FETS FETS FETS	where the plant of	ESTa, Weakly sinitar to AF164780 1 proba orbateratin 2 probassa, santa, 16 (Drymus) E1A binding protein p300 methyl CpG binding protein 2 (Reti syndr	onacion A. AK tinding protein  Akt tinding protein  repotent reputar of cytokhesis 1  repotentire protein MGC2941  protein A carbonylase, bets	gap junction protein, eighta 5, 4000 (con +-ings avian ingelocyformetosis what oncog mycolodyformetod or intrad-lineage butsam dual specificity phosphatrae 7 hypothatical protein FLJ 10902				
. 2					Ha. 139631 E8 Ha. 105104 E5 Ha. 145053 E5 Ha. 251014 E5		He.101433 ESF He.7327 clas He.101689 ESF He.317769 ESF He.317769 ESF He.317769 ESF										
						AA60019 Na AA598594 Na AA509012 AA600200 Na AA60053 Na AA609861 Na											
20 W	2000 2000 2000 2000 2000 2000 2000 200					32071 AA 32071 AA 32074 AA 32083 AA 32083 AA									10012 10002 10005 10005 10005	33298 333058 333058 333057	333123
	'n	10	15	70	25	30	35	40	45	20	55	9	92	70	27	80	8
	٠																
8.44	2522	225B	25.25 25.25 25.25	25 ± 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	25235E	88885	55333	85558	§855 <b>3</b>	52882 52883	207 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	29 <b>8</b> 5	82.885	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		25 6 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	888
25.2	12215	26323	55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22.50		. 650 640 640 640 640 640 640 640 640 640 64							12825	85588	59595	2005 2002 2002 2002	5 8 F
					Karyopheth apha 6 (Importin apha 6) KOAAD103 gene product protease influitor 3, sth-cforhed (SIKA) addrest limiterial group to bestockled adventing a consistent of protein 4	includiments structured by coloran- endogenous refront of crisese guarien micholice betraig protein (0 pr phospacionalice-shinton gradiator su 5100 eadarn-bendra protein Al (rathum tino fingor protein 8 (a cellular retro	Pypoprial A-Actorygenses heptoprial A-Actorygenses (NONE) ph-Human RP1 homotop mRNA, 3UTR region by-human RP1 homotop mRNA, 3UTR region by-more applian school-FLZ1830 fts, done H plasminogen achievas, rotabless	ubkqutin carboxyl-berninal esteraso L1 briogri, beta 4 retuccelibri 2, Eshard calcium birdin 8100 calcum-birding protein A2 junction placoglotin	ESTs. Weakly sentian to ALUT_HUMAN ALU SETs ESTs Hono septens CDVA FLJ 11570 fts, dono HE Vesture, bein 8		EB18 hypothelitza protein FL/20688 EB18, Moderately stratar to ALUT_HUKAN A ES18 ES18, Weakly stratar to iransformation-1 ES19.				Human DIMA sequence from PAC 75N13 on d'y ESTs (NOME) glycoputien (transmembrane) mrb dechéund (Encsophita) homolog	ESTs lorno asplens CDNA FLJ13496 fs, done PL KDA1462 prolein striadro gradient 2 (Zemepus Bewls) hom hypothetical prolein FLJ11088	NADPH oxidese 4 ESTs Moderately similar to ALU7 HUMAN
							588 575	5118 3256 3391 340	29283 293690 11571 22620		H. 274337 Hs. 274337 Hs. 49136 Hs. 105807 Hs. 265398		23748 23748 191358 157148	Hs.21983 Hs.4197 Hs.159283	8469 8469 82228 83331	Hs.23240 Hs.23240 Hs.46901 Hs.91011 Hs.49282	44037
					14.182 14.154 14.822 14.822	Ha.267319 Ha.71642 Ha.6241 Ha.81256	1	22222	f f = f f	22222	e e e e e e e	2222	로 <i>로 코 로 로</i> :	22 ZZ	22 EE	£ £ £ £ £	£ £ £
329764 329316 370017	322000 30000 30000 30000	330085 350084 350093 320100 550100	330107 330120 330123 330123	33263 33330 33333 33336	AA449749 D14659 L10343 L24203	30093 MZTB26 H-25 30093 MZTB26 H-27 30030 MST900 H-62 300512 M80363 H-281 300537 UNFT66 H-281	USS240 USS244 USS316 VSS2419	XS3587 XS3587 X775669 Y07765	AA317045 AA133891 AA233707 AA233707	AA243560 AA297746 AA40979 AA406142 AA428286	AA48663 AA480200 D60374 T48538 AA015730	AAGC0037 AA157816 F01445 H02835	H16568 H98597 N65563 N75081	RA1406 R54737 R81336 T23461	12246 140769 182310 AAGS9347 AAGS9347	AA20125 AA416979 AA416979 AA421562	AA456001 AA505135 F10802

· 4

142

WO 02/08 64443

PCT/US02/12476

WO 02/086443

Summer to the property of the pr

.O 02/086	20084_1 AA47558 AA40248 AA402571 770097_1 77084 A70810 A7081 20003_1 A7082 A70810 A7081 A70810 A707711 F2423 A4631878 2010978_1 D01010 D03110 D03110 D03105 D03463 2010_1 D0442 D0334	318499 3644 310524 3462 307127 458 304122 7727	31709 83725 312094 79788 319312 15401 319407 16888	20007 2296 320018 18155 319484 16916 316865 15355	31548 19718 31528 2030 31238 90308 312437 29147	311896 ST9182. J AVODAU ALAZOSA MAMASA AUGOSTI RIESS3 318034 (1523. J. AUGTEST TESPA TRASIS AAGTISS4 271102 GESS.) J. AUGTEST TESPA OT TESPA AUGTEST AUGSTI AUG	305528 2883 321270 16620 314128 17766	306442 AA976899 306446 AA977348	306458 306510 308557 308572	306582	30668 306761 306892 308106		306588 308589 308643 308673	308378 308808 308878 308888 308888	308958 308979 303011	NGO16 AAZESIN NGOTA AASINE NGOTA		
	\$	10	15	20	. 52	30	33	40	Ş	<del>2</del>	20	55	09	65	92	75	80	85
0 02/086443	1327 7.39 4.10 7.39 5.05.57 4.10 7.39 10.12 7.39 10.12 7.39 10.07 7.39 5.07 7.30 6.17 7.30 6.17 7.30 6.17 7.30	50.5 50.5 50.5 50.5 50.5 50.5 50.5 50.5		0.12 0.00 0.14 0.15 0.15 0.15 0.15 0.15 0.15 0.15 0.15	0.23 6.65 1.17 1.10 1.00 1.00 1.00 1.00		From the exception numbers for floas Prays In Table 84 lecting uniquesIDs. For each probass sections of the second or the second	amberly extp Obstang and Agorment Took (Doobla Twist, Ostiand California). The Gentrank accession numbers for sequences composing each obstenses liked in the Accession column.	Phay: Uhitya Ea probasi kimilia numba O.f. sunber Gene claste numbar Acrestor: Genbark accession numbers	Phy CAT number Accessions		227173 46891, 1 NEASAN AFRENSAN BERBURG 227173 46871, 1 NESSAN AFRENSAN PARTICH 227173 46882, 1 NESSAN AFRENSAN PARTICH 227179 1510(2), 1 NESSAN AFRENSAN PARTICH 271577 1510(2), 1 NESSAN AFRENSAN PARTICH	677492 27771_1 27871_1	17422_1 47422_1 814584_1 862222_1	38927 1 473768	82296_1 85042_1 37372_1 37372_1	20778 (18780) I ANTSTA ANNOTATI ANNOTAT	233842_1 442885_1 333127_1
	٧,	10	15	20	25	30	35	40	45	?	20	55	09	65	92	75	80	85

AW77246 AW77891 AW77891 AW71821 H5522 Ak18689 AW74183 AW74183 AW74183 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181 AW74181

20

Y08250 Y08245

55

8

2

73

8

S

65

PCT/US02/12476

WO 02/086443

PCT/US02/12476

WO 02/086443 205814 AA78786 205837 AA006124 205839 AA006139 205850 AA07709

10

15

2

25

ဓ္က

35

147

8

PCT/US02/12476

X

													•				
29014404-29014590 29027963-29023166 29087731-29087869	983390-985579 985591-4887271 881790-985570 981790-983364	889276-90813 891906-891240 1696402-1696478 2420546-2420616	1023623-10236523 1263206-12692381 1664617-1664692 1782174-17821922 2747893-37478182	239/3606-2394/3686 2397/3949-2397/4016 28071979-2807/2034 2902/2656-29022775 31401509-31401579	3330760-33339381 3474472-34474531 3971764-3971900 4449069-449193 5443027-5443101	6969182-6969270 7697068-7697238 6092128-6097271 10384481-10384621 10391398-10291600	11386829-11385892 11448985-11449085 12808775-12608833 13638107-13638181 18186944-16159091	17039714-17089988 17132477-17132547 18082184-18062402 18074402-18074501 18252026-18252189	18371200-18371282 19345573-19346660 19435506-19435596 2124713-21244828 21221871-21221953	21509763-21509864 24404720-24404899 27226005-27235108 27792166-27792272 28410653-28410734	29160655-29160725 30077787-30078184 30760793-30760968 31141580-31141765 31456454-31456519	31583467-31583536 32216799-32216527 33223671-33223819 133567-1339397 2628236-2628109	26,2606-26,2457 2711704-2711565 30,78925-3028811 3204124-2204036 3308446-2308358	3308538-330831 3310817-3310749 337722-3378309 4308400-4308304 6468335-6465727	6467090-6456768 6217374-6217761 6218238-8218063 11822456-11832508 11921456-11921205	12732417-12732289 12734355-12734269 1320978-13200692 14478333-14478172 1478333-14478172	1629993-16298937 20078117-20077891
		15555	2522	22222	2222	2 2 2 2 2 2 3 3 3 2 3	22222		8888	22222 22222 32222	2222	Menus Brans	Minus Minus Minus Minus	Minus Minus Minus Minus	Minus Minus Minus	Minus Minus Minus Minus	Minus
	Outhern, I et al. Durham, I et al. Durham, I et al. Durham, I et al.	Ounham, Letal. Dunham, Letal. Ounham, Letal. Ounham, Letal.		Dunham, I et al. Dunham, I et al. Dunham, I et al. Dunham, I et al. Dunham, I. et al.	Dunham, I et.er. Dunham, I et.er. Dunham, I. et.er. Dunham, I et.er. Dunham, I. et.er.		Dunham, I. et.el. Dunham, I. et.el. Dunham, I. et.el. Dunham, I. et.el. Dunham, I. et.el.	Dunham, I eleti Dunham, I eleti Dunham, I. et al. Dunham, I. et al. Dunham, I. et al.	Dunham, I. et.el. Dunham, I. et.el. Ounham, I. et.el. Ounham, I. et.el. Dunham, I. et.el.	Ounham, I. et.al. Dunham, I. et.al. Ounham, I. et.al. Dunham, I. et.al. Dunham, I. et.al.	Dunham, I. et.el. Dunham, I. et.el. Dunham, I. et.el. Ounham, I. et.el. Ounham, I. et.el.	Ounham, I. et.al. Dunham, I. et.al. Dunham, I. et.al. Ounham, I. et.al. Ounham, I. et.al.	Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al. Ounham, I. et.al.	Ounhern, I. et.el. Ounhern, I. et.el. Dunhern, I. et.el. Ounhern, I. et.el. Ounhern, I. et.el.	Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al. Dunham, I. et.al.	Dunham, Letat. Dunham, I. et.at. Ounham, I. et.at. Dunham, I. et.at. Dunham, I. et.at.	Dunham, L. et.al. Ounham, I. et.al.
WOON WOOD	336632 336633 336634 336636	33653 33653 33653 33654	336948 337028 337028	337183 33728 33728 33729	25.00 20.00	237958 238008 238033 238110	338145 338178 338178 338197	338359 338357 338359 338359 338359	338418 338418 338418 338501	33862 33862 33854 33836 33879	338937 338933 339100 339114	339121 339170 332858 332858	102091 103091 103097	233122 233122 233260 233260 233260	13360 33483 3483	2222	334787
	S	01	15	20	25	30	35	6	\$	20	55	9	65	92	75	8	82

WO 02/086443 7775 6867964 Minus 7796 6867962 Plus 7940 6249578 Minus

2

ಜ

35

\$

20

150

																٠																													
205138-205269	207533-207690	117397-117483	130314130370	13994-140138	70295-70423 163474-163605	32438-72663	115749-115962	64228-64402	105841-106035	172397-172481	7831-8035	70854-70915	661381-681510	62787-62929	69283-69413 148088-148200	301888-301972	117120-117216	22760-22919	41702-41841 8818-8949	3663-36809 2368-23828	100091-100282	21168-21301	37517-37638	59613-59770	35311-35406	24656-24749	84525-84677	117697-117899	19023-16561	10217-10357	783870-783817	2247267-2247437 4041318-4041431	4734947-4735069 319951-320040	20247-22343	48583-48773	65701-65781 189459-168544	69745-99836	8702-8820	102451-102586	75101-75181	181573-181662 37610-17878	34358-34474	200262-200495	2513-2743	87554-87710 31003-31583
.43 Whas	Minds Minds	2 2	Minus	Minus Plus	Minus	5 £	2 d	Mime	2 2	Pice	Minus	2 3	Minus	Knus	§ §	ž 5	2	2 2	E S	2 2	Minus	2 2	£ £	Minus	Minus	2	2	2			£ &	2 2	2 2	P P	P. S.	2 E	Maria	3	<b>F E</b>	3 £	2	Z.	Par :	Minus	Minus
02/0864	6463828	6682468	6682490	6065793	6624838	5867087	5887124	5867133	5867153	4567168 6671887	5867168	5867178	5867188	5867208	5867212	5867230 4567162 ·	6042048	5867320	5867435	5857439 6138928	8015249	6016253	6015278	6015302	6671869	5867637 641783	6552456	6682502	5967657	6004448	631965	6531965	6531965 6531965	6531976 6866841	5867481	5867525	6249562	5867743	5867759	5867772 5867776	5867783	5867804	600463	5667691	5867910 5867940
WO waste	325782	325685	325819 329764	328643	323816	325883	325925	325941	32697	330020	326163	326025	328099	326165	326204	326230	330038	326589	326393	326515 326592	330107	3000	330088	330085	330123	326605	328720	326692	326983	326936	327040	327075	327085 327038	01.722 02.723	327288	327220	32732	327396	327442	327473	327483	327562	327606	327642	327734
		S		9		:	2		ć	7		25	ì		30			35		;	40		;	42		05			55		5	3		65			20		3,6	?		0	3		83

. **‰** 

		Ha. (91125 Ha. 293441 Ha. 293441 Ha. 19825) Ha. 81221 Ha. 81221 Ha. 81221 Ha. 272822 pt. 42.27822  Ha.288036 Ha.288036 Ha.236301 Ha.237260 Ha.117183 Ha.67846	Ha.75431 Ha.20234 Ha.71376 Ha.27776 Ha.246759 Ha.28414 Ha.2850 Ha.2850 Ha.3850 Ha.3850 Ha.3850	H. 11269 H. 12891 H. 12891 H. 12891 H. 12891 H. 12891 H. 128073 H.	H, 4428 H, 18233 H, 4527 H, 4573 H, 4574 H, 2548 H, 25	
WO 02/086443	10541 10544 10576 10577 10532 106137 106139 106139	405621 X57809 405621 A245210 405562 U24683 406671 AA12954 406678 X62399 406678 U17534 406678 W11753 406678 W11753 406679 W31126			407782 AA60396 407780 AA6114 40781 AW19392 40781 AW19392 40784 R2408 40500 L11690 40500 L11690 40500 AW14882 40500 AW14882 40501 AW14882 40512 AA4382 40512 AA4382	406151 BE43803 40838 F61438 40838 AF12303 40838 AF12303 40838 AF12303 40858 AF12303 40858 AF123403 40858 AF123403 40851 AF123403 40851 AF123403 40851 AF123403 40861 AF123403 40861 AF123403 40861 AF123403 40861 AF123403 408771 AF123573
5 10 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	15 20 20 20 20 20 20 20 20 20 20 20 20 20	25 30 56 56 56 56 56 56 56 56 56 56 56 56 56	35 35 35 35 35 35 35 35 35 35 35 35 35 3	50 ### ### ### ### #### #### ##########	65 55 55 55 55 55 55 55 55 55 55 55 55 5	408353 408359 408359 408359 408329 408329 408329 408359 408359 408439 408439 408439 408439 408439 408439 408439 408439
PCT/USO2/12476  Exal/Agricos, anall cell carchenes, gradenativa and carched Exal/Agricos, Hall Geneckly array. Exal/Agricos Hall Geneckly array. Exal and infiltuda. These sequences were clastered based on sequences ion manifers for sequences completing seach claster are stated in the	cell carthornes, prandomibjos and carchold tumos) devided by the trais, globertatis, saltmai devided by the severage of normal time earnifes	77 1.00 1.00 8 2.24 8 2.24 0 1.00 1.00 1.00 1.00 1.00 1.00 1.00			1.4.1 1.18 1.6.4 4.7.00 1.6.6 1.19 1.6.6 1.19 1.6.6 1.19 1.6.6 1.19 1.6.7 1.10 1.6.7 1.1	
WO 01/0864.43  Table St. Phenist Thereault, Disprate and Propriate by Thereay of Lung Cancer  Table St. Above about 131 gream up-regulated in high lamon (hording agrantous and controlled.  Table St. Above about 131 gream up-regulated in high lamon (hording agrantous and controlled.  Table St. Above about 131 gream up-regulated in high lamon (hording agrantous and controlled.  Table St. Above about 131 gream and agrantous and agrantous and agrantous agrantous and carchottes.  Table St. Above the accession number for method thereof the form of the form of the person of the person of the person of the form which the disperson of the form	Play: Unique Eds probesies identifier number EUAcci. Emmigra Accession in marker Unique (EMM): Unique enteries in marker Unique (EMM): Unique enteries in marker Unique (EMM): Unique enter side ILIQUE (EMM): Unique enter side Ri: Average of lump tumore (including squarous call carchemes, scheoceamhornes, small cell carchemes, genuidomischa end carchemes, denoceamhornes, semall cell carchemes, genuidomischa end carchemes (including sycarous call carchemes, scheoceamhornes, semall cell carchemes, genuidomischa endered by the sevenes of normal blue samples RC: Average of normalization of stesses a semble (including transchills, emphysieras, stillorist, stabilitation by the sevenes of normal blue samples RC: Average of normalization of stesses a semble (including transchills, emphysieras, stillorist, stabilitation of the sevenes of normalization of normali	X0628	AA28778 H.179139 U.V. I porth, estopen reputeds AA28774 44.180027 Perspector 2.A Fl-Adming cressists, sub-AA28245 Fabrillo Cre	## ## ## ## ## ## ## ## ## ## ## ## ##	141   142   142   142   143   144   145   145   144   145	EUS-SPOROZIOZI, ALF. Schorby on his linger  INI_CZZZZ-Binno sperie kirasin proseh 6  Terpel E.m. N. (2000/22)-(1910/22)-(1910/21

		•																					_								40							wo			~												
	14.65	25.5	83	6. 8.	2 2 2	8.5	55	S	g 9	2	98	8 5	3 5	2 6	8	9	38	9 8	27.7	8	8	8	43.42	ដ្ឋ	18	B.92	<u>\$</u> 8	3	E 5	100	38	3	- S	13.61	8 <del>2</del>	83	88	22.22	2	2 2	<u>§</u> ₹	2 5	8	5 <b>5</b>	3	82	5	38	8 5	200	85	ន្ទន	32.51
	offactumed a related ER localized proteil	trypothelical protein AF301222		zho finger protein 28 i H2A histone family, member Y		- 0	_	ESTs	hypothetical protein DKFZp547J036 stam.hypothetical hypothetical hypot	Interferon-etiructated protoin, 15 kDa	panecipoon lactor BMALZ fidgeth-like 1	Indolesmine-pyrrole 2.3 doxygenese	UEALTH (ASP-CH-ABANDARTH) BOX polytep ESTs	hypothetical protein FLJ12443	-	hypothetical protein MGC5350	ESIS chrRC1.HT0373-120200-011-e08 HT0375 Hemo	•	email inductible cylokine subjectly A (Cy length, pers 1 / April / 1817), tellin	ESTs, Highly similar to unnamed protein	centromers protein E (312/d)		Home eaplans cDNA PL112981 fs, clone NT	syntacin 1A (brain)	Hamp sepients CDNA FLJ 14438 fts, clone HE	Homo saplens cDNA FLI 1448 fts, clone HE	WAS protein family, member 1 Chamill exten crystal problem	phosphoduconate dehydrogenese	hypothedical protein FLJ10038	: 5	hypothetical protein MGC2721 ubleatifa carboxyldeminal estocase L1	S	F. 5	-	Nament-PCK disease, type C1 Homo sapiens cDNA FLJ13522 ffs, clone Pt.	۳.	E 8	enhancer of zesto (Drosophila) homolog 2 decretores activator unbinesa			epidermal growth factor receptor (avian DNA (cythalha-E-Lmethyltransferase 1			Imphocyte anigen 8 complex, locus E KIAADDIS cene omduct	· w ·	3-hydraxy-3-methygrulary-Coonzymo A sy tissue factor pathway inhibitor 2	ш	EST8	ESTs KIAA0071 ordein		i iii ii		Home sapiens CDNA FLJ 11381 fts, done HE ESTs
	Ha.74376	Ha.335851	Hs.74619	Ha.59757 Ha.75258	Ha.76117 Ha.821	Hs.76182 Hs.76184	Hs. 104613	Ta.191868	Hs.21433	2	Hs.137516	Hs.840	Ha. 128065	Ha.179882	Ha.149089	Hs.71331	4.17183	Hs.75478	Hs.76498	Ha.35406	Ha.75573	HS.54310	Hs.144687	Hs.75671	H-33465	Hs.120905	Ha.75850 Ha.889	Hs.75888	Ha.21331	Ha.75939	Hs.76084	Hr.76473	Hs. 296278	Ha.76888	Ha.288735	Hs. 107907	#.72 #.72	# 7778 # 7771	H.7328	H.77367	14.7432 14.7482	4	H.77613	H.77687	H <sub>2</sub> 24951	15.23594 15.23594	Hs.72402	Ha. 130853	H.6546 H.739	H 78589	Hs.278558	H.225841	Hs.127797
WO 02/086443	7753865		H06362 AL037159	018422	5901 VD68115	12221	292100	V732182 ·	4858	583085	A061271 E536218	34455	129640	E250788	733859	V295847	V3UZB85	023173	439580	32246	5005	133338	7294416	048146	V368397	963304	148072	263280	824298	17.0	V409985	0285	204500	9829	310440	5348	1410370	2419	1691	7755	6370	926960	1884	BE076358 BF283782	V95A064	044872 8356	W21113	(948033	1450	NM_005025 RF394784	649850	653718	AA886115 AZ87700
OW	112859 AV	222	112811 HG 112817 AL	17863 AV	13001 13011	13048 MK	(13129 A	H3223 AI	613248 T6	413278 BE	(13364 BE	M SSES M	13453 A	(13527 BE	M3573 A	(13562 AV	ALSSY AV	_	413719 BE		413833 ZI	413926 A	113943 AV	413995 BE		14180 A	614245 BE		414334 24	H4369 W	11416 A 11430 A		614618 AI	14683 S	# 14 14 A	H 4718	114747 CE	414761 AL	114806 D	14808 X	14826 X	44883 A	4514	14945 BE	1801 1801	15091 15138 C	(15227 A)	45263 A	415235 P.	415669 NI			415857 A
			S			2		•	≏			20			52				2			35	2			6			45	2		Ş	2			22			8			65		,	2			25			02		88
							•																																														
2776																																																					
PCT/11S03/1374			•																		•																																
7	;																																					٠															
	1.07	8.8	888	38	3 %	195.00	<u> </u>	40.00	35	88	23.00	8 8	8	2.10	8	28.2	17.00	88	8	18.12	5.00	8	8 5	2.12	5	52	8.00	88	3 3	8 5	8	8.5	1.32	8 8 8 8	8	- 58 - 13	18.00	\$ 5	8 5	87.6	5 22	8 8 8 8	2	255	202	= : :::	8.6	8.5	2 62	¥ 8 8 8	7.6 200 200	2 2	85.98 85.98
	1,02 81.14	24.67	38	8	3 <b>3</b>	112.42	9.7 20.7	4.0	9 6	22	1.80	8.5	8	£ 5.	8	3.97	8	28212	8	Q.12	8 8	8	8 2	7 S	212	5.5	<u> </u>	88	35	1.12	8.	9; <b>5</b>	2	82	8	9.8	8	2 Z	0.0 9.0 8.0	8	38	28	<u> </u>	77	35	9	8 2	22.7	2.13	# 8 # 8	118.48	1.98	41.52 17.90
	s				Spenso				0 -			0									1321 (1	٠,					Homo			ų	Į.								I			aug.	m				¢						
	e, type C1, gen		Minase, dell	rotain (G pr	WADH dehydr	BED (DOAN 15			tase 1, miloch	9260A B cell		72 solvitat homolo		90) pare				o Parioto	ssociated prof	euroblast	Asset An	A NIH MGC	ce deficient (S		Mh AB e		Le09 BTCC19 Homo	144		Te fle about VE		-				fro 4	2	einese doma	044 fis, clone I		polypeptide	TSLRE pr Hota BTCC79 Homo	108 fis, clone l	Here-ESSOC	otalu	:	a protein L8m	rotein (G pr		ih 18 is viral oncog	(rathines	lory factor (	edpha .
	n-Pick dhese	Linase 1	hosphorytae	Ode binding p	mo seplens	cytokine substately, XP_CS			or marronan sphate synthe	imilar to 210		teh FL/133		2 (nicain (10 cainine/seda		Otem 1		ine) proteins	oreth furnor a	chantified in	THENY: CON	#4110U	ne majnipenan		activin A, aci	PESO 1	120200-014	-6	o in cencer, i homolog	, C 440	tein FLJ1265	tels FU 1051 In 281	te protein 2	Jeh FL 11314		orotease, se	telo KIAA 13	f metalloprof	ONA: FLZS		nogodymia se activadno	6 258 - CT	ONA FLIA	Motic centror	e ectivator pr	-6	clated Sm-10	6de binding p	remeal or '	ocieted prets etocytomatos	dein FU1090 a. Kinesh-Bu	gradien inhibit	ntein FLJ 1334 plion factor Y
	NPC1 (Nemans-Pict disease, type peundandis bushe bitana, men	vaccinia related	B commodulin 2 (phosphorytase kinase, deli	Quantine modeo	Dycoprotein (FI	smad inducible Hypothetical pro	EST <sub>8</sub> CG-04 protein	XAGE-1 protein	carberroy-phos	ESTs, Weathy s	EST	hypothelical protein FL313352 sine cours homeofox (Onesothla)	ESTa	laminin, gomma 2 (niceln (10040)), solicina factor, archime/serbe-rich	EST	NCK adaptor protein 1 chrom@TiO1 at Strategory availant concess	ESTs	sorina (or cystoine) probehasse inhibito	Homo saplens	thymosin, beta,	Homo sapiens	CHIF-BRO	minichromosom	ESTS	Inhibin, beta A	hyatuman synthese i	de:RCC-870319	KAAAB18 prote	riging expressed in cencer, non in te profine coddase homolog	ESTS	hypothelical pro	hypothetical protein FLJ 10514 who finner contain 281	hyporda-inducts	ESTs hmothefical rm	ESTs	carbonic anhydrase IX Vansmembrane protes	hypothetical protein KIAA 1335	nypourence pro a dishtagrin enc	Homo saplens c	ESTa	severytan cyclase activating polypeptide	cell division cycl ob: OVA-BT0379	Homo sapars o	MO-2 protein Mnesh-like 6 (mitotic centromere-essoc	GW2 ganglosid	MAA1077 protein	US snRNA-associ	guarine mucleotide binding protein (G	Adlican	microtubuse-essocieted protein 18 v-myc evfan myetocytomatosis vir:	hypothetical pro RAB6 interactin	macrophage mi ESTs, Weathy s	hypothetical protein FLJ13346 ructear transcription factor Y, othhe
143	1000	H-48269	H. 18227	Ha.71642	H5.49787	Ha.50081	Ha.19072 Ha.50441	Ha.11220	Ha.50968	H-27169	Ha.18757	15.22972 14.54418	Hs. 129058	Ha.246735	Ha.67688	Ha.54589	Hs.190721	Ha.55279 Ha.66077	Hs.108681	Ha.56145	H.35263		Hs.57101	Hs.278025	Ha.727	Hs.57697	17.00	Ha.58009	HS.20109	He.7991	Hs.15830	Hs.59346 Hs.59757	Hs.61762	Hs. 278153	Hs.95469	Hs.63287 Hs.63325	Ha.45207	Ha.64311	Ha.6994 Ha.66425	Hs.165028	Ha.68137		Ha.334605	Hs.69328	Hs.289082	Hs.70623	Hs.70830	Ns.71842	Hs.72157	Hs.103042 Hs.92137	Hs.73239 Hs.73525	Hs.73798 Hs.22828	Hs.266273
WO 02/086443	F192522	59012	1046017	A058325	E383387	97450 BICCO025	A401369 E243834	72127	154830	1554298	4625304	A576953 V 005982	E220023	15008 21945	581173	M,006153	M01359	17601	769160	4125985	W675258	W502152	W247090	4511413	W103364	M 001523	E065985	8020725	78467	15387 N748608	E311928	11259	(381807	E043077	W182663	11382	9037756	77.235	E\$40255 N246890	375672	30435												AA766268 ALG31778
WO	408783 A	106905 H	406873 A	(06992 A	409015	1000 A	409077 A 409093 BE	409103 A	409187 A	409228 A	409268 A	409289 A	408404 BI	409420 Z	409448 AL	A09505	409582 A	409632 W	409719 A	4 15794	409744 A								410048 W					410309 BE										411263 BE									412530 AV

	PCT/US02/12476	
	2.22 2.22 2.22 2.22 2.22 2.22 2.22 2.2	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
•	proportion convertions utilitativistic in protection of the convertion of the conver	and gradiench promit 18 (comitie) micking (seate promit power 18 (comitie) and produced promit 18 (comitie) and produced promitis to the house 20 of 16 concrete trained 2.04 (16 concrete trained 2.04
	9018 9018 9018 9018 9018 9018 9018 9018	777 777 777 777 777 777 777 777 777 77
	0.2/086 20.2/086 20.2/08/20 20.2/	18.00 House to the control of the co

6 (1712) 4 (

		-																																																																			
	EST	hsuftoma-estociated 1	Ebis hypothetical protein FLJ21620	hingda, beta 8	paratheold homona-like homona	protein lyrosine phosphatasa, receptor l	cylochrome P450, subtamby XXIV (vitamin amel industries) a contribute subtambly B (Cv.	ESTs	hypothetical protein FLJ12888	apolipoprotein H (bata-2-gh/copresent)	KIAA0007 protein	gb:HUM316G108 Contach human sorta polyA	PTK7 protein tynosine kinase 7	ESIS ESTs Weath strike in masmed multip	nucleochosmichtedeoclesmin 3	fibricosn. A state por peofice	Hamp septens clones 24522 and 24523 mRNA	chilinges I (chilotrosidase)	(agged 1 (Alagille syndrome)	topolsomerase (DNA) II binding protoin		equaporn 4	portexpectual mod_con_col mano aspenta	sho (dicten handra), the frase and	ESTa, Moderately similar to 2N91, HUMAN 2	phosphotpase A2, group VII (platelal-ec	gbod91d05.y5 NCI_CGAP_Xdd8 Homo saplens	DIG-ZPASAND14 protein	Homo sapiens mRNA; cDNA DKFZp588E1624 (t	EBIG	Consecut Annualize purine recognize	cycle-droendari kinnse 4	Human DNA sequence from clone RP5-1103G7	calctum channel, vollage-dependent, PAD	ESTs	ESTs, Westly single to ALUS HUMAN ALU S	SOUTH (OF CINCIPAL) (FOCULARS WINDLE)	chendramodella lareamen	skraler to rab i 1-binding protein	hypothatical protein	ESTO	CSTs.	ZAP3 protein	Homo sapiens cDNA FLJ11381 fts, clone HE	lectin, galactoside-binding, soluble, 7	ESTS	Emiliar Processes cyclone & Sublamiry (C)	FeTs	EST	EBTs, Moderately similar to 138022 hypot	metratasis eseccialed 1	Galveptan E	EST	hay oxidase	Homo sapiens mRNA; cDNA DXF Zp43480425 (f	SAMS	ESTa	echtle cerrier family 1 (ghulamate trans	thymidine kinase 1, ecluble	Solution alpha 2 Anishttemstores at 1	GDMF family receptor alpha 1	DKFZP564O0823 protein	secreted itizzled-related protein 4	German, Dolla 2 beful factor 1 (hasest Canate estimate	sorting nexts 10	protocodharin 17	ATP-binding cassetts, sub-tamily 8 (MDR)	ESTs DEPONT	HSPCUS/ procen
43	Ha.87113	H. 69584	H. 18878	Ha.52820	Ha.89626	Ha.89655	Hs. 83663	Ha.87507	Hs.284137	HS.1252	Ha.90315		Hs. 90572	H-155649	H 90691			Hs.91093	15.91.E3	18.91417	128151	75.700050	H- 93002	Hs 92005	Hs.152818	Hs.93304		M. 93836	H-94000	H. 133294	1000	Hs 95577	H-348112	Hs.96263	Hs.323494	H. 21766	He 102408	HA 97872	Hs.98510	74.98806	Ha.69115	N. 98678	Hs. 159471	Hs.127797	Ha,99923	Hs.44269	16.1004.31	No. 100305	Hs.197653	Hs. 14691	Hs. 101448	1 19072	Hs.189902	Hs.102267	Hs. 103305	M.324728	Ha.50831	Ha. 104637	Hs. 105097	H 10516	Hs.105445	He.105460	Ha.105700	ME TUDSE	Ha.106260	Ha.106511 Un. 20207	Hs.107911	H. 112457	M. 105150
WO 02/086443	AA350392							AA256106						A 4 4 8 9 1 2 1			AF070690						NA monto																AK001978														A913562				AA291377											W69233	
3	418971	1907	1908	1988	19121	419171	459180 45978	419288	418335	18354	28.5	286	419452	127	188	(19502	4195.79	419656	18569	182	9/6	7/617	440741	419745	419752	419809	19936	1661	19983	50003		20162	(2025	420269	42028	98	72032	420A67	120520	20252	2020	420689	420721	(20759	420783	00602		20107	21037	421041	21073	213	21150	421165	751307	21318	121451	421474	421506	21515	121524	421526	232	4/012/4	51633	421659	52120	513	1117
			S				2			1				20	ì			ě	3				ç	3			36	ç				40	?			YV	7			Ş	20			;	22				9				65				2				75				8			8	3

25	1500 213 213 213 213 117 117 110 110 118 226 226 226 226 226 226 226 226 226 22
	UDP dycostrustiense 1 turn), polyse PCIATE protein times 1 turn), polyse ucidio monochospitus synthetias (orotal edition monochospitus synthetias (orotal edition orotal) edition turnospitus (orotal) edition turnospitus
H 133 H 14256 H 14256 H 14256 H 14256 H 14256 H 14256 H 14256 H 15256 H 152	Ha.77834 Ha.77834 Ha.778304 Ha.772316 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319 Ha.772319
WO 02/08/443  WE RESTIT THE AVESSURE THE AVE	AVESOX8 NML 005201 AVESOX8 XSS480 VS3749 AVS3515 AF105365 AF105365 AF105365 AF105365 AAR01359 NML 001196 NML 00008 AAR03739 AAR0739 AAR0739 AAR0739
W	26692 AVE 26691 INA 26691 INA 26752 X30 26754 X30 26807 AA 26807 AA 26801 AA 26801 AA 26801 AA 26803 INA 26803 INA 26803 INA 26809 AA 26809 AA
5	0/ 75 80 85 85
•	
PCT/US02/12476	
19 19 19 19 19 19 19 19 19 19 19 19 19 1	53.00 3.30 68.00 68.00 1.00 70 70.00 70 70 70 70 70 70 70 70 70 70 70 70 7
112	51.50 52.53 52.53 52.53 52.53 52.53 52.53 52.53 52.72 52.53 52.72 52.53 52.72 52.53 52.72 52.53 52.72 52.53 52.72 52.53
ESTS  ATPACHING casseth, auckning C (CTR  SET Altering casseth, auckning C (CTR  EST Altering C (1984) A records  Bearing A (1984) A records  Introduction of the CTR  From the Control of the CTR  From the Control of the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  From the CTR  EST Altering parked  EST	MONAGE OF IL (UNIVED MEMORY)  ROANISED POSES  O subsolist protein Care of Readen  Propries and protein 53 LOs with strong homology  Propries and protein MCS (179 M)  From supries CAM FL 14(34 M, Cher VT  Serve (or cystein) protein are inible  Prof cystein profession and profession are inible  prof cystein profession and profession are inible  prof (1844 Extramellat turn benn said  prof (1844 Extramellat turn benn said  profession inibitation and initiation and deficient  Getting of Committee (194) profession  deficient profession  EST (1844 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn said  deficient profession  EST (1845 Extramellat turn benn benn benn benn benn benn benn be
100 CONTROLLER STATEMENT OF THE STATEMEN	18, 1925 H. 1986 H. 1956 H. 1927 H. 1927 H. 1927 H. 1927 H. 1927 H. 1937 H. 1937 H. 1937 H. 1937 H. 1937 H. 1937 H. 1937 H. 1937
WO 02/08/443  WO 02/08/443  WASSISS THE WA	11568 WASS164 WASS177 WASS177 WASS177 WASS177 WASS160 WASS178 WASS178 WASS178 WASS178 WASS178 WASS178 WASS178
WC 4019 1	

WO 02/086443	429653 MSB874 HL.21559 phospholipse A2, group IVA (cyhoodis, 429736 AF12504 HL.21259 hunor neorosis bathor receptor superfami	ALI34197 Hs.93597	AW873986 Hs. 118383 AA249027	AF092047 Hs.227277 AA464510 Hs.152812	430114 AA847744 Hs.99640 430134 BE380149 Hs.105223	R60704 Hs.234434 AWIR2459 Hs. 125759		5 NM_004283 Hb.238147	Ha.239600 Ha.2556	A356923 Hs.240770	430393 BE185030	430451 AA636472 Hs.297939	Hs. 105635 Hr. 241517	130/81	430486 BE062109 Hs.241651	AA480895 Hs.57749	430563 AF146074	430678 AA401369 Hs.190721	NM_001942	X54232 Hb.2699	430935 AW072916	20893	BE041395	AX32764 Hs.125757	431164 AA493650 Hs.94387	431211 M86849 Hs.323733 gap Junction profess, beta 2, 26x0 (conn. 4312)1 AW207837 Hs. 286145 SRR3 (enroquescor of RNA columnates R. ve.	AA501806 Hs.345824 E	AW971018 Hs.21659	BE158000 Hs.285028	AA991355 Hs.280312	431548	431630 NM_D02204 Hs_265829	BE221890	BE019924 Hs.271550 u	Hs.271988	431858 X63629 Ha.2877 ca	432023 R43020 Hs.238223	AIS67421 Hs.273330	X81334 Hs.2936	BE382679 Ha.285753 AK001739 Hs 274763	AX001106	432375 BES36069 Na.2962	432407 AA221036 432441 AW292425 Hs.163484	A/B04855 Hs.207530	432652 AIS37170	432683 AW023624 Hs.162282 432606 NM 00210M Hs.3068	A1243596 Hs.94830 N82096 Hs.293185	432677 NM_004482 Hs.278811	427753 NIA, 1014076 Hs. 2359338 Home sapiens PRO0353 mRNA, compute cts 427789 A6271031 Hs. 178499 Home sapiens pRO0353 mRNA, compute cts	432842 AWS74093 Hs.334822 432857 AWD16936 Hs.233384	432917 NA_D14125 Hs.241517	
		4	n		10			15			20	3		36	3			္က			ž	ડે			<del>4</del>			45	!		20			55			S		. ;	65		Ę	?		ž	C		80	3		82	
PCT/US02/12476																				-																																
3	888	888	88	3 p 8	8	3 3	978 878	7,5	6200	00.64	97.00	2.63	88	82	12	69.00	8	£.	3 8	8	211	8	81.8	15.90	1.43	8 8	8 t	8	58.00 50.00 50.00	8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5	888	3 23	92.00 6.15	22	8	238	3.31	67.00	9.6	3 2	25.82 25.82	₽. E	1420	2 S	98	8 8	17.00	55.00 1.37 1.37	8 8 8	28	8	
	838	2 2	-==	200	2 9 9	≥ ₽	8 <b>2</b>	9-	. 5	6,	. 12		<b>.</b> 25	2.	2 50		<b>.</b> 23	٥,٤	9 50	<b>9</b> 7 (	- ·	, ,	8.	- ~		30	<b>3</b> ,	20		ء -		2 50	<b>e</b> ~		ئوڭ	9.9	E ~	. g =	٤.	200	۔	= ^	. e	28	<u>5</u> 2	٠ ـــ ا	2 80	ഇ ത	<b>2</b> 6	* O	•	
	ubduttin carrier protein gb:ea70b08.s1 Stratagane achtzo brain 81 gct.	G antgen 78	1853 1873	surfaciant pulmonery-excelaind protein	SPANX family, mamber C	grutansis receptor, metaboropic 4 268 protessome-associated pad1 homolog	small nuclear RNA activating complex, po minichromosome maintenance deficient (5,	hypothetical protein FLJ23188	collegen, type X, alpha I (Schmid metaph	Homo saplens cDNA: FLJ73228 fs, done C	hypothetical protein FL14904	FGFR1 oncogene partner	noted a superingent spain prozen pro solute carrier family 25 (machonomial	ESTs hunchalical apptain El 120118	serine/threatine kinase 12	tumor necrosis factor (igand) superfami	giviamate-cysteine ligase, catelytic sub	Homo suplens cDNA: FLJ23602 fls, close L	E.S.1.5, Model areny terrorat to tubusz nypox E.S.1.5	protein disutide Isomerase-related prot	ESTS order observational sin 2	ESTs, Westly similar io GGC1_HUMAN G ANT	small inducible cytotine sublamily B (Cy	eovamie intoliary lector (chominary): matrix metalloorolehase 7 (matrihrin.	Home sepiens, Similar to DNA segment, Ch	stretting gaine product	cell division cycle 2, G1 to S and G2 to sold to carrier form? 7 features arrives	chromograph B (secretograph 1)	TBP-Interacting protein ESTs, Weathy similar to 2017205A Ghydro	similar to SALL1 (sal (Drosophia)-like KIAA 1888 emich	hypothatical protein	hapsi protein hypothetical protein FLJ14303	KIAA1089 protein E8Ta	riting adde synthase 24 (inducible, hep	KAAUTSI pana produci	WNT1 Inducible signaling pathway protein artemin	teizure related gene 8 (mouse)-like Homo azniens cOAA FLJ 13103 fla. clone NT	ESTs	KIAA0704 protoin	group-spectro component (Ntarra D ting gap function protein, beta 5 (connexin 3	ESTs .	ESTs, Highly shaller to 550712 band-6-pr ATP-bindion cases the sub-family A /ARC1	G protein-coupled receptor 61	matrix metalloproteinasa 14 (mambrane-in POU domain, class 2, associating factor	DESC1 protein	Spocatin 2 (ancogana 24p3)	ESTs	ESTs sukaryota translation krittation factor	a dishipgin and metadoprotehase doma LUNX protein; PLUNC (palate hing and nas	pliulizy tumor-transforming 1 ESTs	neurofisment, fight polypeptide (58KD)	
13	Hs.174070	Ha. 251677	Hs.97649	H-17582	H-343875	Hs.178761	15.178012. 15.178585	Hs.36793	Ha. 179729	15.17121 14.180121	H. 180191	Hs. 180296	H. 180406	H. 134726	H. 180655	H. 181097	Hs. 151393	To assess	Hr.104830	Hs. 182428	H8.26912	Hs.293317	Hs.2248	4,2256	Hs.65551	H-184510	Hs.334562	Hs.2281	H. 184788	Hs. 189095	Hs.191381	Hr. \$8502	Hs.193143	Hs.193788	Hs. 163810	H. 194680	Ha.194768	Hs.116588	Hs.197955	H. 198249	· 12.326447	Ha.292911	Ha. 198612	H-2407	Hs.201877	H.204238	F. 190721	Hs. 2437	Hs.2442 Hs.211092	Ha. 120845	H. 211584	
02/0864	77239 BE270447 Hp.174070 77250 AA683848 Hp.102869	(448542 7804	V023482	100	112608	361562	7542	(188763	1152	741320	238760	50000	1659	393122	W11425	022310	149563	038843	294506	077258	244311 178984	386042	321849	223	909938	28.	2072	035481	431400	857778	C016825	433988	1028992 1277724	902890	157579	120274	023513 752247	538563	1014504	052693	W207208 153633	01900	056085	C 006235	1,014058	9133	401369	819413	024937	382722	<b>9</b> 608	
W <sub>0</sub>	26 E	182 182 183 183 183 183 183 183 183 183 183 183	A 25.		2	7505 2 2	7525 1528 ≥×	7546 A		200 200 200 200 200 200 200 200 200 200	2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	E	71.9 A	7 <del>7</del> 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	₹ ? 26.50	7	8053 F 150	2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	8698 A 8	7 ¥	1132 BE	823 823 823	22 22 23	SA34 AL	22.2	24.75 74.48 74.48	₹ ¥ 5	86.52 86.52 86.53	3564 AV	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	9758 ★	4 1089 4 4 4	8810 AF	2 T T	₹ 53 53 \$65 54 \$65 54	9038 A A	M 010	26 26 27 27 27 27 27 27 27 27 27 27 27 27 27	25.5	₹ ₹ 828 858	9259 A	22.5 27.5 27.5	3328 27.78 27.78	24.03 E. E.	2 Z	9547 B	3851 A	9610 AE	9616 A	X 9596	

	17.00 112.00 775.00	32.5	25.50 20.00	3.00 5.00 5.00 5.00	252 252 253 250 250 250 250 250 250 250 250 250 250	83.00 31.00 90.00	22.39 36.90	00.00 00.00 00.00 00.00	24.0 24.0	257 257 257	283	588	7 7 5 8	87.5	3.07 52.00 122.00	2 3 E	288	885	2 5 K	8.5.8 8.5.8	2 4 2 8 2 4 2	22.00 22.00 22.00	382	385	88.00
	8888	82 82 83 83 83 83 83 83 83 83 83 83 83 83 83	1988	8888	1.68 1.68 74.03	1220	3 5 7 8 3 6 7 8	202 E 202 E	29B	3883	2525	528	3 E 8	33 6 20 33 6 6	25.23 25.23 25.25	E 22.5	85.8 8.0 18.0 18.0 18.0 18.0 18.0 18.0 18.	86.58 86.58	8 28 E	1,00 32,68 21,28	25 E E E	25 E	2.55 10.85 10.84	2888 2752	141
	ESTs, Whathy similar to KVAADTS8 protein ESTs, Weathy similar to ISS214 s silvery from services mRNA, cDNA DKFZp5402071 (f evr.	Csystein resistance related protein CRR Homo septera mRNA; cDNA DVT-Zp5580134 (# Homo septera mRNA; cDNA DVT-Zp5470023; (# Front septera mRNA; cDNA DVT-Zp5470023; (#	ESIS Homo septens mPNA: CDNA DICT2547C136 (tr hypothetical protein DVFZq782H1311 ESIs			hypothetical protein FLJ23142 ESTs ESTs			type I transmembrane receptor (selbure- ESTs. Human DNA sequence from chone RPI 1-16.2)	Human melanoma-essociated enligen p97 (m nucleoter protein 4 ESTs ESTs	ESTS Williams-Beuren syndrome chromosome regi Human DNA sequences from chroe RPA-85/ESP		Immunoglobulin kappa constant UL16 binding protein 2 honorihedical periesh El (2009)	G proteh-coupled receptor 66 hypothetical protein FL/11608 ESTs	ESTs haterochronatin-lite protein 1 B-cell CLI Americans 118 (zine finost pro	Unroid homone receptor interactor 13 ESTs, Moderately emiliar to GFR3_HUMAN G ESTs.	E8Ts E8Ts G protein-coupled receptor 87	ESTS, Westly similar to ACCOUSES 3 UT km ESTS ESTS, Westly similar to DAP!, HUMAN DEATH	Genta Gontan, ermulocopolates comes (VI), Homo sepiers m7414 full length forset cDN Homo sepiers m7414 full length forset cDN ch-Homo sepiers m7814 full length insert	GDNF temily receptor dipha t ESTs ptatabst-ectvating factor acetyfhydrda	hypothetical protein FLJ 10430 hypothetical protein FLJ20510 ESTs, Westly similar to T17227 hypotheti	KIAA1603 protein hypothetical protein FLJ (020) Home septens cDNA: FLJ2523 fs, done L		claudin 1 Insulin-tita growth factor thirding prote Propulatical protein MGC2408	0 th ea
	5000 5000 5000 5000 5000 5000 5000 500	H. 255763 H. 25646 H. 161962	15.24.4 14.27.27 14.27.27 14.27.518	H. 156135 H. 5719 H. 127812 H. 135474	Hs.282014 Hs.28687 Hs.2894	Hs. 20999 Hs. 121655 Hs. 307526		H. 292206 H. 130163 H. 130163	Hs.6314 Hs.54618 Hs.114670	Hs.184727 Hs.6414 Hs.192375		Hs.28273 Hs.35598 Hs.163069					Ha.185029 Ha.68399 Ha.68581					Hs. 127699 Hs. 316127 Hs. 325335			
WO 02/086443	AL110216 AL110232 AL110232	R18087 AL137445 AL359567	A125659 BED69268 A1306152 H46008	A954795 D63680 A581344 A068192	AA684838 BE001836 BE262082 AIG37993	BE566249 Al917222 Al886258	AW373062 A467908 AW963217 A918906	AM970529 AAB05507 AAP08578 AW707704	A1245820 A1879064 AW612553	AIRESB15 NM_003787 AAB26425	AA280174 W00947	AA745978 R96696 AI942771	AW138909 AW238299	AW837046 AF086161 AA401369	AA632012 AF086270 AA918317	BE264974 W89813 AF086310	W72348 AF086413 W79123	AF088078 AW085525 AW072527	AL159053 AL159055 AL159055	AW449211 AW014875 AW247529	AW600291 AKD00517 AW473675	AA864968 AB033023 AI805392	NM_003812 R39127 AV657117	AF134160 N69241 AW082298	AA401369 AI110684
×	407781 407205 407205	944			437852 437873 437873			C00078															440482 440482 440527		
		'n	10	15		8	25	. 65	2	35	9		\$	20		55	5	3	65	1	2	75	8	8	85
																·									
PCT/US02/12476																									
	8 5 6 6 5 6 6 6	8888	95.00 95.00 95.00	8 8 8 8 8 8 8 8 8 8	6.00 6.00 6.00	888	35.85 35.85	8 <u>5 8</u> 8	8,8,8,8	888	8888	888	9.62 38.09	00 00 00 20 00 00 20 00 00 00	288	3.00 2.00 2.00	72.53.8 78.89	8F3	2520 100 100	# # # # # # # # # # # # # # # # # # #	3 2 6	7.00 2.75 5.00 5.00	0.00 7.00 7.00 7.00	8 6 8	<b>23</b>
	- # <del>-</del> =	- 86-			- 42	<b>→ &gt;</b>	-64-		- 20 50						0 C4 F5	- (4			_						

Mens clones 24714 and 24715 mRNA

	E816 E85	poly(A)-Unding protein, cytoplasmic 14		_	Homo espiens done 24859 mRNA soquence	ESTs	ESTS . Month semilant of NAI- El 179587 for along la	hypothetical protein FLJ 10540	Rh bypa Cghcoprotein	ESTS	ESTA, Weathy similar to ALU4, HUMAN ALU 6			secreted phosphoprofem 1 (osteoporalo, choo phosphoprofem chool phosphoprofem contractions and contractions)		mitatic spindle colled-coll related prol		every Contraction of the Contrac	Homo saplens CDNA FLJ 14934 fts, clone Pt.	small inducible cytokine subtanily A (Cy	hypothetical protein FLJ 11036	E318			relindic acti receptor responder (lazaro		Homo septems club mRNA, partial sequence	-			ESTs, Hohly similar to 602392 atpha-2-m	-	ESTE, Weakly strike to KF39_HUMAN KINES		ESTS broothalical entieth FL 120607	·w		MAD2 (mito8c arrest deficient, yeast, h	Homo kaplens cDNA FLJ14597 fis, clone NT	SEC24 (S. cerevisiae) related gene famili	ESTs, Weatly strater to T23110 hypothed	smiler to a, coronities bows membrans-examina 4-domains, subfamily A	Transmembrans protouse, serine 3	ESTs	Homo saplers cDNA FLJ11245 lb, chore PL					solute carrier family & (neurotransmitte	hypothetical protein MGC5469 TATA box binding grotein (TBP), essociate	much (muchoside diphospitate triked moi	ESTs, Washy strick to putative p150 (H hypothetical crotsin 4/3/10013.3	ESTS	~~			similar to 558401 (cattle) glucose induc		G protein-coupled receptor
5	Ha.174870 Ha.138017	Hs.251946	F-127699	He.132781	H-33355	Hs.156061	13.75	He. 14559	Hs.279682 Hs 149777	Ha.150120	Ha. 12498	Hs.15243	Hs.335933	Ha. 15767	Ha.141867	HS 16244	Hs.16251	H 15362	H. 108545	H.16530	H. 15740	Hs.157601	Hs.9914	Ha.17287	Hs. 17468	H4.326	Ha.17518	Hs.192417	H3.17883	H 19322	Ha.236894	70714	Ha.28149	Ha 18573	He. 18791	Hs. 190721	140726	Hs.19400	Ha.320831	H. 19822	Hs.313413	Hs.20141	Hs.298241	Ha. 11782	Hs.20843	H. 108923	Ha.21058	Hs.21486	Hs. 106823 Hs. 275106	Hs.187958	Ha.19574	Hr.388	Hs.23246	Ha.177164	H8.22785	Hs.389	Hs. 22831	Hs.22920	Hs.22934	Hs.23016
WO 02/086443	AIS70830 REDARGO	W250970	V734009	1347487	SEMBAI	U339982	W168067	WZ63155	VF081497	W139665	W082270	U075640	U310135	0000563	(W13834)	3E091978	10076817	85026	(1811807	(B012113	W001898	1357412	WISSTT	13896	JM 004585	35.299857	1402041	W594641	1878309 117747017	1199268	W256841	(U) 33/2	W837335	U963747	JA6258	VA01369	7,0043	VF157482	W873704	VB018298	181728	50714	US38613	M07369	K002107	ET74398	L035414	E382657	3E614599 1955511	IM_005629	3E814567 U366784	(8025237	U580252	USB1518	09763 U471630	78342	726369 F040704	145051	F148848	W205847
0M	445669 A		445888			446078	446102	692977	446292																														447769			48030		448278			4,8390 4							448844 A				449048 2		
			\$	,			2			15			Š	₹			35	}			30	3			35	3			ΨV	?			45			Ş	2			55	1		9	3		;	3			2			75	!		6	8		8	82
PCT/US02/12476							٠												•										-						-																							•		
PCT																																																												
. 8	38	8.8	3 P.	85	25	211	S 22	<u>e</u> 8	8	027	95	9	88	314	£ 5	3 5	80.08	345	8.5	88	83.00	8.8	8	3 5	850	3	2 2 8	88	200	88	8 6	61,00	£.	20.00	16.00	88	8	8	2	97.	 	25	8 8	29:00	8.8	<b>=</b> 8	658.00	95.0	11.00	900	8	900	8	8 6	90.00	<u> </u>	2	272	<u> </u>	76"
:	5	130.23 12.23	165	<u>\$</u>	3 23	1.47	231	8	8	8.5	8 4.	8	28.85 28.85 28.85	19	8.5	3.0	27.73	8.8	181.59	109.73	8	29:02	8 8	3.5	223	3.18	5. 5.	38	1242	128.84	<u> </u>	18.52	2 2	8 8	8	8 <del>\$</del>	48.74	ន្ទ	. 13 5 5 7	8	3 5	3	3 5	8.	88	15 S	469.00	12.88 24.08	8	800	8	7.02	7.55	8 8	<b>2</b>	<b>5</b> 8	503	<u>.</u>	<b>5</b> 1 5	<u>.</u>
# 10 TO THE TOTAL COLUMN	ests, wasny arrest to 1232/3 hypothet cholinergic receptor, ricosinto, alpha p	RADS1 (S. cerentsiae) homolog (E coll Re	EST8	ESTa	183	neuronal cell acheston molecule	Homo saplens mRNA; cDNA DKFZp5656183 (fr	adenosine dearninase, RNA-specific	ESTa	ESTs	ESTs Fanconi anemia, complementation group G	CDA11 protein	neural precursor cell expressed, develop Norm seriens oftne 2000 mONA sersence	ESTs	ESTs.	Edil, Yogany amena to 21s2_howan 2000 betweenstrain-five projeti 1	choncome 2 open reading frame 2	ESTS, Wealdy similar to ALUA HUMAN ALU S	hypothetical protein FLJ23458	FSTs. Weath similar in All III HUMAN A(1) S.	Homo saplens mRNA; cDNA DKFZpS86L2424 (1	ESTa, Weddy shuller to AF154793 1 prote	ESTA	ESIS, Wessey samuel to 1239/6 hypotheti	Procedural projects Come 1 CCC 1 AUG 142 minute serpe	bramodomain adjacent to zinc linger doma	E8T9	Homo serviens cOVA FL13103 fa. clone NT	ESTB	o-Myo larget JPO1	EST	ESTs	chromosome 20 open reading frame 1	Cezvage and polyaderylation specific is FSTs. Whathy single to A1111 Hillidan A111 S	fbringen, B beta polypeptide	similar to pregnancy-associated plasma p	erdin El	syntacin 8	NAV. 1291 protem folistatin	ESTS	gb:rb47t98.1 Soares_letal_tung_Nb14.19W cofasskm-thtmmediatekmati conductance	type I transmembrane protein Fin14	ES18 neuro-chodical ventral antigen 1	E918	Cholinergic receptor, elcothic, elpha p	boths at box M1	ESTs, Wealty similar to 664054 hypotheti	ESTe, Weakly straker to 2109250A B cell	ESTs	ESTs, Moderately similar to A45010 X-in B socressive hypothema cane	desmocollin 3	hypothesical protein FLJ13057 similar to	antifin (Drosophila Scraps homolog), act	hypothetical protein FLJ 10814 ESTs	CGI-147 protein	Homo sapiens cDNA FLJ10196 fis, clone HE FSTs	hypothetical protein MGC3077	nypomenta process EGF-tra-domain, multiple 5	skb ( S. pombe) homolog	DVOTEGOZIN TEGUCISTO I
	8	₹ 5	3 = 3	R۴	22	~ ?	<b>.</b> _	~ 5	2 28	2:	₽~	2	<b>8</b> =	÷	ĕ:	3 %	3	÷:	2	3 5	6	<b>3</b> :	2 ;	8	8 5	-	83	=	2	# 3	38	3		ຸຊ	2	- 5		≠,	0 =	2	딺	8	욛_	5	5 S	_ 9	35	25	F	~ 🏻	8	2 2	8	5 5	=	86	3	33	23	£
WO 02/086443	M27501	BESIGNED	A1692660	RS1064	44281219	NM_005010	A081848	KT94K9	W242799	4553802	R41782 U744935	4W887434	AW95659	W452649	AW664964	WIRES	W383842	11352430	BE093589	A The Say	L 137761	2877444	AOISEO	KBSJ52	WIRES	AA457211	AW167087	WZGS878	A1128388	BE614387	K44013 U792453	428424	AF038158	AAU25610 1078022	AV655386	AL031290	US83187	A)14442	W 013409	44401369	W24187	BE395085	A330792 U04840	N63620	AMEMAZIA U62432	BES40274	BE387335	RS3734	A1151010	BES38082 9E613128	AI188613	BED19923	AK001468	AK001676 4635931	AA151342	AKDO1058 AVESTATE	AA378778	V245871	AF167572	/97L6X
Ž,	200	1362	1 30	11.07	2 2 3	41607	41636	121	18	61617	11937	17025		12108		12769	67124	H2328	77	177	42558	HZ819	1210	/1/78	12314	M2932	720	100	1727	143247		13400	62828	143572	71907	200	Maris	1203	1,3839	75837	1997	90077	44003	1219	44279	44371	144381	14461	64448	144819	44707	524	183	M5236	MS4 13	257	29757	4887	445680	£2824

ø
~
-
ri.
-
_
~
•
S
=
_
-
-
ťΣ
_
-

PCT/US															
2.38 5.15 16.10 161.00	2120 2120 2120 2120 2120 2120 2120 2120	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	83.08 83.08 83.00 60.09 60.09	1.50 2.00 2.00 3.00 5.00 5.00 5.00 5.00 5.00 5.00 5	22.5 23.5 23.6 23.6 23.6 23.6 23.6 23.6 23.6 23.6	220 63.00 2.10 1.07	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	S22 800 828 800 838 br>830 830 830 830 830 830 830 830	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	51.00 13.00 13.00 52.00 12.00 35.00 35.00	102.00 25.00 1.12 1.00 1.00 1.00 1.00 1.00 1.00 1	75.00 1.92 1.00 1.00 1.00 1.00	2522	8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	134.00
1.81 2.36 1.15 208.65	25.00 25.00 25.00 25.00 25.00 25.00	255888 8888 8888	822288	807 128 128 128 128 128 128 128 128 128 128	<u> </u>	28835 2885	888 <b>8</b> 8	E 3 5 8	13.42 13.42 13.42 13.42 13.43 14.43	25 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	25 8 8 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	7.91 3.16 174.35 153 153	5325	25555	흌.
YOAN1694 protein Richards protein Richards (18 post 18 protein retained with protein setting with protein retained with proteins in retained with proteins and branching near the ATM TO ATM Atmos sentement in the BERG OF at MAT TO ATM Atmos sentement	Homo sapana, Sirdaa lo RREN 4204, 6730 ESTA ESTA Choron for Combine plant 6 charactera (C-C motil) neeplant 6 opelin 81	Human DNA sequences have now RP-8-50E9 solvin carrier termly 6 (perucharantha hypothatic atrief Endin ELJ (1016) Human hobel in RRNA sequence Zo lamb, marrier 2 (odd-point Dracoph Homen septem Enough emerite complemental richardelon stroads and real complemental richardelon stroads and real	e debiteurin end meritaborouskrase doma hypotheurin poutum P115.2 Homo saplema CDVA FLJ 10784 fts, chone N7 ESTs historium i necetor, hype II	Homo septens cDNA FU 12280 fb, done NA Egypush bameabox protein 2A (IRX-2A) ( Egyp ATP-dependant interferon response protein ERDI (\$\$ ceremistable lites	governous is in the Loan-Loss name aspera governous in the transformation darsh 10 E81s derytypean thass, zela (1040)	posto paraglegia 4 (autocomel dominant hypothedical protein FLJ 11011 hypothedical protein FLJ 20350 hypothetical protein FLJ 10604	ESTE ESTE Cryptogene ESTE ESTE ESTE ESTE ESTE ESTE ESTE EST	ESTs EBTs thresh ramby member 4A KAAGOZ protein	Locard recognitions, cannot assure a constraint of the constraint	programmed cell deal) of SET, Wandy sinfer to SUGSO cytake GSI transcripton leave, (IMMonsochus A Piez, Gaze M, Igni A. Gaze M	ESTS ESTS ESTS ESTS ESTS ESTS ESTS ESTS	transcription factor 14,100A transcription factor 130 5 (paste hear NAAO124 protein preferrationly expressed anligen in mola ESTs. Whatky strifter to AAV562 Bont or	hypothetical protein MGC18007 EptA3 EptA4 ESTs Recq protein-like 4	Hizzko (Dresophitz) homotog 10 ESTs Pregnarcy Articael growth lathblor ESTs Histone lands, member L	ESTS, Westry similar to ALLS, HUMAN ALU S
14.3 Ha.19597 Ha.27255 Ha.211579	Ha.78531 Ha.197042 Ha.64443 Ha.23860	Hr.13058 Hr.406 Hr.8109 Hr.137863 Hr.15607 Hr.15607	H-25010 H-25010 H-25159 H-202578	Ha.283467 Ha.28351 Ha.26257 Ha.26257	Hs.265393 Hs.26126 Hs.8702	16.2834 16.2834 16.2834 16.2834	H.20337 H.213897 H.127178 H.190721 Hs.27076	Hs.270563 Hs.270766 Hs.27657	H. 28721 H. 28721 H. 28721 H. 28732	H.2868 H.61311 H.2918 H.2979 H.2932 H.2932	Hs.24685 Hs.23459 Hs.216062 Hs.246063 Hs.222707	Ha.30743 Ha.30743 Ha.30743 Ha.190721	Hs. 2013 Hs. 2013 Hs. 201139 Hs. 201139	Ha.15344 Ha.15344 Ha.2436 Ha.2436	Ha.109057
O 02/086 T05058 ALGCTT2 ALGCTT3 BEE11348 ARGSTST	AW235021 D60730 AW205006 NM, 000679 BE280074	778 H05350 Hs.13. 201 NL,001044 Hs.40. 201 NL,001044 Hs.40. 201 AVAPSSS Hs.24. 149 AVSSST81 Hs.13. 153 ASSSST82 Hs.15.	BEZ18107 AA009647 AF212233 AL050078 A1701505 AA872605	H38960 U90304 AA401369 R48131 AA305384	A1955040 A1955040 H48259 R53228 AW498974	AB029008 H24143 AK000387 AK001466	BEZ78383 A805416 AA016699 AA401369 NM_003729	A821005 AL120173 AA307703 AB018345	AW340281 AA401369 AK000933 TE3500 AF015592	BE379936 AA025386 HW_002202 AB028944 U71207 NM_007115 AL130619 N78223	W31518  AA461538  AW285390  H43805  AF180477  AW294022	AB012124 BE55981 U65011 AA401359 AW173720	AASB1322 X95425 R44214 AB006532 AW795960	NM_007197 ACD1052 AA297891 NS2893 A783307	AIS16269
W 449167 449284 449284 449305	449318 44948 449523 449722	45001 450001 450101 450145 450183	45047 45047 45058 45058 45058	450703 450837 450837 45083						\$228 \$220 \$220 \$230 \$230 \$240 \$240 \$240					
•		~	0	δ	0	Ś	٥	٠ .	0	ဂ ဇ	ν <sub>2</sub>	0	S	0 '	S

PCT/US02/12476		4.58 80.00												ss aaasadt autosss awagags alztabi 1857 Robsa aarootst awootet nessed	A MASSY IB AWROSST ABSSOR A BITORS	34 AABSTD AASI TRY AASSI 18 RESERVENTER AANDERS BEGONZY SELTASI BAAKI ZBO AAND 14 AAASD 14 ZED AZDAGA AANTZOTO AAAASD 18 ZED AZDAGA WYZSTO AAADD 14 AAASD 18 ZED AZDAGA WYZSTO AAADD 14 AABSTS ZED AZDAG AWYZSTO AAADD 14 AABSTST ABDD 55 ZED AZDAG AWYZSTO AAADD 18 ABBSTST ABDD 55 ZED AZDAG AWYZSTO AAADD 18 ABBSTST ABDD 55
ş	255 25 25 25 25 25 25 25 25 25 25 25 25	1.60 1.60 1.00	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	889 889 889 889 889 889 889 889 889 889	25.55.25.25.25.25.25.25.25.25.25.25.25.2	28.888 888 888	85 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8488E	5895	8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<b>385</b> 55	87.00		38226 AW2728 506598 AW46	2876 A5511	65394 AA1889 2 BE069121 AV BE160316 BE1 563 AAA36132 A1862076 A331 AW360810 AA
Ę	2828888 282888888888888888888888888888	15			828852									A058396 AW3 1 AA805864 AA	W601031 AAS	AASB6369 AA66 648 AW835042 26 AW877527 ( 64010 AA4050 783 A167568 ( 105 AW380823 (
	mypochaeta powie II (1997) mypochaeta powie II (1997) leardin, leaf, schite, i sonin, carte inneh; 29 (undeadle tra cohn carter inneh; 29 (undeadle tra ESTs STV (sext demindre graph V)-box 11 graphen sonicitic, belt graphen motochic blackup protein 4	ESSIE Ha. (81103) hypothetical probibli FLJ 20764 replication factor C (extresion 1) 4 (37	DATPAGEE (£21 protein hypothatical protein DAT2A4341165 chacker required for 601 trenscriptions KAAA0186 gens product ESTs, Wasder springs to ALUS, HUMANAALU 6	budding uninibihad by benchridazaka i Bboni syndrama ESTs Honna paplera, dona IMAGE.CO31298, mRNA ESTs	hyprobletist porthin L12403 addebyds dehydrogenises 3 temly, member hypobletise protein F11,2023 statherin statherin ESTA, Hight stallarise to solve perfectively and the solve perfectively temler to solve perfectively temler to solve perfectively temler to solve perfectively.	gb-CM2-HT0178-O41099-017-e02 HT0178 Hamo Muchoedde repeat contacting 9 DMC2P95801948 protein gb-RC2-BN0032-18020-014-M9 BN0033 Homo CRV hav debendina sealen Vi hvv 9			# C 9 m	ESTs, Mg/ty strike to unserned protein ESTs, Mg/ty strike to unserned protein KUAAZZS protein remail protein remail muclean formation-protein aud U.2 cms muclean cOMX-FL2/ESSS ts, clone H			Unique Ese probesal Mentifica number de de de bien Aurel Gentelle ezcessen numbers	idan ' 982 regalis bealglos aalibes9 aags223 aalasobs a 1982 aatsoosa aast6507 aags1217 aats2067 al985bb 1773 ya aa marka aa medono deeta	962 BESIOSS TITTA AUGSALA ACSTETT ANYTIZEI AUGSATSE 202 AUGS131 ENEZ WI 2021 HESTTZ SUBS BEDSALD BESIOSOOD BESIOSOOD BESIOSOOD	ALTERS ALVIETE ALTERSEA MUSICIZA ALGESTES ALVESSES ALGESTES ANT ATTERS ALVESSES ALGESTES ALGESTES ANTERS ANGESTES EGGESTES ALGESTES ANGESTES EGGESTES ANGESTES ANGESTES EGGESTES ANGESTES ANGEST
443	H-12954 H-12954 H-12954 H-12975 H-12975 H-12977	H-3406	£22388	Hs.36708 Hs.36820 Hs.12744 Hs.62711 Hs.163714	H-575 H-575 H-37048 H-37058 H-37058			Ha.100623 Ha.1619 Ha.17772 Ha.171545 Ha.197764			Hz.709194 Hz.147813 Hz.24783	Hs.172004	s probesel ide or number coession num	AKOO!	AW14 AA28 AA078 BEDGE	A16794 BE069 AWB2 AL031 T2940 AW95:
980/20 C	2210 A.133161 14.32 2317 NALOZZIT 14.41 2317 NALOZZIT 14.23 2313 A.204063 14.23 2313 A.204063 14.23 2313 A.204764 14.23 2313 A.204764 14.23 2313 A.204764 14.23	AWEDESOG.CC AAASTOO! NIA_002918	ALDB0735 A1928383 A1638518 AA355925 AW003582	AF053306 U39817 AI961486 AA847843 BE463830	AA933527 NA_000691 119228 NA_003154 X00358	BE 144666 A124459 AW819152 AW893247 AM58680	AA203682 NW, 001327 NW, 000144 AA502764	X91185 AWZ48217 BEZ59150 NM_DD4504 U33749	AW968360 AW301344 A1693815 AA725650	AW974812 AA057484 BE545684 BE550224 T28472 BE299588	R14439 AW675480 AW451034 A638429 AV840383	F01020 Alz04995	Unique Ex er. Gene clush Genbank a	CAT Mumber 10125_1	102668_1 10729_1 113735_1 115652_1 1170435_1	1,234221
×		6363 6363 6363 6363 6363 6363 6363 636	453887 453887 453884 453884		2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3						658247 658373 658373	459870	TABLE 90 Pkey: CAT number: Accession:	Pkey 407746	408070 408660 409866 410032 411089	411152
	'n	01 ·	15	20	52	30	35	40	45	20	55	9	99	92	75	80

PCT/US02/12476 AM77777 ARFOLDE ARFOLDE ARFORDE AUDITOR IN 1877 TO ARFOLD	ANSESTI ANGESTI ANGESTI ANGESTIS REGESTIS REGESTION TO CONTRACT ANGESTICAL ANGESTIS	BE 161409 BE 15750 ANGTOSON DARSON WYZET WYZETO WYTER ANGTYT DE ZETZEN HENIB AMESSON BERSIS ANGTYSON DE ESTSYTS ANGTYS EEGEGZUS AMESSUS HYTTER HETTER WITHOUS WITHOUT BE DECEMBER WALTHOUGH WITH THE DEST BETTER THE MAINTHAIN THE THAT HE CONTR	AASTASI ANTINGA MAL OO IRBY SKIRAN IEETI KESI AAGGOTTA INTRODA SEETII TASSOETIIN TAAKSISTASI AANTINGA MAL OO IRBY SKIRAN IEETI KESI AAGGOTTA INTRODA SEETII TAASSA AAGGOTTA INTRODA SEETII AAGGOTTA INTRODA SEETII KASSA AAGGOTTA AAGGOTTA INTRODA SEETII KASSA AAGGOTTA	AAKIZED WHASI ARRI ERRO BRISTROZ ANDOGZO ANDOG	AVESCHAN HITTER FREAZA MARTIN DE AZERGEN RESET MENDE ELZOTO IS RESEZA ANDIZEA NEVETE RATION HITEZO PITZEZO HUZDES ELZIBIS BANTESEZA JAKRONI DA ASTICA MARTIGES ALZOTZA ANNIATZE VIZSEN I WESONI TEREBO HUSIS I TITZEO RESES WESONS REGIOD AANZEZA ENTESI AMBIENSE NEZARIA MARTINIA ANZEZA RATIONAL ANZEZARIA MARTINIA ANTESA MARTINIA MARTINIA MARTINIA MARTINIA MARTINIA MARTINIA MARTINIA MASTA MARTINIA MARTINIA MARTINIA MARTINIA MARTINIA MARTINIA MASTA MARTINIA MASTA MARTINIA M	WYDOS KUNDSK ALANISTY AREJESTS AREJESTS AREJESTS BETTER THE TOTAL	1982D 17467 171800 1883S 1812Z 18278 18817 18389 174682 77388 17389 17381 18894 77385 77340 16884 17457 7738 1738 1738 1738 1738 1738 1738 173	KUSSA AJALAS ANRAGOA AVDYAFT REITAJ AAGOTIJI HA189 AAGOSSA AAGUROG TEGOAL SEDDIZ TSYSSA ANTITLI AASIJIZKE AAJIJISH PURISAZA ANRAGOS EVZIZIR BRESI AKKOZOO RESPON WASHA AASIJISH BANGOSTA AAALASISA AMYIDTA AKRISTSA KAKIT AAGUSEA AWINZASA AHINGO REKUS PITOKOO AAJAKOSU RAGOA AZITTSI AKKSU BA AZIZOSA TUTOKO AAZISSA TITOSO TATOS REGIAG HTORZO AAVDAAS ANRAGO EGOSTA ANGOTISH TITOSO TATOSO TEXASO TEKSOS TATOSO TAXAS TEKSOS ANGOTISH SEGOSTA	1822.0.1730 1771 77426.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	ALAKSON 18758 AMTHAT 1800K HAZAK ZANDEST 184219 WASDIT 1870K 1810K 14431 1810K MENDAMI 1800 J ALAKSON 18758 AMTHAT 1800K HAZAK ZANDEST 184219 WASDIT 18422 RANDES 1811, ALAKSON 1816 1813 TANDES ANGENCE ZANDESD RENAL 1800K 1730K 1740K 1740K 1750K 1811, TANDES 1870K 1800K 1830 TANDES 1870K 1746K 1750K 1740K ANGENCE ZANDESD RENAL TANDEST 1740K 1740K 1870K 1870K 1880K ANGENGA I HIGNES ANGRESIS 1870K 1750K 1750K 1850K	NIETZYN BE (1572 AALSTYN). KRIOTTS KOOTH KSKOOL SKOOD NIE, OOZIZE AALSTYS AAKBUD AASSTET AAGHEZ MISTIGHE AASTIGGE AAGHEZT AAGSTRU BERGH AASSEZ AAGHUR AAGDTSTA AASSEZ AMSOOLS ABUDOS HIZDYS EEDVUEZ AMKOOLSEA AASTEGH AAASTON EEDVUAS BECHATS EEDVUH AAKSTYTT AASSESAD EERVES EHVINGE AMKOOLSEA AAKSTON EKSANDA AAASTON EERVUAS AAKSTOOLSEA AASTEGH EERVUAS AAGSTON EERVUAS EERVUAS AAASTON EERVUAS EERVUAS AAASTON EERVUAS AAKSTOOLSEA AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAASTON EERVUAS AAAASTON EERVUAS AAAAASTON EERVUAS AAAAAASTON EERVUAS AAAAASTON EERVUAS AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AMBILITA ANADTI BURGAT ANADATS TUGGT ANATAS ANADA FINIS BELIFIELD BELIFIELD ANADA FINIS FI	AKODISSA AKININSO ANISTOSA ALOKSKBA ALOKSKBA AKININSOA AKOSBA AA AKINSO KAAOLOK AKOSSKB TOSKBA AKININSOA AKOSBA AA KINSOB GEKACI AAKOSSK TOKOK AKOSSKB BESSOODB AAKOLAKI HATOOLAKSKBO KANIOZRIZ AKINIOSTI AKINIOSI AKOSBAS AKOSKBA AATOORI AAXOSSK TARLAKO KAYOSKBA BAKINIOSBOS AAKOSTISI HATOOLAKSKBA AAGTARIA ALOKSKA AATOOLAKSKA	MOZAZDA WING SIZA PUZIS ANNOTRA JANGBERA JAZDE SIE ALANGESER ANNOTRAG BEGGGESE BEGGGETA MOZIGO O TZGAL MAGAZDA ALZUZIO JACENGOS WINZAD ALIZOZO ZA VIREMA ANNOZGOS ANNOTRAGA ALBOROZO ALIUGOSE ALZOTITA ALAZDA MAGAZDA WAGALTA JALABI SIGA MOZOGOS ANNOZGOS GANGESER ANALGOST AND SIZA ALGOZOSIA AND SIGA ALZOSAGA WIGOSTOS MAGAZDA ALGOZOSIA ALGOZOSIA AND SIZA BEGGGZOS ANALGOST AND SIZA ANGOZOSIA AND SIGA AND SIGA ALGOZOSIA WIGOSTOS	THEORY STREAM DECORAGE ACCOUNT WHICH IN JOIN IN WIT WAS IN ALCHES, MANDER ALCHES, ALCHES, THE MENTAL ALCHES, THE MANDER ALCHES, THE MENTAL ALCHES,	MMOTORIO MISSI AMERISSA MARGSAA MARGSAA MARGSAA MARGSAA ZAZBOZSO AZZEOGO XAATSBOZ AATASBOZ AATASBOZ AATASBO A BEEN USEK AAABEES AAKZEOGA AATISBO AAKSEOGS TEPIES AAKSTIGGES THE SEXUNDES GAATSBOZ AKSEOGS TEPIES BEEN USE DEDOOGSOA MARGIT TO AMERISTO KANSEA AMERISTA AMERISSAS CAUSOS AATTSAST AAKSBOZ AATSTAT AAKSTASTASTAS	AMBITROI ANDESKOB AALISSTO AALTROED TOXOT ANTFALDB AAZZIADT AALISDOA AASTONG COBSOS WYDDIA SE GADON ANDRIENT FANNED BEING SE BELLOZOF ANTFALDB AAAZZIAGA FALESSES AMEGEZIA AMEDISKI AMBITTAN ENGEN ANDRIEN AAZGOS AALTZIAGA AALISDOA AAAZZOB AAAZZOB AAAZZOB AAZZOB AAAZTOB AAAZDOS AAAZDOS AATZOB AAAZTOB AAAZDOS AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAAZTOB AAATZOB AAATZOB AAATZOB AAATZOB AAATZOB AAATZOB AAAATZOB AAATZOB AAAXAAATZOB AAATZOB AAATZOB AAATZOB AAATZOB AAATZO	arazara karisty presi parata a trali samusura mdakadi Punda aka valara dan inda ulumiaka dan singa Karitara (karitata akatersis berba issi 1855) Arazero Besamis
WO 02/086443	132949_1	138256_1 15824_1			156454_1 166714_1 17690_1	1784125_1 184788_1 16535_1					169181_1 2041_1		77415_1 776539_1 28589_2	301384_1 31150_1		25772.1 27722.1 201543.1 34624.1	38585_1	42361_3
×	412811	413590			415989 417324 418574	418712 419443 419502					421582	42128 423034 424200 424999 424999	426991	429220	430439	430935 431089 432407	137117	136508
	٠,		9	15	20	25	30	35	40	45	20	55	09	. \$9	20	75	80	82

VO 02/086443 4184_1	ANNASAR, AZBEÇAS ATBEÇAS DESES DESEST DESEST DESTOT DESTO DESETS AZBETAS HINSTRA MESTAN HINSTA MESLA BETACITA AAALSET I ABBISSA LAZI SES MESKEZ ALTISSES DESTOTE DESENDE AZBEZA AZBERA DESTOTA DESESTA DESESTA RADESA AZBERA MESTAN DE ANISTEZDO AZBETA SERVESTE A RESTOR AZBECOS AZBETA AKSTOTO A ATBETAS XESTES AKBETAS ALTISTA ALBETA AZBETAS ALTISTOS AZBETAS ALTISTOS AZBETAS AZB	467716_1 47065_1	47673_1 51021_2 658874_1		79225_1	44505 60424, AASTSON MENSSEN 45105 65002, ANTISLEA AMERICAN MENSSEN 45120 65502, ANTISLEA AMERICAN AASTSON FOR SACIO 450552 AMERICAN 1907 ARTISLEA AUTISER TUDSIT RELEAS 45120' 85502, ANTISON AMERICAN AASTSON FOR SACIO 5500 ANTISON AASTSON FISH OAKTSON AASTSON FOR TUDSIS TUDSIS TAXED	. 8865_1	9163_1	1087807_1 1257335_1 168730_1	47395_1		Play: Unique number corresponding to an Eas probless Sequence unique. The J degli numbers in the column are Genhant (denliner (G) numbers. "Dusham L et al." refers to the profiberdian entitled "The DNA sequence of number abendances 22". Dusham L et al. Hature (1909) 402-493-455. Strand: indicates to NM strand from which exams were prefeted.  NI, position: indicates numberidia positions of predictid exams.		8118496 Plus 8118496 Plus 7331445 Milmus 8131618 Milmus 7230983 Milmus	8516137 Minus 974387 Minus 9858408 Plus 7799787 Minus	622791 Minus 6682791 Minus 6715702 Pilus 9789672 Minus	9928699 Phas. 27249190 Menus 27249190 Menus 27249190 Menus 27249190 Menus 6730720 Plus 6	4581193 Minus 2560474 Phus 4152858 Minus 8117407 Phus 3399665 Minus	3287873 Plus 6598824 Plus 9796239 Minus
V 438091	٠,		439780 441128 443068		448993		451807	452410	454241				Phey 400512 400517 400560 400560			401484 401714 401714			402265 402297 402408
		10	7	-	20	25	30		35	9	45	. 20	55	99	65	70	75	80	85

7.7.700/40 City	W.O. (12/1/864433 418319 A.B.15801 1 *kr.1913 C.033 antigen (acheriad 6 hymphocyes, 1 418402 N.B., 200715 *kr.1012 complement component 4-briding protest., 417355 0.13189 *kr.80202 environish mesator tone 8	AL138201 HL82120 AL049176 HL82223	18 =	BE387038 NM_000216	AV470411 Hs.269433	AAZ78036 Hs.124232 AAZ78036 Hs.187638	AW064897 AW070211 R20893	W79117 AW967969 NM_002837	H04507 Hs.9218 AA464840 Hs.131987 NM_005785 Hs.152175	X92521 AW956889 AJ006278	AU076629 Hs.155950 NM_019865 Hs.171731 T89832 Hs.170278	427559 DJ9153 H5.2171 growth differentiation factor 10 427833 M17706 H5.2223 colony ethnulating bactor 3 (grandocyta 428167 AK002121 H5.184465 hypothatical protein FLL11259	AAM1837 Hs.80250 ES AAM53800 Hs.182783 ES NN_004673 Hs.241519 an	BE176536 Hs.11080 IN. 207351 Hs.268107 AST8857 Hs.128768	A42727 Hs.117037 E A221311 Hs.130704 E W57554 Hs.126019 N	A1823593 Hs.27688 AA644669 Hs.183042	AM72330 Hs.283022 AM721522 Hs.177043	37140 AA312799 H <sub>2</sub> .23369 activator of CREM in tasta 37211 AA382207 H <sub>2.5509</sub> ecotropio viral integration sile 29 37960 A669938 H <sub>2.222194</sub> ESTs	AW169287 AC302471	AA627640 AA913488 AW292830	AL120214 NM_005408	NM_004469 Hs.11392 R41900 Hs.22245 N98238 Hs.55185	AB020722 NB9013 AI375922	AI800470 Ha.171941 H25899 Hs.201591 AW450848 Hs.205457	A1694722 A1654223 AW204600	NM_004657 Hs_28530 R67837 Hs_169872 A1000341 Hs_220491	AA022888	10,500 H. 3708 the floor probably 145 foruspedies, e 41225 AW080228 Hs, 11176 polyk-blading probab, nuclear I 414571 H24481 Hs, 78305 surfacient, pulmonary-sesocialist probab	NB1037 Hs.1074 U70867 Hs.83974 T28469 Hs.89485	AF111856 Ha.105039 N74880 Ha.28677
2 D TO TO TO THE A CONTRACT OF	PC I/US62/12476	S		10		15		20		. 57	30		35		04		<del>.</del>	20		55		09	yes	65	70		75	08		88
	8737108 8077108	2996543 Minus 9211494 Minus	8058545 Plus 8516120 Plus	996328 Plus 9965328 Plus	8565879 Manus 7239569 Phus	9931752 Menus 9931752 Menus 8075923 Menus	9926489 Minus 4572584 Menus	5006246 Phus 9067202 Minus 2326514 Plus	9944763 Minus 9833195 Plus 7528051 Plus	9855648 Maus 4826439 Plus 7143420 Plus	1519284 Plea 7342002 Plea 6007890 Plea	10644) 1122457 Pra 42215-4250 10588 20005P Pra 142215-4550 10557 20005P Pra 6520-6558	4914350 Pus 4567087 Pus 2735037 Pus	7767812 Minus 9166422 Minus 9256107 Minus	9256288 Minus 9795551 Plus	ASI.E. (Dr. Pobantis Therspecific Despressio and Prognostic largest for Therapy of Long Cencer and Non-malignani Long	able 24 thors about 30) genes up-regulated in non-milignant long das are retires to him burnes and normal body tissues ander dom-regulated in heig burns retaken to omit knig and non-milignam ung das sen. These penes wen selected from about 63800 probests on the CoulAdynestra Hill Genethig stray.	side 108 show he accession rambers for Draze Puty's backey, Uniquesid for table 104. For each probasel we have lated the great challer from which the experience of promodeless were despined of Bore challer were compiled using approaches of before the Electrical Service of Service Service Challer (Berling 1882) and proper to experience of the Challer (Berling 1882) and probability to the Challer (Berling 1882) and probability to the Challer (Berling 1882) and probability to the Challer (Berling 1882) and the	oceation column.	iske IOC throw he genomic positioning for those Pary's lacking Uniques (T), and accession numbers in laths (OA. For each predicted even, we have kited the genomic accurace and lar prediction. Numboddes locations of each predicted even see also baied.	ker., Untue Eco probesti Untuffer number Adozt Fermina Assession number Gebitsch nember	Judges (Ug. Unique number Judges (Ug. Unique profits) Judges (Ug. Unique profits)	Average of non-malignant lung	EcAcon UniquesID Uniques TUP RRAP PROTEIN. 873 Tennal Economy 1175; TRRAP PROTEIN. 170	MZ5079 H±158376 hamoglobit, bela 0.17	A43253. Hs 1914 Hone appears m3NA for KIAA1588 postein, 1.00 A470533. Hs 1917 E EST: 1.00 A470513. Hs 1919 E Hs 1919 E Hs 1919 1915 E Hs 1919 E Hs	740226 H.167790 ESTI 1.14 AL113960 Hs. 37828 T-cell south hymphocytic louternia ( 0.37	113.17 R0538 14.328.52 Proprieta protein FLIZOZO 1.00 113.00 113.00 114.	NAL, C02543 Hs. 77729 coddsed fow density Ropprofela (actin 0.94 0.07 0.007) NAT 778729 coddsed fow density Ropprofela (actin 0.07 0.07 0.07 0.07 0.07 0.07 0.07 0.0	H0717

S

190	88	26.6	88	8.75 0.52	888	388	888	88	88	8 2	323	388	353	828	<b>8</b> 5	88	86	85	88	88	32	5. 8.	<b>8</b> 8	888	5 <b>8</b> 5	365	39	88	3 5 5 5 5 5	355	88	888	388	88	88	528	888	88
	ESTs small nuclear ribonuchoproteth D1 polyp	oylochrome b-245, bets polypeptite (chro erachtomete 54poxygenzea whodess-kna MATV integration site fant	solute carter family 1 (neuronal/apilite hypothetical protein	interfautan 6 (interferon, beta 2) cacherin 6, type 2, VE-cacherin (vascula	ESTs. Moderately strater to ZNS1_HUMAN Z ESTs		ernexin A.s ESTs, Moderately similar to S29539 ribos granutysis:	early growth response 2 (Your-20 (Drosop ESTs, Modershely similar to ALUA_HUMAN A	ostogych (asteahductive tacko, mime ESTs, Modernsky similar to AF 161511 1 H	Prenacription factor EC heperan suffate (glucosamine) 3-0-suffot	GTP-binding profesh hypothetical protein FLJ11004	Vasoacove massuna pepase receptor i prostaglandin D2 synthasa, hematopoletic PXCTDsection 1 socialis	Sushi domah (8CR repeat) containing		UNC(1) (C. elegans)-like Briting exemperators Africa America Mass		colony stimulating factor 3 receptor (gr	ESTA, Moderately strater to A53959 throm broothefted portion E121940	ESTS		gt;nc5704.s1 NCI_CGAP_Pr1 Homo saplens advenents, bela-2, receptor, surface			Industrytamine N-methytransferase Rho GTP ase activeling protein 6	enesin, beta 1	CLST 11240 protein CLST 11240 protein CDWS2 enform (CAMPATH-1 antioen)	phosphatch finocial of year, class A (pa matrin 3	emplotensin receptor 2 semaphorin sem2	EST8 EST8 EST-	ESTs. Weekly stimfar to transformation-r Homo sapiens beta-1 advenantic receptor	Homo seplens cDNA: FLI21326 fts, clone C ESTs	hypothedcal protein FLJ12910 SWISNF related, matrix associated, ecti		SEC24 (S. cerentsias) ratated gene terral ESTs		ESTs ESTs ESTs	ESTs ESTs hypothetical protein FL/12666	
443 Hs.83393	ES	282	82	22	£ 2:	H. 1043	× 50 50	20 英	33	58	88	Hs. 128433	10702	Hs. 143131	Ha. 155001	82	£ g	ž	E	Hs. 185305 Hs. 2465	Ha.2551	Hs. 12532 Hs. 120385	Hr.162080 Hs.119514	Ha.250830	25	28	£	≥ 8	H. 133386	1 B 2	53	#.15929 #.9458	Ha 122147	Ha.7239	Hs.176379 Hs.265660	Ha.127346 Ha.235768 Ha.253569	# (329) # 23767	. Ha.49265
O 02/086 A127959	C01566 JCG796	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	U08389 AK001989	X04430 UB4722	AAZSB124 AAZ78438	AA913059	AI683243 NM 006433	NN_000399 F06504	Al934365 AA300900	D43945 AF105374	R34385 AK001868	AF15024)	292546	AW3/5/3 NM_005814 RE2424	AF020202	BE178285 AF240467	NM 000760	AA765368	AVZ07175	A1928355	AA469153 BE245562	AW292053 AW365665	AA482900 AI734149	AF128847 NM_013427	AW090386	AA309977 NS0866	D11466 AJ224741	X87723 A8029496	AI732837 AI066872	AW840171 U29690	A1248584 BED48860	727503 AA370041	AW016539 W72062	AJ131245 AJ799488	AA813880 AA447849	A1738875 AW590572 AW206560	957 Al949952 Hs.49; 282 T47764 Hs.13; 547 AW271273 Hs.23;	A15977655
W 418067	418298	41832 418345 418281	419584	419968	42028 42027	255	421478	42156	421913	42232	423196	423624	423696	424212	425175	425486	427618	427952	58763	42883	430212	430378	430656	431217	432176 432176		412522	432850	4358	435496	437157	525	436199	440815	441384	4 2200 4 2832 4 2832	4 4 2 8 5 7 4 4 2 8 5 7 4 4 5 6 7 4 6 8 5 7 4 6 8 5 7 4 6 8 5 7 4 6 8 6 7 6 8 6 7 6 8 6 7 6 8 6 7 6 8 6 7 6 8 6 8	44330
		જ		10		7	2	;	70		25		30	₹		32		40	2		45		20		5	3	;	99		65		2		75		80		88
PCT/US02/12476																																						
. 937	10.14 0.35	0.00	252	588		0.32	0.46	85	8 6 8	355	888	90.0	0.97	000	88	1.37 0.88	 100 100 100 100 100 100 100 100 100	3.5 3.5	8 <u>8</u>	<del>2</del> 2	86	80	555	# 8	25.55	88	83:		252	18 00 E	888	80.0	25 25	88	888	1825	0.70 0.70 1.00 1.40 0.88 1.30	
cathim channel, vollage-dependent, alph	atiway trystin-lita protesse progastrican (pepsinopen C)	activin A receptor type II-the 1 hypothetical protein FLJ10970	utarogłobin Interfactin 7 masptor	surfactorit, pulmonary essociated protein Homo sepiens mRNA; cDNA DxG-Zp564B2062 (f. cor.	acherced phosyletion and product-speci ESTs	ESTS	receptor (calcitorin) activity modifying ATP-binding cassetts, sub-temby A (ABC)	solute carrier family 6 (neurobansmille MAD (mothers against decapentaplegic, Dr	straign to hypocome-associated membrane Target Exps	NA_016582*:Homo sepiens peptide transpor	ENSPRODOZZEZBERMB. CZ (DODZZO-elgst-SBMM) DGZSEZ (1 AT	NM_031419". Homo saplens molecule possess NM_037037". Homo saplens a disnigatival	NM_005463:Homo sapiens heterogeneous nuc NM_019111":Homo sapiens major histocompa	NM_002944":Hono sapiens v-ros avian UR2 CDB3 antigen (activated B lymphocytes, I	C11001637*;gi5032241/reip\P_003732.1  z Targat Exon	Target Exon major histocompatibility complex, class	hemopobin, gamma G amerin A2	major histocompatibility complex, class terricocyto immunoglobulin-lite receptor,	gb:Human trophoblast hypoda-regulated f complement component 8, beta polypeptide	ayfacetamida deacetylase (esterase) E8Te	ESTs forthead box F1	interleutin 12A (natural killer cell sil	riyponeoca protein FLI20022 cytochrona P450, subtamily IVB, polypept Home seelent mONA PACTAGAGET A	Homo supplies mRNA, chromosome 1 specific are homobov three (SKI) and existing it	ph:PM3-HT0605-270200-001-a02 HT0605 Homo macrophaga receptor with collagenous str	gt:QV1-HT0413-010200-059-h03 HT0413 Homo ATP-binding cassette, sub-family A (ABC1	ESTs bone morphogenetic protein 2	cardio envyra repeat protein CXC chemokine ligand 16 CXC chemokine linand 16	Interleukth 8 receptor, beta cb:CV4-HT0222-011199-019-e05 HT0222 Homo	zina finger protein, eubfamily 1A, 5 (Pe hypothodical protein FLJ 1268	ESTs. Weakly similar to 565657 alpha-1C.	Caroutypaproses of Upasing ESTa, Wealdy similar to 16.7Kd protein [ hypothetical ordein FLJ20992 similar to	ESTs found in Inflammatory zone 3	ESTs neutrophil cytosolic (sctor 2 (65kD, chr	ESTS Homo expiens cDNA FLJ14237 fts, clone NT cST-	COSTS  Searched 2 guarine exchange factor (GEF)  coagulation factor VIII, procoagulant co	exhalour I (allour) illustrat enhancer of Gamentation I (cra-lite do hypobetical protein FLJ14902 bypoplemy-IRNA synthetae	ESTa
粤	8 . 3	68	្នន្ន	825	3 8	2 2	28	;	<b>₩</b>								Hs.266959 Hs.217493	Hs.198253 Hs.94436	Hs.38069	Ha.587 Ha.245123	Ha.155591	H.673	H.687	Ha.301281	H-16291	Ha. 15780	H. 24172	Hs.82407	H2.846	Hs.20631	Ha.192235 Ha.32241	H, 66915	Hs.28363	Hs.949	H-165195	H-79307	H-293885	Hs.16355
WO 02/086443 42334 AB01130 Hs.127	AB002134 N16567	NIA_000020 AA001732	T\$2248 AA381258	X65018 AWOS8350	AB036432 AW449467	AID82692 AW152618	A1904740 NM 001089	X70697 AF005528	NM_014338					Al815601		M33500	AI219304 AA505665	MCM996 UB2Z75	U96191 NM_000068	NM_001088 AW138959	R20723 AW025430	AF050083	AA780473	A8007979 D86840	BE178622 NM_006770	8E160198 AW576555	AL035668	AA290712 N22788	U11874 BE146973	BE157288 AA131486	AW964490	BE353858 A1058548	H63202 AA311223	N84464 BE269352	M92445 H16761	BE244050 NM_000132	AA159996 728651	187281
W 423354	2521	126828	128043 130280	01430	M 835	M3709	50054	0 SS 5	00752	5000	0220	10367	104277																								7148	

	PCT/US02/12476 840 430 430 1510 1510 1510 1510 1510 1510 1510 15		<b>9989</b>	<b>2</b> 50	800.0	88		DS:XX2 AW134897 AAR34157 AAA48943 AISSB20	20 104 FREMENDE PRODUCT PROGRAMMENT REPORTS BE 140787 BE 147044	UN BELVI WAS DE 1917/22 DE 1917/23 19 FR94 105 T83923 21:06 MAY 40809 T81 1622 T709517 T29519 FR94 105 T83923 11:08 MAY 2004 AWR 4004 AWR 72917 AWR 72915 AAS EKS 55 10:0920 F7339, AWR 84009 AWR 84005 H7344 T80038	V32571 R7280 H45409 R72085 R46356 R46758 1733599 A1572251 A1872488 AW193282 A124716 H1681 A A336477 AA336070	000000		et al." roters to the publication entitled 'The DNA		. (209)			
	\$25.52 \$25.55 \$5.5	233 protein 0.05 Weatry entale in USD022 hypother 0.02 efficial protein FJ USD92 1.00 1.00 404 person 0.42 44th observent Bindfug protein A 0.17	888888	2 2 4 0 2 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	nnia critivi Fillitzz Bi, ctma HE 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00		ke number	os n najelom aaztosta aazusts aattaisi aworskob aaziosis amilisto	DOBRA WINGSSE, ITS.O. WUXSOD A WESSOD A WESSOD A WESSOD A WESSOD AS ELATOR BE LATOR	10 ECT-NOT TO ECT-NOSO EL TATOS ANGONTO EL FONT TO EL TROSO EL TATOS ANTO EL TATOS ANGONTO EL TATOS EL TAT	173145 FEDSHQ ADDALST AKEBTYB RT3.002 AIS64346 WD1956 AA418562 V 5 AAH18TYB T3375 FEDSHQT T18115 AZRZB185 AADDOSS AV330286 AISTUSE AHYAH187 AIRZTVGO AAY28656A AIRZTVB BAD16593 A HISTSKIN A ABYDHAA AIRZTVGO AARADVGA AAVTSHGA AIRSTTVGA AARSTVGA AARADVGA AAR	AAGSTS ANTRGGO AAGSZS AATTGC AAGSTS TUGO AATTGG AAGSTS TUGO 6 EL SAGS AVRETOG BE LEASTS		Unique number corresponding to an Eca probeed: The contractive power, I have digit unimented in this submanue Genthank kidentifier (3) jumiban. "Omhlam), et al." refers to the problection entitled "The DNA sensons of homes characterises."	which exons were predicted.  As of predicted exors.	M, position 1.4559,4489, 8004,40114,8111-1345 3027,5428,8159,859,87104,771 1.468,1.1518, 1154,11564,11504,11766,1177,11904,1	12079-12069 12600-12071, 13090-14005 10072-0013 10050-6114	0.05579194 50.05579194 60.05579187 10.05579188	60877-6148 73121-73273 7838-054
,	56979 3438 4623 7917	Hs. 18705 Hs. 28792 Hs. 22837 Hs. 22839 Hs. 29117	Ha. 20365 Ha. 20365 Ha. 26956 Ha. 26954	H-2017 H-2017 H-30343			Unique Ecs probasel identifier number Gene clusies number	w accession number imber Accession	4_1 8E1801			1 AA4691 5 AA478 9.1 BE1542		number correspon ce source. The 7-	ONA strand from as muchacitide positi	Strand Plus Mirra Mirra	2828		
9	WO UZ/086443  S AWZ04908 Hs.18  8 A134471 Hs.2  8 R13500 Hs.18  1 RES97753 Hs.17  7 AGA7893 Hs.11  1 NA_066591 Hs.13  AWS6A73 Hs.3			ANN22585 AAS98509 C18825 BES37217	AWES4374 AASE2496 AA417940 BE154396 AA287827 AK287827	AFEG2906 F18572 F03027	· ·		12334	1,4172	ו"מווג	314437_1 421802_1 97026_1 1232559_1	8	Sequen		Ref 733144 811761 324274 754717	754727 986504 971967	183458 276864 313303 . 8151988 7341828	807939 732931 600692
•	45515 45508 45508 47508 47509 47509 47509	44787	25053 25053 25153		2002 2002 2002 2002 2003 2003 2003 2003	457.18 4577.18 459636	Pley: CAT rumbe	Presy 108074	411667	423387	423696	490212 496532 454721	TABLE 10C	ž ž	Strand: N. postlon:	Phay 400754 401045 401083 402474 402808	63421 63421 63438	00000	405106 405257 405381
	~	10	15	. 20	25	ર	35	6	Ą	2	20	55	9		65	70	25	80	85

ani king disease, and normal king. These genes were selecte faths 11A shows about 84 genes upregulated in lung adentocarchomes relative to other lung lumons, non-from about 59880 probesets on the Eos/Affirmstix HeGS Genechty array.

ided ITC show the generalizabilitying for brose Peny's section Uniques ID and accession surthers in table 114. For each predicted exists, we have listed the general excessors used for prediction. Hubborides locations of each predicted exto see also black ನ

aplens cONA FLJ 14035 fls, clone HE in, gartima (breast cancer-specific hosphate synthetase 1, mitoch protein FL13352

ificity phosphatasa 4 ing cascette, sub-family A (ABC) stehr, PLUNC (palate lung and nas side-binding, soluble, 4

R.7.75 Horne septem micht All lang in kent cith 1.00 71.00 R.7.75 Horne septem micht All lang in kent cith 1.00 71.00 R.7.75 Efficie Efficie 20 71.00 R.7.75 Efficie 20 71.00 R.7.75 Efficie 20 71.00 R.7.75 Horne 20 71.00	TABLE 118 Plany: Library Eco probest Mentifier number CAT number: Gene duta's number cate duta's number of categories of the categories of	acesian Betroor Betroot acast acasti appitas na oodbit appitati appita aastoga betroot betroot betroot ababod Aististi aarasti aasagit aatoot aabasa betitiii aatzaa matood aarood aasoot aasoot aaroon antoot ait	MATIOT FRESS FRESS TATEST THE STATE THAT THE STATE STATEST THAT THE THAT THE STATEST IN HATEST TATEST THE STATEST THE STATEST THAT THAT THAT THAT THAT THAT THAT TH	THE TOTAL THE TREE THE THE THE THE THE THE THE THE THE T	TREASES TITES IT THE RESH HYDRO ANNOLES AND REMOTE CORRESPONDED IN 11 IT TITES IT TITES IT THE RESH THE TREASE THE RESPONDED IN 11 IT TITES IT THE RESH THE	TERES EGGS TERES HASKEDS TTEST TEST TAKES THESE THESE THESE THESE THESE AALDED AALGED AALGED THESE TESTS THESE TESTS THESE TESTS HASKED ALGED THESE TESTS HASKED THESE TESTS HASKED TESTS THESE TESTS HASKED TESTS THESE TESTS HASKED TESTS THESE TESTS HASKED TESTS THESE TESTS HASKED TESTS HASKED TESTS HASKED TESTS HASKED TESTS THESE TESTS HASKED TESTS THESE TESTS HASKED HASKED TESTS HASKED TESTS HASKED THE TESTS HASKED TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED THE TESTS HASKED	TBYRDT TZERT TAZET TEACH TBAZE TAZEN TREBE TATAF TBOOK TREBET TAZET TAZET TEACH TEACH TBAZE ALSTAR ALFORGO ASSETT ALVECT ASTED TAZET ASTED TREBET AGEST A MOLINE ALTDET AGENCY ESTANDED AND TRES BLITTH GEORGES AND MOLES AND AGENT ALBERTA BEDVASS GEOTHEN BEDVAG ALFATTA AGENCY BEDVAG TEACHES BEDVAG ANTOGRED ALTDET RESERVADORS AND TAZET AND AGENCY BAZET AND AGENCY BEDVAG TO TAZET AND AGENCY BEDVAG TO TAZET AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AND AGENCY AND AGENCY AND AGENCY BEDVAG TAZET AND AGENCY AGENCY AND AGENCY AGENCY AND AGENCY AGENCY AND AGENCY AND AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGENCY AGEN	BEDT OAG AUDTACT ANNEZZOO BEDTASTA AZZEZIZ AASZEZA ANTWEDA PARDASTA BEETAGUTA AUGUTAR RESERVE AAKTARI A MAZDESA AAZLAGA AAZLAGA ATALAGA ARANGA OA MASZA TEBEROADI BEHOAT BERENDER BEHOZIZ BEHOZIZ BEHOZIZ BE AAKTARI AMABIALA BEHOSTO HANGKOTA ALASTETA LABIHTSA ALASHASA AKRISTA ALASTATA ALASHASTA ARANGTA ATALAGA ARANGTA	AASTAIS ANBTATAT AATHBED WAAAZI AA16680 Waxaa aliitsoo beessiii beesdratabeessessa karsaas aastaib beioom beiugso waxoo aabsaan noosi ahaysosa ahaassa arbossa arbasso aastasa aastassa aastassa aasaasa aastasa aataasa aataasa		
150555 110534 1216239 12172 12172 12173 12	B Unique Ecs pr er: Gene duster : Genbent acci	CAT Number 11995_1	18535_1				1,1905	4433,2	8865_1	•	
4,0718 4,1071 4,	TABLE 118 Phey: CAT number Accession:	Play 410099	419602				421582	437866	451807	TABLE 11C	i
. 5 10 15 20	25	30	35	40	45	20	55		8	65	

	Pteg.	Unkque mumber comasponding to an Eos probesal
	Ę	Sequence source. The 7 digit numbers in this cotumn are Genback identifier (GI) numbers. "Durcham I, et al." refers to the publication enfled The DN
ě		sequence of human chromosome 22." Dunhem I. et al., Nature (1999) 402-499-495.
2	Strand:	Indicates DNA strand from which exons were predicted.
	N. position:	n: Indicates nucleotide positions of predicted expms.

Per (1982)

7,

PCT/US02/12476

TABLE 124: Genes Ostingishing Squemous Cell Cerdinoms from Other Lung Chasses and Normal Lung

Tobis 12A slows about 72 genes upraptished in equamores call cardionnes of the lang resident is other lang thmore, non-marginaris Lang desister, and normal lang. These genes were selected from about 55600 probasets on the Equilibration hand. Genestly array. S

Table 178 show the acceptor number for those Play's lacking Uniques[7] to table 12A. For each probased we have lated to gene dualwr cumber from which the observationableds are an elastimate. Gene clatter areas compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were challend based on required self-areas areas dualway lated on required probables are all places of the Genbank accession numbers for sequences computing each clatter are listed in the "Accessive colors."

2

domaious and carechoid lamon) drivited by the son devised by the son person of recemble two semples					-					
rchomas, gran (ebclasis, estir	4.00 2.22 2.70 2.70 47.00	62 62 62 63 63 63 63 63 63 63 63 63 63 63 63 63	51.00 3.27 1.10 1.10	25 25 25 25 25 25 25 25 25 25 25 25 25 2	220	1,00 1,00 1,00 1,00 1,00 1,00 1,00 1,00	1.18 1.00 1.40 1.40 1.40	8 2 2 2 2 3 3 3 4 5 5 5 5 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	14.00 139.00	1.00 11.00 147.00 1.42 38.00 1.00
ia, email cell ci ema, fibrosis, a	R1 132.45 3.26 26.47 10.33 4.13 61.84	1.00 173.91 151.17 1.00 1.00 24.30	53.29 1.00 112.17 1.18	112 112 110 110 110 110 110 110 110 110	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	137.82 137.82 33.45 4.24 51.83	201 201 11.80 12.28 1.58	25 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	8.55 6.55 8.55 6.55	1.00 1.00 62.88 1.53 31.11
une no protector, recentive recents or sect practical train as and sect.  Esemblar from problem laurifor cambar  Esemblar controller cambar  Unique none de marche  Manage de marche  Arrange of card marche  Arrange of correct and garden as acceptations, séenocarchemas, small cell cardnomas, grandomatious and cardnot burson) divided by the  Average of normality cardious garden.  Average of normality cardious	Ungene Tibe matir mraflorpordeisses 10 (stronelysh NM, 0024283/stome applear meter metalopro NM, 003577/stome applears kerath 18 (scea Tangel Eson NM, 00379/stome applears kerath 18 (pQFT) Tangel Eson	ELISTOMOSS (0.68: Flazma membrane calcium Targel Econ Estis permityola erigen I (2002/00) Ecol prelievich protein SPR (Parma, Homo septens CINA: FL/22A4 III, doze H Shydrova-Schnipfystark-Corazyma A sy errothin Protein obseshutas, neocid-	Steffin 2 (congenital contractural are neverolatins) annal rotate-st-probin 18 (comility) desmocalin 3 certicalists emitpen	per en primer indication per en primer per en principal per en primer per en primer per en primer per en primer pe	adoctas mander, a monomero losos, adoctato reductase family i, member 810 hepath-briding growfi lector briding pr hypothelical grotten LOGST822 dewny hystol-lector	umo fronce no Lus aire resign tempora erral profine-for profines shallon temporal profine-for profines Horno septem cOM A.1/1070 ft, chea HT descroptia, (Jernythjan viginis airigen odd Coltene-honolog 2 (Drosophita, mous G. Editjon 19 G. Editjon 19 G. Editjon 19	ESI I, was printed to DOI/1004 chaptor Kipp?) protein ESI II, May Partia to SOI/10 band-b-pr arrall profess of pratein 2A cyclin-dependent latense 5, regulatory su cyclin-dependent latense 5, regulatory su physican i	gap junction protein, bela & (connecth 3 unojdakin 18 hymbrogra aufgan & complex, locus D ESTs cylcohorne P450, amblamly VF, polypept	menteurun-i nomotog 1 ESTs ESTs Phytochestcal protein FL/20093	O protectional designs to the control of the contro
uneuro prentatat. rocesous le Europita Accession number, Ge Uniques number includio Uniques gene illa Average of horizo Includin wavego of normal lung dempes Average of nor-malignant lung de Average of n	UngenetD Hs.2258	Hs.161566 Hs.620 Hs.6320 Hs.6934 Hs.77910 Hs.78167	Ha.79432 Ha.60962 Ha.1076 Ha.41690 Ha.87725	Hs.9923 Hs.312457 Hs.31309 Hs.110198	H.152127 H.132127 H.132137	H. 1320 H. 13322 H. 13322 H. 1336 H. 23167 H. 23137	HS.98765 HS.98765 HS.11281 HS.93597 HS.241651 HS.241651	H-48956 H-271580 H-127780 H-127780	Hs.291523 Hs.291502 Hs.292506	Hs.59507 Hs.59761 Hs.7164 Hs.127728 Hs.9029 Hs.12569
R	ExAcen X07620	AA045144 L11690 AIS41214 BES40255 AL044872 UB8967	U02272 NIM_006183 BE185289 AK001100 NIM_001327	A658038 W69233 L42583 AJ243662	AW853908 AJ403108 AB002134	AF027866 AF077374 AF077374 AF077374 AF072853 AAA448542 BE385042	AA431400 AA420450 BE182592 AL134197 BED62109 XS4232	BE149762 BE019924 Y12642 AW015415 U02388	A4721252 A4721252 A466607 A4133916	W/8123 AFD8076 AW872527 NM_003812 AW741867 T49951 R41339
Ptoy: ExAcort Uhipenelit: Uhipene Tils: R1:	Pkey 400289 400668 401780 401781 401785	402075 404936 407639 408000 408522 410561 415091	41658 41734 41736 41853 41853	20173 20173 20184	2007 2007 2007 2007 2007 2007 2007 2007	42404 42404 42434 42733 42733 42733 42733	42845 428748 42853 428903 430458 430890	431009 433091 43480 43480	4552 4552 1255 1255 1255 1255 1255 1255	43870 43870 40325 41325 44376 44378
15	30	35	9	45	20	55	65	6	75	80

Struct includes Office Arm when predicted comman.  **London: Includes in nucleoting positions of predicted comman.  **London: National Nat
7249190 Minus 7249190 Minus 4153858 Minus

WO 02/086443

(the 1St shows about 7) genes upopulated in non-refigurating disease retains belong turners and normal lang. These genes were selected from about 19600 probesses on the East-Appreaded HADO Generation array. PCT/US02/12476 TABLE 134: Genes Okthoushing Non-Malignari Lung Disease from Lung Tumors and Normal lung

S

2

Table 108 alow the accession number from Poys' lacking UniquedDe for table 134. For each probest we have listed the great dutier number from which the object-accessions are constructed was sometimed to an expension of the security state Qualitative are constructed and on expension in the security state Qualitative and Algorians (Toots (Dooble Texts). Obtained California). The Genbark accession numbers for expension compatible each obtain real kind in the Autorested Colorum.

fabe 100 chow the genomic positioning for those Play's lacking Uniques (10 and accession numbers in liable 134. For each predicted coon, we have kind the genomic sequence source used for prediction. Noticelide booklops of each predicted room are also libited.

Ungare gene life Averge of they turney faculties as celectricines, diencoardnomes, small cel cardnomes, grandometous and cardnoid lumos) divided by the Averge of those large services Averge of coordingtoned turney disease earrybes (broading broadins, emphysema, Broad, alabediach, estima) divided by the average of normal lung sample Averge of coordingtoned turney Unique Eos probesei identifier number Exemplar Accession number, Genbank accession number Unipene number 2 12

54ht2r1 HCI\_CGAP\_Ew1 Homo saptent ESTS. Moderately similar to ALUS\_HUMAN A ESTS ESTS gbzk15004.s1 Soares\_pregnant\_uterus\_NbH ESTs ESTs, Weatly stribar to unknown protein membrane-spenning 4-domains, subfamily A Unigene Tite Home septens mRNA for KIAA1568 protein, als receptor, tenotropic, AMPA 1 hypothetical protein FLJ22029 chemokine (CX3-C) recaptor 1 thordin-libs Hs. 222194 Hs. 22588 Hs. 101689 Hs. 7117 Hs. 201591 Hs. 220491 UnipenelD Hz 31141 Hz 76728 Hz 26543 Hz 26543 Hz 191721 Hz 131967 Hz 131967 Hz 191731 Hz 191731 Hz 191731 Hz 191731 Hz 191731 Hz 191731 178538 Hs.11090 L007351 Hs.268107 RABLE 139 25 ဓ္က 35 8 45

Pray: Unique Eos probessi identifer rumber CAT number: Gene duster number Accession: Genbank accession numbers

20

CAT Runder Accession 327826\_1 BEON1305 AA491828 AA621948 AA718980 AA686102 421802\_1 AA721522 AN975443 TB9070 55

Dequive a nonex compaced to the separated of the common as Certain's leave the common and the common and the common as Certain and the common as Certain and the common as Certain as Certain and the common as Certain as C TABLE 13C 8 65

121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

2

Strand

 $WO\ 02/086443$  TABLE 14A: Preferred USINy and Subcalding Locatzation for Polential Lung Disease Templa

PCT/US02/12476

Tota IVA inton the stockbire boetlathon and preferred offly for the series appearing in Testes 54 and 10A. mAs symbolizes monocheral entitled symbolizes and second of the series of the

S

2

Table 149 show the accession numbers for those Pay's backing Uniquesity for table 144. For each problem, we have fixed the gene chaste number from which the algorithms were designed. Gene destine were completed table preparates defined from Centerint ESTs and mRNAs. These expensions were obtained based on expensive surfacely using Obstering and Algorithms 100k (Double Table). The Genberk accession numbers for sequences computing each distance and label in the Deceased or Colority. The Obstering or Algorithms 100k (Double Table) and Cellbring). The Genberk accession numbers for sequences computing each distance are listed in the

ithe IVC show the genomic posibilistic for these Pays Lechted Uniques ID's and accession numbers in labb IVA. For each practical ector, we have labed the genomic equences sources used for practicion. Nucleoidal becades of each practicad ecton are 6sts based.

2

yr. Unique Ges produced lentifier number Commerce Energie Acceptation number, Genbert, accession number genetic. Uniques number genetic. Uniques number program (Test Uniques per set all Littory. Present URIP ed.Loc. Predicted soutenhear localization. 2

Pref Usility mAb & disg & s.m. mAb i mAb & disg diag diag diag diag mAb 8 s.m. mAb & diag 8 s.m. Uniques Title matter controllers 10 (strone) sin m multur inschoologises 10 (strone) sin m ENSP0000051 (106-7 teams membrane calcium nu GNSP0000051 (106-7 teams membrane calcium nu epistem but especiamily 1 (BNP settagen recomplyibly (youther kines), receptor, second your benefit of the second your benefit of the second you will be second you wil arbono enhydrase IX crassmembrano prolease, enfine 4 XABE interacting, timesin-tibe (rebitines 23 30 33 9

s.m. dag s.m. CTL & dag mAb & dag & s.m. mabb 4 sm.
CTL
days
mabb 8 sm.
mabb 8 day
mabb 4 day
mabb 4 day
cTL
cTL
cTL
cTL
cTL
cTL
cmb 4 day
mabb 4 day surfaces to the control of the control of the control of the control of contr COC28 protein technitis, utobinase COC28 protein thress 1 Basse factor patimes inhition 2 parties (or cystem) proteinase inhibito protein (prostine prospitatese, rospital floritina 2 (congenital contractural are A4976590 C16339 WW, 05052 U8850 U8850 WW, 05052 U8850 U8850 U8894 WW, 0504 U8894 WW, 0514 S 25 8

a handle cytokine sutdamby B (Cy in carier famby I (ghtamete trans rebed frizzled-related protein 4 2-binding cassette, sub-termly B (AIDE) 2-binding cassette, sub-termly C (CFTR COOKS (seel division tyche 45, 6 centrels
COOKS (seel division tyche 45, 6 centrels
to backward full emission taxor
to backward full emission taxor
to backward full emission foliar
to backward full emission foliar
carding onlymorate matter probable (see
the probable of the matter probable (see
the probable of the matter probable (see
the probable of the matter probable of the matter
the probable of the matter probable of the matter
than the probable of the matter probable of the matter the matter probable of the matter the matter probable of the matter the matter probable of the matter the matter probable of the heleasing peptide ise inhibitor 3, skin-darhed (SKAL 2 23 8 જ

38

v
•
-
~
_
-
₽.
•
Š
5
_
u
حَد
_

PCT				
cytolismic cytolismic getra-editar escritoli cytolismi emitrane plasma membrane plasma membrane plasma membrane plasma membrane plasma membrane escritolismic escritolismic cytolismic cytolismic	cytydamio estheodylar nocker nocker plasma membrana artrachdur mitohodra mitohodra mitohodra plasma membrana plasma membrana secritica	plasma membrane echrochites plasma membrane plasma membrane plasma membrane plasma membrane nuckara ecutida cytoplasma aucitara	pastra membere plasma membere plasma membere plasma membere extrachiar	ectrició ectrobiliza ectrobiliza ectrobiliza de principal de principal plates enembras ectrobiliza electrobiliza electrobiliza
		the first state of the first sta	and the second s	mich & Gag dag dag CTL & Gag CTL & Gag mich & E.m. mich & E.m. mich & E.m. mich & Gag dag dag dag dag dag dag dag dag dag d
length  The control of the control o	the anticolous in the anticolous of the anticolo	chardin channes is equiting as charding as charding as chardin channel chardin activated from prompting an extraordinate profit prompting the charding of the	LU In Greating protest.  Construction of the control of the contro	EGF-Da-donald, multiple 0  Fig. 19  Fig
443 Fe 148585 Fe 15728 Fe 15527 Fe 15537 Fe 15337 Fe 15337 Fe 15337 Fe 15337 Fe 15337 Fe 15337 Fe 15337 Fe 16940 Fe 1694	Ha. 180655 H. 2.256 Ha. 184339 Ha. 184301 Ha. 184601 Ha. 184601 Ha. 184601 Ha. 184601 Ha. 182403 Ha. 182408 Ha. 182408 Ha. 182408 Ha. 182408 Ha. 182408 Ha. 182408 Ha. 182408 Ha. 182408		15.2500 18 15.2500 18 15.2500 18 15.2501 15.2501 15.2501 15.2501 15.2501 16.25	H. 1284 H. 1513 H. 15761 H. 15762 H. 17764 H. 17764 H. 17864 H. 17864 H. 17864 H. 17864 H. 17864 H. 17864 H. 17864 H. 17874 H. 17
WO 02/086413 WO 02/086413 WO 02/086413 WH 00000 Hr, 000000 WH 00000000000000000000000000000	AW411423 1.155708 1.2524 NM_014781 Y00772 AF00122 AM62773 AM62773 AM62773 AM62773 AM62773 AM62773 AM62773 AM60788 AM607883 AM607883 AM607883	AL134197 AW621109 AW621109 AW621109 AW621109 AK63120 AF211511 AF200492 AM77819	AMEGRIS WAS A WEST A WE A WEST A WE A WEST A	AUNSEN AUDISIN AUSTRIZ
W 6250 6250 6250 6250 6250 6250 6250 6250	19827 19827	42993 421462 421516 421948 42194 423001 423001 42301 4001 4001 4001 4001 4001 4001 4001 4	43973 439606 43973 44373 44373 44383 44408 444381	46519 46619 4672 4773 4773 4874 4884 4904 4904 4907 4907 4907 4907 4907 490
\$ 10	15 20 25	35 30	45 50 55	65 65 77 75

TABLE 148

WO 02/086443

83327\_1

TABLE 14C 20

450375

12

2

Uktyra number corrasponding to an Ecs probesed becomes process. The 1 defin numbers in Escapanes of Gorbant Identifier (GI) numbers. Tombarn I, at at " relats to the publication entitled The DNA requires of human primaryones. To Cabimers I at all, Marian (1959) 402-4054. Requires DNA start from which strongs warp particles, identified the process of the process of the process numbers of the process of the 23

121907-122035,122804-122921,124019-124181,124455-124810,125672-126076 Stend S

ubiquifin carboxy-larminal estaras L1 integris, bets 4 CO44 unitgen (horning turction and indian RAN binding protein 1

PCT/US02/12476

fathe 15A shows the Seq ID No, Phay, Exhcor, UnigenelD, and Unigene Title for all of the sequences in Table 16. TABLE 15A: Information for all sequences in Table 16

WO 02/086443

Table 158 show the accession numbers for base Plany's backed Uniquestics for table 154. For each probless we have based by great drafter number from which for adjunctedidar were deciried. Gene datatan were contract target or any proposed that granitories of which from Gentaria ESS is and mONAs. These requirement exist of based on requestic statement code (Double Nets). Outstand California). The Genthert accession numbers of respectives computing each dictair are Estad in the Ausstrand Colorum.

Table 15C there the genomic practicenty for these Placy's Lacking Uniques (DT and accession numbers in table 15A. For each pradicted occur, we have itself the genomic sequence source used for practicion. Nucleodide locations of each pradicted occur are also listed. 2

2

Seq ID Not. Sequence ID rumber:
Pher: Unique Eco probest it benifier number:
Educar: Ecompte Accession number, Genteats accession number
Uniques Tale-Uniques ammobe
Uniques Tale-Uniques gene IDle 15

centrocate and the control of the co Still cackan binding protein AZ Still cackan before protein AZ Still cackan before protein AZ Still cackan before protein AZ Still cackan before protein AZ Protein Still protein AZ 2009 I statis burn protein Still still statistical burn burn protein Still still statistical burn burn protein Still statistical burn BASS intereding treased as fraithers make mediaproteinses 12 (mescralappo preferratising operassed entypen in mela desmooths. carbonic anhydrasa IX ESTs MANDER 10

BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
BEG11982
ALICI3916
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
AMOG1100
BEG13231
ABG28377
BEG13231
ABG28377
BEG13231
AMGG377 Seq ID No: ಜ 23 2

L 10343
AF200422
BE 182528
E 182528
WY9233
MAL 000094
BE 182592 1
BML 000094
BE 182592 1
BML 0005429
BE 182592 1
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
BML 0005429
B

8

8

8

A the part of cases, sub-lenk-C (CFIR escriptions of cases) and a sub-lenk-country of the part of cases of case CAN desiry grown in cycle-deported in these shokes 24 (me cycle-deported in these shokes 24 (me cycle-deported in these shokes 24 (me cycle-deported in these shokes 24 (me cycle-deported in these shokes 24 (me proported a point Full (1340) Executed 124 (me cycle 24 (me 18-70; 50 proble mark to the shokes con a citizate and metalportalises doma 16-10, 100 proble metal 81 (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 58 pers product (MAM) 59 pers product (MAM) 5 tomo explens mRNA; cDNA DIG-Zp547C136 (n. tomo saplens cDNA FLJ13103 fts, done NT saplens clone N11 NTeraZD1 terabors vergites-type MATV integration tills farm COCKE (position for the cocket of the cocke pin-2 occopers

typicos (base, reta (10410)
hydra com synkes 3
adelnyfor dulydnosene 3 Jamil, membe
bookenenses (Duly 1 gehe (170c)
potesh (you'de potential prospiration
potesh (you'de potential prospiration
potesh hydride potentials, respicapotesh (you'de potentials, respica-ES1s cystath 8N cell division cycle 2-8ks 1 (PTSLRE pr quanina nucleotida binding protein (G pr ESTs cell division cycle 2, G1 to 8 and G2 to cell division cycle 2, G1 to 8 and G2 to HA 7859 HA 3185 HA 3185 HA 2744 HA 23453 HA 23453 HA 23453 HA 2021 HA HE 104613
HE 1727274
HE 11600
HE 60205
HE 60205
HE 60205
HE 165246
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807
HE 70807 (1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988)
(1988) 890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 16 |
890 (10 ft : 1918 | 1 S 8 25

88

	1														_		_																															
٠	BE001838	A/250717	97577 27577	AF019225	BE246502	AM411425 Al623693		NM_014398 Y15221	U65690 XS4232	NW 001650	ALCOST37	AU34361 NM_007115	NM 007115	X66839	AW341663 AW016610	NM_006183	U1760	NN 001944	AK001100	AK001100 AB024907	0758270	L10343	X83629	AF 104032	AF052693 BE260964	BE149762 JOA129	BE613348	U92649	J05070 BE001596	AA381807 W79123	NM 014400	NM_005328	U88967	198987	U88967	MM_001327	Z15008	AW580227	AWZ36289	AF120274	AF120274 AF120274	AF120274 H39960	H39960 X02419	724008 724008	AIGS3816 AWD09168	M18728 M18728	M18728 BE395085	
4:13	437852	2112	451668	2223	439738	E003	405932	421379	430890	12.51	413063	452401	<b>\$240</b>	1000	309931 412719	417034	1375	475650	418653	479610	06990	422158	431958	78484	1763	431009	449230	410555	424687	439606	404877	418543	188	12817	415817	418678	409420	408790 408790	200	428969	428969	450701	450701	1	457489	407242	444005	
WO 02/086443	88	3 65 8	8 = 1	Seq 10 No. 474 & 475	:2:	= E	2 2	Ic. 488 & 489 Ic. 490 & 491	Vo: 492 & 493	Vo. 496 & 497	No: 500 & 501	Vo: 502 & 503 Vo: 504 & 505	Vo: 506 & 507	Seq ID No: 510 & 511	Seq ID No: 612 & 513 Seq ID No: 514 & 515	Seq ID No: 516 & 517	Seq ID No: 520 & 521	Seq ID No: 622 & 623	Seq ID No: 526 & 527	Seq ID No: 628 & 529 Red ID No: 670 & 531	Seq ID No: 632 & 533	Seq ID No: 534 & 535 Seq ID No: 538 & 537	Seq 10 No: 538 & 539	Seq ID No: 542 & 543	Seq ID No: 544 & 545 Seq ID No: 545 & 547	Seq 10 No: 548 & 549 Seq 10 No: 550 & 551	Seq ID No: 552 & 553	Saq 10 No: 556 & 557	Seq ID Not 558 & 559 Seq ID Not 560 & 561	Seq 10 No: 562 & 563 Seq 10 No: 564 & 565	Seq ID No: 568 & 567	Saq 10 No: 570 & 571	Seq 10 No: 574 & 575	Seq ID No: 578 & 579	Seq 10 No. 587 & 583	Seq 10 No: 588 & 587	Seq ID No: 580 & 591	Seq ID No: 594 & 595	Seq 10 No: 598 & 599	Seq ID No: 602 & 603	Seq ID No: 604 & 605 Seq ID No: 606 & 607	Seq ID No: 608 & 609 Seq ID No: 610 & 611	Seq ID No: 612 & 613 Seq ID No: 614 & 615	Seq 10 No: 616 & 617	Seq ID No: 620 & 621 Seq ID No: 622 & 623	Seq ID No: 624 & 625 Seq ID No: 626 & 627	Seq ID No: 626 & 629 Seq ID No: 630 & 631	
			<b>√</b>		9			15	:		2			53			ಜ			35	:		40	2		45	<u>•</u>		8			22		Ş	3		65		Ę	2		75			8		82	
				•	·																															•					-							
PCT/US02/12476			-			-																																					-					
	glutamate-cystrâne ligase, catalytic eutr ESTs, Weathy similar to 117330 hypothell	ESTs, Weatly similar to 117330 hypothell FSTs, Whathy similar to 117330 hypothell	ESTs, Weathy striker to 117330 hypothes ESTs, Whathy striker to 117330 hypothes	High modify group (northistone chromoso NM 022342-Horm sapiens kinesin ordien 9	ESTs	nitro axide synthese 2A (inducible, hep	lerthead box E1 (thyrold transcription )	peptidylglyche alpha-amidaling monowyg	hypothetical protein MGC5350 ESTs	unnamed protein product (Nomo sapiens) minichromosome mainlenance doficiont (8.	web enthroblastosis vina E26 oncogan	guarine nucleotide binding protein 11	calcitorin receptor-like catherin 5, troe 2, VE-catherin (vascula	singed (Drusophila)-like (sea urchin fas	complement component City receptor	ESTs northeast labilities 3, ekin-derived (SKA).	plataphilin 3	paratyroid homona-fite homona	iow density flooprotein receptor-related	collegen, type XI, eight 1	SRY (sex determining region Y)-box 4 constitue monotox charles synthetizes	plutary tumor-tensionaling i	Insular-like growth factor binding prote SRB7 (suppressor of RNA polymerase B, ye	butyrate-induced transcript 1	small proline-rich protein 18 (cornilin)	HZA ristone temity, member X gb:Homo sapters full length insert cDNA	ghycoprofeth (transmembrans) nmb striba-fetoerdeth	Integrin, alpha 5 (Stronectin receptor,	matrix metalloproteinasa 1 (internatibal	maurix metanoprotemasa 1 (metanua solute carder family 7, (cationic amino	tissue factor pathway inhibitor 2 G protein-coupled receptor 39	perfosth (OSF-2cs) monokine induced by gentima interferoe	514 encotatal trochodissi ghopprotein . 514 encotatal brothodissi dhopprotein	cartiage ofgomeric matrix protein (pse	ESTs, Weakly similar to \$64054 hypothed LIV-1 protein, estimoen regulated	Adilcan XXA1888 protein	hypothetical protein FLJ21080 secreted ffzzlad-related ordein 4	to superfamily receptor LNIR  a distribution and metallocrateiruse domo	standocalch 2 matrix metallombianese 11 (stromebsin	Transmembrane prolease, serine 3	ESTs; hypothetical protein for IMAGE:447	gap junction protein, beta 2, 20kU (conn ESTs	EST <sub>1</sub>	c-Myc target JPO! Vantamembrane professe, serfine 4	Hypothetical protein, XP_051860 (VIAA119 Hypothetical protein, XP_051860 (VIAA119	bone morphogenetic protein 2	orskine knd superfamily 1, 6MP antegon	
	PA-151300 PA-127812	Ha 127812 Ha 127812	H 127812	H2.62711	Hs.127728	H 193788	He.159234	Hs. 159396	Ha.71331 Ha.292206	Hs.57101	Hs.279477	HS.83381	Hs.152175 Hs.76208	Hs.118400	Hs.97199	Hs. 816	Hs. 26557	Hs. 69626	Hs.54481	Hs.82772	H. 5359	Hs.25287	Hs. 286145	Hs.260622	H. 1076	Hs. 147097	Hs.82228 Hs.155421	Hs.149609	Hs.83169	Hs. 6682	Hs.295944 Hs.85339	Hs.136348 Hs.77367	Hs. 82128	Hs. 1584	Hs. 79138	Hs.72157 Hs.334838	Hs. 8109 Hs. 105700	Hs.61450	Hs.155223	Hs.298241	Hs. 128899	He.157601	Hs. 157601	H3.123833 H3.63125	H-50031	Hs.73853	Ha.40098	
	M90656 Al581344	AISB1344 AISB1344	ALSB1344	AAB47843	AW241887	AF068238	U89995	AF056209	AW295647 AAE06607	AW247090	BE245360	AW161552	NM_005795 UB4722	8E259035	AW580939	AW016810	BE279383	AA374372	D88407	AW067903	A1075141	AF062849	AA449015	AF181470	BE165289	X14850 AF086009	X76534 J00077	NM_002205	M13509	AW388633	C18356 AA084248	D13668 X72755	BE270268	L32137	BE387336 AA242758	AF245505 AA852773	W27249 AF026592	BE 153855 AA003647	AW863419 NM 005940	A1538613	AW664964	M85849 A1357412	AI357412 AI357412	BE614387 031382	AB033025 AB033025	AL03566	AW190902	
113	424629	637789	637789	451968	441525	428810	423934	425734	438403	403329	119073	102283	103280	102012	134299	412719 472158	128921	419121	409459	417866	418113	428612	431221	431563	1323	103768	417512	424503	418007	416738	415138	423961	417433	422867	400300	411789	450098	452747	426215	525	42117	47003	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	115522 410418	40804	12420	407811	
086443	38	22 2	SA	22		::::	369	, z	22	22.52	5	38	28	133	3 8	5 5	<b>5</b>	3 2	55 55	8 8	33	<b>1</b>	8 E	21	851	2 2	<b>3</b> 5	20 5	128	3 8	<b>A A</b>	<b>5</b> 3	8 8	\$ <del>=</del>	55	5 5	55	85	85	8	35!	5 5	33	33	58	359	8 5	

H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 10877
H. 1087
H. 10

187

œ .

COST   ALCOHOL   PARKED   PA	MONATED TO THE PROPERTY OF THE	CONDUCTOR CONDUCTOR CONDUCTOR CONCOCCO CONCOCO CONCOCCO CONCOCCO CONCOCCO CONCOCCO CONCOCCO CONCOCO CONCOCCO CONCOCCO CONCOCCO CONCOCCO CONCOC CONCOCCO CONCOCCO CONCOCCO CONC
14.00   14.00   14.00   14.1		GCCTGCGCT CCCCAAAGTC CGCCGGCATG GGGGGGGGGC GGACCGCGTC GATGGCCCAG
14.13 14.23	MASTIGEN MESTED OLIVER TO AND LIGHER MESTER MESTER MESTER OLIVERS AND MESTER ME	
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2011 AGAINTOS HE 2021 DE 251 AVAGOS PROTOS DE 251 A	
WO 02/0864413  Seq DNx 524 557 557  Seq DNx 524 57  Seq DNx 524	Seq Diver 51 4 55 5 45 5 46 5 40 5 40 5 40 5 40 5 40	7528051 1519284 2735037 7767812

⊋	_		_	_	_		
	MAPLCPSPWL GPRD1. DEPUD	PLLIPAPAPO	LTWOLLLSLL Pri. priestilb	LIMPVHPORI.	PRINCEDSPLG KREREGGILEI	COSSOCIODAL	9 2
	DPQEPQNNAM	KDKEGDDQSH	WRYGODDPWP	RVSPACACRF	DEPUDIRPOL	AAPCDALRPL	8
¥	ELIGPOLPPL	PELRLRANGH	SVOLTLPPOL	EMALGPGREY	RALQLALIMO	AAGREGSENT	2 5
2	FEGSETOVEG	HVVHLSTAPA	PSRYPOYBOB	LITERCAGGY	INTVENOTVH	LEAKOLHTLE	200
	DTLMGPGDSR	LOLMPRATOP	LNGRVIEASP	PACVDSSPRA	ABPVQLNSCL	AADILALVE	2
	GERFAY 18VA	PPOMRKOUR	KULNGOOR	A PART OF THE			
Ö	Seq 1D NO:	Beq ID NO: 3 DNA sequence	900				
	Coding sequence:	Jence: 438-1391		•			
٧.		11-	<b>:</b> -	<b>-</b>	<b>\$</b> _	81	
•	AGCGGGGTTG	TCTATTACT	TOTTCHAMA	GTATCAGGAG	TOTOMOGC	AGAGAAGAGA	9
	GTGTTTGCAA	AAGGGGGAAA	GTAGTTIBCT	OCCICITIVA	GACTAGGACT	GAGAGAAAGA	130
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TONGCOCCAG	GCTTAAGCCT	TTCCAAAAA	180
8	TGATCCTGAT	TCCAOTTTGC	CTCTCTCTTT	TITICCCCA	ANTIATICIT	COCCIONTITI	9
	TCCTCGCGGA	OCCUPACT	CCCGACACCC	COCCOCCT	CCCCTCCTCC	TCTCCCCCCG	360
	22000000000	CCCCANAGTC	2000000000	COADOGTCOO	0000000000	0000000000	430
	COCCCACAG	COCCOOCATO	TACAACATGA	TOGAGACOGA	<b>OCTOANACCO</b>	000000000	9
	AGCAAACTTC	G0G0G0GCGC	GGCCGCACT	CCACCGGCGGC	000000000	GCCACCAGA	240
ŭ	MANACAGCCC	GGACCGCGTC	MAGCGGCCCA	TOWATOCCTT	CATGOTOTOG	100000000	9
-	AGCGGCGCCAA	GATOOCCCAG	GAGAACCCCA	AGATGCACA	CTCGGAGATC	NOCANGCOCC	9 20
	TOOGGGCCGA	GTGGAAGTT	TTGTCGGAGA	COGNONANGCO	accorrector.	GACGAGGCTA	720
	Adeadcraca	Agederace	ATGAAGGAGC	ACCCODATTA	TAMATACCGG	CCCCGGCGGA	280
5	MACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	COGCOGGCTG	CTGGCCCCC	
2	GCCCAATAG	CATGGCGAGC	gagactcaga	100000000	כבוממכמכם	DOCUTORACE	000
	AGCGCATGGA	CAGTTACOCO	CACATGAACG	OCTOONGCAA	COCCADCTAC	AGCATOATOC	96.
	AGGACCAGCT	GGGCTACCCG	CAGCACCOO	OCCICATOC	CACAGOOCA CACAGOOCA	COCCADATOC	1020
	STATE OF THE PARTY	CCCCINCION	A COLUMNIA C	TOTAL CITY	Character	ACCUPATION AND ADDRESS OF A PARTY	9
2	TOCCICITOR	CTCCATOGOT	TOOOTGOTCA	AGTECGAGGE	CAGCTCCAGC	CCCCTOTOG	1200
	TTACCTCTTC	CTCCCACTCC	AGGGGGCCCT	OCCAGGCCGG	GGACCTCCOO	DACATGATCA	1260
	<b>GCATGTATCT</b>	CCCCGGCGCC	GAGGTGCCGG	AACCCCCCCC	CCCCAGCAGA	CTTCACATGT	1320
	CCCAGCACTA	CCNGNGCGGC	ccoaracco	OCACOOCCAT	THACOCCACA	כשמממשכ	90
ç	CACACATOTO	AGGGCCGGAC	AGCGAACTOO	AGGGGGGAGA	AATTTCOM	GALAMACGAG	2
ž	CCANATCOCA	000010CM	AGAGGAGAGT	AAGAMACAGC	ATCONCANA	CCCGGTACGC	1500
	TCAMAAAA	AMANAMAA	AMATECAT		MATUACAUC.	TO COMMON	200
	AACACCAAIC.	CAICCACA		A THE PERSON OF	ACADA A POR	TOTOTAGOT	1680
	GOLD GOLD CO.	COCCANTICA	CONTRACTAC	ATCTOCACGOA	AAGAAGCTA	CONTANACT	1760
35	TITANAGIT	CTAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTOCKNO	TCTTTACCA	1800
	TAATATTAG	AGCTAGTCTC	CAAGCAACAA	AAAAAATOTT	TTAATATT	CANGCACTT	1660
	TTGTACAGTA	TTTATOGAGA	TAAACATOOC	AATCAAAATG	TCCATTOTT	ATAMOCTOAG	1920

26
7
=
3302/
Š
2
₽
ن
يتم

7			
1980 2040 2100	2160 2220 2280	2340 2460 2520 2580	2640
CAGCTGAAAT TTTAATTOTT CTOTGGTCTT	TTAMAGGAA GATCCCAACT TTTTCTTATG	TTTCCCCCC TTTATTTTCC CASTCTGCC GAGAATCCAT TTCAACTTA AGTTTTTACT GAGACTGAA AMAAAAAAA ACAAMAAA AMAAAAAAA	CACACAAAA
TTGCTGAAT TTTGATTCTG ATTAGACATT AAATACAA ATTAGACATCT	DOCTITIONS OF STREET	FFFGA	CACACACA
045	CTAAATTTA ATTTATAATA AAATTACTGT	TATTTAMOO ATTATTTAMA ACAGGTACAT TTTGAMATAT AMACAGAMA	MAMAMAGA MCMACACA CACAGAGGG
AAAAAAAAAA AAAATTAGAA			CACAGAGGG
WO 02/086443 ATTRECEA TATTTTCAA TAGGACAGT TACAAAGGAA MAAATTGT ACAAAGGAA	GCALANGTT GCAGGTTCAC TTCAGATAAA	THOTAIN THEIGTAN TAGHOTAL THAMAGA TATALATH GACHATAL CATALGCA CAGHTIGAGA AMANGA ACAMMA	CACAACACA AACAACAAAA AAAAAAAA CCACAACACA AACAACAACA CACAGAGGG
WO 02/086443 ANTITOCON TATTITICAN TAGGRACATT TECANAGES TANANATTOT ACANAGEM	ANATOGOCAT TICCATTITIO	OTTOTANTA OTAGTICIAL CLATATATT CCATTATGCA AAAAAAACAA	CACACACACA
	S	10	

Seq ID No: 4 Protein sequence: Protein Accession #:CAA83435.1

15

	ADRENDIA 60	RPRRKTKTLM 120	(SPONGDQLGY 180	OTPOMALOSM 240	ALHMSQRYQS 300	
ī —	PHY WSRC	YXY RPRE	NGS YEN			
<b>:</b> _	VICEPICIA	HMKEHPDYKY	APPRICASNOS 1	PTYSMSYBOO	AEVPEPA	
<b>-</b>	GOLIDINIBDE VIRPIGIAPHY WSRGGREK	IDEAKRLRAL !	AGVNORMDSY .	TSSQTYPINGS	RDMISHTLPG AEVPEPAAPS	
₹_	GOGNSTAAAA	LLABITEKRPP	BOVOVGAGLO	DVBALQYNSM	SRAPCOAGDL 1	
=-	INNORTELK PPOPOQTECO COCKSTAAAA	DENPKHANSE ISKRLAAENK LLASTEKRPP	UCHATLEOG LLAPGGNERA	AAOMOPHGIRY	SPPVVTSSSH TLPLSHN	
	MYNNORTBLK	QENTRADASE	XXDKYTLP0G	POLIPGLNARG	GBVVKSEASS SPPVVTS GPVPOTAING TLPLSHN	
8	3				22	

8eq ID NO: 5 DNA sequence Nucleic Acid Accession \$: U91618 Coding sequence: 29-541

Seq ID NO: 6 Protein sequence: Protein Accession #: AABSOS64 S

55

Seq 1D NO: 7 DNA mequence Nucleic Acid Accession #: NM\_006516.2 Coding sequence: 109-2940 છ

•	9	120	180	240	300	9	420	480	240	9	9	720	780	940	900	960	1020	1080	1140	7200	1260	1320	1380	146
<b>n</b> _		GACCCAAAGG	CTTANGITCA	TOGATTOCTC	TAAGGAAATG	TTTCAGAAAT	MAMCANGA	AGATGATCCA	CACCACCTAAT	GITTGICCAT	ACCITICIAC	AGGCATTTT	TTTTAAAGAA	OTTCA TOCAA	AGCACCANAC	CTCTGCTGAC	ATTCTCCCTT	GATGGCAGAG	GATTOTTGAA	AGCCCAGCTA	CACCACTOTA	<b>GOTOOTTOA</b>	AGATGATAAG	CTCCATTOCC
<b>;</b> _	CATATTGAAA	TCTACACAT	TOCTOOTTICC	ATCCCTATA	TCTCAAACAT	GAAGAGTATT	ACAGCAMAT	GGGCACATGG	ACATTCATTT	CAGGCCCAGT	ACMATGACAA	CTGACATCAC	TTAGTAAGCT		ACAACCAAGA	TATCACAGA	CTCCTCCCCAC	TOTOCOGCAA	ATTITION TOCA	GAGAGATICAG	CATATCTGCC	AAGGATTTOA	TOACCAGOO	CUCUATICA
<b></b>	CATCTGCATC	TOGAGGCTTC	TITOTOTOTO	CTTCANGACA	CAGAACCTCA	<b>actaccasas</b>	GCTAATAATA	DACTOSTATO	GAGGGAAAAT	TACOGATICAC	GATGAGTATA	AGOTTOTATA	AACTOTATTA	MATCOMCTO	OCAMOTACCC	CCATCOCATO	CADCTTCCAC	<b>CTOCTOGATO</b>	<b>OCNOBATITI</b>	GACAGCAAAG	TTOCTOOTT	<b>ODGCTTANGA</b>	ATGATATTAG	AGCAGTGGTT
<b>12</b> –	AGGAAGAAAC	<b>OTGAGTGAAC</b>	CAACCTOAAG	TOGAGTACAG	ACCTGAGGAT	CCTATTIMI	CACATGGAAA	CATAOTOACT	<b>OTOTOGALALA</b>	AACAGCTOGC	OCCUPANTIC	TAMOTOACA	CCCCCAAGAA	TAGCACCCAA	ATTITITION	CCTCADAAGT	GANTOGGACT	GOTCTOTTTA	ACAACAAGCC	TROCOURTE	TGATCGAAAG	CATTEMENT	TOCCICION	CACTGTGCTC
<b>a</b> _	TTCCAAGTTC	CAGGCTCAGT	<b>OTCCTATTE</b>	TCCTOCOAGC	ATCCTCAGGT	ATTENDED.	TAATACCTOC	AGGCAAATGT	AATACAGAGG	ATGATAACTT	ACCTCCOTTG	AAATCAAT.	AAGGTCCTTG	TTATCTACA	CTOTOOTTOA	ADATGTGCAG	COTTOCCAT	<b>GTGACAAAGT</b>	TOCTTCAACT	TCOTOGGCAT	ACAGCAATGA	CAGACATCAG	GAMAGETTA	ATTGCTTACC
		ATOTATOCAG	AGCATTGCAG	<b>GAACTCCCAT</b>	ATTROCASTTA	ATAACTGAAG	ATAAAGATTT	TCATATOMA	TACACCCTAC	TTCCTACTGA	GAATOGGCCC	ATAAATGGGC	<b>STOTOTOMAA</b>	GGATGCACCT	AGTITATET	CTACAGAACC	TTTCACCACA	<b>GTACAGGCTG</b>	<b>OCTOACADAC</b>	ATTCATACCT	CACCAMATTA	TCAGCTAAAA	AAACTGAATG	CTTCTTGGCA
	;	S				ć	2				;	2				ć	20				ě	င္ဆ		

ACCOMMENT TREABART CONSIDERAL MACCOUNTS TREABLE AND CONTROL TREABL 2 22 15 2 3 35

Seq ID NO: 8 Protein sequence: Protein Accession #: NP 006517.1

<del></del>

45

S

55

	<b>1</b> -	<b>- 5</b>	<b>-</b>	<b></b>	<b>3</b> –	
HTORSTAGPI	CHEKEVILLY	ALSSELPFLO	AGVOLQDINGY	NGCTIAINPO	VPENCHLIBN	
KEMITEASP	YLFRATKRRV	PPRNIKILIP	ATWXANNAK	INCESYBKAN	VIVIDAYGAH	_
CODPYTIOYR	COCKECKYIH	PTPNFLLNDN	LTAGYOSROR	VPVHEHAHLR	MOVPDEYAND	-
KPPYINGONO	INVTRCBEDI	TOINCRIOR	CPOENCIISK	LPACEDCTFIY	HETQUATABI	-
(PNQ5L68VV	EPCHASTHNO	KAPKILONOHC	SLRBAMDVIT	DSADPHHBPP	MOTRLPPP	_
<b>LPSLVQAGDX</b>	VVCLVLDVBB	EMAEADRIE O	LOOMEPYLH	DIVERHTEVIO	IASPDSKGEI	~
PACLHOINEN	DDRKLLVSYL	PTTVBAKTDI	BICSGLKKGF	EVVEKLANDKA	YGSVMILVTS	•
CODXLIGACL	PTVLASGSTI	HSTALGSBAA	PHLEKLERLT	COLKPEVPDI	BNSNBMIDAP	•
BRISSOTODI	POCHTOLEST	GENVKPHHOL	KNTVTVDNTV	GNDTMPLVTW	OASCPPEITL	4
PDPDGRXYYT	NNFITNLTFR	TABLMIPGTA	KPCHNTYTLA	NTHRELOALK VIVIERABNE	VTVTSRABNB	_
AVPPATVEAP	VERDSLHPPH	PVHIYANVKO	GPYPILNATV TATVEPETOD	TATVEPETOD	PVTLRLLDDG	۳
AGADVI RNDG	IYBRYFFFA	ANGRYSLKVH	VNHSPBIBTP	AKB I PGBRAM	YVPOYTANGN	•
COMMAPRKSV	GRHEBBRING	PSRVSSOGSP	SVLGVPAGPH	PDVPP PCK11	DLEAVKVEER	•
LTLEWTAPGE	DPDQQQATSY	BIRMSKSLON	IODDFWNAIL	IQDDPNNAIL VNTBKRNPQQ	AGIRRIPTPE	ŵ
POISTNOPEH	<b>QPNGETHESH</b>	RIYVAIRAND	RNBLQBAVEN	IAGAPLPIPP	IAQAPLPIPP NGDPVPARDY	^
3	GLIGITCLII	LILKGVITAN GLIGIICLII VVTEHTLBRK KRADRKENGT	KRADKKENGT	Kil		

Seg ID NO: 9 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 136-632

65

8

	100	120		000 340	_	_	۰			_	_	٠.	_		_	
۲.	CCCACTOTO	OCTOOTO	OGCINONOG	AAGTTGGGC	1CTCCTTCC	CTGGAGCAGC	acchante	TTTGTGGGG	AACAGTGACC	ATOTOCALTO	CTCCCATOGA	TITITION		CCTCCCAAAATC	CCAGCAAAA	TAAAAAAOGC
<b>;</b> _	CCTCCCACTT	CCCTCCCCCA. OCTGOTGOTC	GAGTGGGAAT	TTAMATOCC	acracerrae	gracionica	CCANDAGGGC	GCTGCCCAGC	<b>CCTGGATGAG</b>	CATCACTOTC	TCTTGACTTC	THOMTAMO	COUCTOOCTC	CTCTOACTCT	ATTECANCA	ATAAAGATAT
5-	CCCCACCACA	TODOCCTAGAG	OCCADOCAAT	TITIOGITICS	таоомасста	GATCCATGAT	AGTACTOCTO	TGCACAAGGA	TGATGGGCAG	TOCTOOCACT	GAAGCAGAAC	<b>CAUTITIONS</b>	TTCCATAACC	CCCTTCTOOG	CATTITION	ATTTTOTCA
<b>11</b> _	GATGCCCAGT	<b>OCCULTANCE</b>	DONGOGGCT	TTGAGGCAGG	ATCCTCACCC	OTCIDOCACA	ACCETOCACA	AAGGAACTTC	CTGAAGAAGC	TATGCTGTTT	OACCOACCCT	TOATCOCTIT	CTCAGTGATG	DOATCCTGCT	CTTTAGGTCT	acraacmm
<b>=</b> _	CCCCGTCCAG	TC000007	TETETOGGAG	TOGGATCAGG	CCACATATAA	CTOCCACCTO	GCTCOTCACT	GCCCCAAATG	TOADGADOOG	CTTCCAGGAG	GOCCTGCCCA	CCAGGACTGT	ATTETALTO	ADDOCCTOCT	CADADCTATO	GAGATAGGTT
	CTCCCCTCAC	OCTODOTO00	GAGCTGGCAC	CAGGGTTTOG	CCAGTGGGGC	<b>ACCIPITATION</b>	CCCTCCCTGT	AGCTGAOTAA	AGAAAGTOGA	AGCAGGTGGA	ACTICITICGA	TCTCTTGGGC	TOTTOATAAT	CTOCOLATO	TCTCCAAGOC	ATTGGAAATC
	6	2				i	2					2				58

Seq ID NO: 10 Protein sequence:

13

8

8

45

S

ଓ

8

2

75

စ္တ

83

Seq ID NO: 17 DNA sequence Mucleic Acid Accession #: Bos sequence Coding sequence: 919-2172 WO 02/086443 TOTCHARTA ABITATAN ANGOCANT ACCA Sag ID NO: 16 Protein sequence: Protein Accession #: NP\_005969.1 2 15 ನ 23 ಜ 33 45 8 65 8 82 THE CONTROL OF THE CO Beg ID NO: 11 DNA sequence Mucleic Acid Accession #: Eos sequence Coding sequence: 116-626 Seg ID No: 15 DNA sequence Nucleic Acid Accession #: 20s sequence Coding sequence: 62-358 Sos sequence SCORGONING S | HOCBBLEGAL AVLVTIPHKY SCOEDDKFKL VHLFNPVIGD LRNGSPEGKS DCPKITGHWR Seq ID NO: 14 Protein sequence: Protein Accemeion #: NP\_005969.1 1 WO 02/086443 Protein Accession 8: NP\_005969.1 Seq ID NO: 12 Protein sequence: Protein Accession #: Eos sequence Seq 1D NO: 13 DNA sequence Nucleic Acid Accession #: 1 Coding sequence: 58-354 MICBELEGAL AVLVTTPHKY CSLDENSDOG VDPOSYAVPL

TRICKTANA KOOGONT TCTCANAGE KANACATE COCCUTTCT CHARTTECT TCTTANA KOOGONT TCTCANAGE GOCCUTTCT CHARTTECT AND TO TCTTANATO CHARTTECT ANACTITTO ATTECTOR A TOTOTCATA TOTOTCATA TOTOTCATA TCTTANATOC ANACTITAT ATTECTOR ANACTICA ANACTICA CHARTTECT CHARTTECT ANACTICA CHARTTECT ANACTICA CHARTTET TOTOTCATA TTTANATO ATTENATOR TTTANATO ATTENATOR TTTANATOR ATTENATOR TTTANATOR TTTANATOR ATTENATOR CHARTTET ATTENATOR ANACTIVATOR TCCHARCE MATTETT ATTENATOR ANACTIVATOR ATCHART ATTENATOR ANACTIVATOR ATCHART ANACTIVATOR ANACTIVATOR ATCHART ANACTIVATOR ATCHART ANACTIVATOR AN

Seg ID NO: 18 Protein sequence: Protein Accession N: CAAS3571

15

2

12476	
÷	
N	
-	

WO 02/086443

	Ĭ	PAGAGETCCA	TGCTGGGTGA	AGAGTTCCA TOCTUGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG	COCATCCAGA	OTOTOAAGAC	AGAGGCAGAG	•
	_	AGCTOTTE	GOGGGGGGGT	PROMONENT OCNOCATOR OF CACAGOATOR ANGACATOCA OTTOCAOCTO	GACAGGATGA	AAGACATOGA	GTTGCAGCTG	
	•	TOCCOCCA	GCCAGGCCAT	SCHOOLEN CATOCTOCOC TCOCCOORCE TOACAGGACT GGAGAAGCOT	TODOCOGACC	TOACAGGACT	CONGAGOOT	
•		TTGGAGCAGA	TCCOTCACCA	TROACCAGA TOCRETACOA CATCAATGGO COCRETOCTOT ACTATGCCAC CTGCAAGTGA	COCOTOCTCT	ACTATOCCAC	CTGCAAGTGA	• •
n	_	TOCTACAGG	TCCAGCCCGT	INCIDENCE OF THE TOTAL STATE AND THE TOTAL STATE OF THE S	ATCTGCCGCC	TITISCITITIO	OTTOGOGGGA	
	Ĭ	ATTGOOTTG	GAATGCTTTC	NATIONATIO GNATOCITIC CATCITICAGO NOACITICAT OCAGCITANA	AGACTITICAT	GCAGCCTAAA	GTACAGCCTG	٠.
	Ĭ	SACCACCCCT	COTOTOTAGE	ACCACCCC GOTOTOTAGC TAGTAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT	ACCCTGAGCT	GCAGCTGAGC	CTGAGCCUAT	٠.
	_	BOGACAGITA	CACTTGACAG	AGRICACITIA CACITGACAG ACAAAGATOO TOGAGAITGO CATGCCATTO AAACTAAGAG	TOGAGATTGG	CATGCCATTO	AAACTAAGAG	•••
•	٠	CTCTCAAGTC	AAGGAAGCTG	TETERABLE ANGUARDETO GOSTOGORO TATECTERCE CTITAGITET CEASTOGODA	TATCCCCCC	CTTTAGTTCT	CCACTGGGGA	•
2	_	CONTRACTOR	ACCAROCACA	SGRATCCTOG ACCAGCACA AAACTTAAC AAAGTGATG TAAALATGAA AAGCGAAATA	AAAAGTGATG	TAAAAATGAA	AAGCCAAATA	•
		C. COLLEGE OF STREET						

11420 11420 11480

Seq ID NO: 20 Protein sequence: Protein Accession #: NP\_000219

200200

HORNIANGO MANIMOTON LIVOGRBANA ACPRECICAS BITACEDDES GIVAPPILES PROPERTE ACRESTICATION GENERALE TAGENGRAPH PROPERTE PROPERTY GENERALE TOGENGRAPH TOGENGRAP

2

25

8eq ID NO: 19 DWA sequence
Nucleic Acid Accession 8: NM\_000228
Coding sequence: 82-3600
11 31

8

35

<del>수</del>

5

12							
		<b>=</b> -	11-	<b>1</b> -	<b>\$</b> _	- 21	
	MAPFALLCRA	LPGLLHAGOA	CSRGACYPPV	GDELVGRIRE	LEASSTOULT	KPETYCTOYG	Ī
;	BWOMKCCKCD	BROPINIYEN	RVENVASSED	DMRWWQBQND	UNPVELQLDL		ä
2	MEPOGPMPAG	ML I BRABDPG	KTWRVYQYLA	ADCTSTPPRV	ROGRIPOSNOD	VRCOSLPORP	=
	NARLANGGRVQ	LATABLYBGI	PATOSOKIOB	VCBI THLAVA	PTRLAPVPOR	<b>OYHPPSAYYA</b>	ň
•	VBOLRLOGSC	PCHGHADRCA	PKPGAGAGPG	TAVQVRIDVCV	COHNTAGPNC	ERCAPPYNNR	ă
	PWRPAEGGDA	HECORCOCAR	HERTCHFOPA	VPAASQGAYG	GVCDNCRDHT	BOTONCERCOL	m
;	HYPRNRRPGA	BIOSTCIBCE	COPDOAVPOA	PCDPVTGQCV	CKEHVQGERC	DLCKPOTTOL	¥
3	TYANPOCCHR	COCNILGBRR	DMPCDRESGR	CLCLPMVVGP	KCDQCA PYHW	KLABGOOCEP	Ŧ
	CACOPHINSPO	PTVQPVHDRAV	PCRZGPOGLM	CBAAAIROCP	DRTYGDVATG	CACOCINO	ň
	TEGPGCDKAB	GRCLCRPGL7	OPRCDOCORG	YCHRYPVCVA	CHPCPQTYDA	DLREGALRFO	ĕ
	RLRNATASLM	SOPCLEDROL	ABRILDAKBK	IZQIRAVLEB	PAVTEQEVAG	VABAILELER	•
6	TLOGLQLDLP	LEESTLBLPR	DLEGLDRSPN	OLLTHYORKA	EQFBK186AD	PECAPRICUET	*
ટ્ર	AYEOSAGAAG	QV5D8SRLLD	QLRDSRREAB	RLVRQAGGG	OTGS PKLVAL	RLEMBSLPDL	F
	TPTFNKLCGN	SROWCTPIS	CPGELCPQDN	CTACOSRCRO	VLPRACCAFL	MAGGVAEGLR	ě
	GPNAQLQRTR	OMIRAMEESA	SQIQBBAORL	ETQVSA8R5Q	MREDVARTRU	LIGOVRDFLT	ă
	DPDTDAATIO	EVSEAVLALM	LPTDSATVLO	KNEELQAIAA	RLPNVDLVLB	OTKODIARAR	ă
į	RLOABABEAR	BRAHAVEOOV	EDVVONLACE	TVALQEAGDT	MOGTERBLRL	IODRVAEVOO	2
સ	VLRPAEKLVT	SMITKOLGDIM	TRMEELRHOA	ROOGREAVOR	COLABGASEO	ALSAQEOPER	2
	IKOKYABLKD	RLCOSSMLCB	COARIOSVET	RABELPOSTM	<b>EMEDRAKENS</b>	LELLROSOAI	ž
	MLRSADLTGL	BKRV SQ I RDH	INGRVLYYAT	ಕ			

Seq 1D NO: 21 DNA sequence Nucleic Acid Accession #: NM\_003722 Coding sequence: 145-1491

令

		<b>=</b> _	17	<b>:</b> -	<b>\$</b> _	18-	
45	TOTTGATAT	CAMBACAGT	TOMOGRAF	GAATTTOA	ACTTCACGGT	graceaccer	Ç
	ACAGTACTOC	CCTOACCCTT	ACATCCAGCG	TITICOTAGAA	ACCCAGGTCA	TITCICITION	730
	AAAGAAAGTT	ATTACCGATC	CACCATOTCC	CAGAGCACAC	AGACAAATGA	ATTECTIONAL	780
	CCAGAGGTTT	けつこうないしょう	CTGGGATTT	CTOOMCAGC	CTATATOTTC	AGTTCAGOCC	9
S	ATTGACTTGA	ACTITIOTOGA	TOMOCATCA	GAAGATOGTO	CHACAMACAA	DATTOAGATT	200
3	AGCATOGACT	GTATCCGCAT	OCAOGACTOS	GACCTGAGTG	ACCCCATOTO	OCCACAGTAC	260
	ACGAAOCTOG	<b>GGCTCCTGM</b>	CAGCATGGAC	CAGCACATTC	MONCOCTC	CTOSTCCACC	<b>5</b>
	AGTCCCTATA	ACACAGACCA	COCCCAGAAC	AGCOTCACGO	COCCCTOOCC	CTACGCACAG	480
	COCAGCTCCA	CCTTCGATGC	TCTCTCTCCA	70,000,000	TCCCCTCCC	CACCGACTAC	340
	CCAGGCCCGC	ACASTITICGA	COTOTOCITO	CACCAGTCGA	GCACCGGCGAA	OTCOOCCACC	9
ያ	TGGACGTATT	CCACTGAACT	GAAGAAACTC	TACTOCCAAA	TTOCAMOAC	ATGCCCCATC	9
	CAGATCAAGG	TOATGACCCC	ACCTCCTCAG	CONSCIENTA	TCCGCCCAT	OCCIPATOTAC	720
	AMANAGCTO	AGCACGITCAC	CGAGGTGGTO	AAGCGGTGCC	CCACCATOA	<b>OCTOACCOT</b>	96
	DATTCACO	AGGGACAGAT	TOCCCCTCCT	AGTCATTTGA	TTCGAOTAGA	GGGGAACAGC	9
5	CATGCCCAGT	ATTEMATA	TOCCATCACA	DGAAGACAGA	OTCTOCTOCT	ACCTTATICAD	8
3	CCACCCCAGO	TTGGCACTGA	ATTCACCACA	<b>OTCITOTACA</b>	ATTTCATOTO	TAACAGCAGT	96
	TOTOTTOGAG	GCATGMACCG	CCGTCCAATT	TTAATCATTO	TTACTCTOGA	AACCAGAGAT	1020
	OGGCANOTCC	TOGGCCGACG	CTOCTTTGAG	<b>GCCCOGATCT</b>	<b>STOCTTOCCC</b>	AGGAAGAGAC	1080
	AGGMAGGCGG	ATGAAGATAG	CATCAGAAAG	CAGCAAGTTT	COGACAGTAC	AAAGAAGGT	1140
;	GATOGTACGA	AGCOCCCOTT	TOSTCAGAAC	ACACATGGTA	TOCAGATGAC	ATCCATCAG	1200
65	ANACGMAGAT	CCCCAGATGA	TGAACTOTTA	TACTTACCAG	TOAGGGGCGG	TOAGACTIAL	1260
	GANATOCTOT	TGAAGATCAA	AGAGTCCCTG	GAACTCATGC	AGTACCTTCC	TCAGCACACA	1320
	ATTOMACOT	ACAGGCAACA	OCANCAGEAG	CAGCACCAGC	ACTTACTTCA	GAMACATOTO	1380
	CTTTCAGCCT	<b>OCTTCAGGA</b>	TOAGCTTOTO	GAGCCCCCGA	GAGAAACTCC	MANCHATCT	140
6	GACOTCTACT	TTAGACATIC	CARGOCOCCA	AACCGATCAG	TOTACCCATA	GAGOCCTATO	1500
2	TCTATATTT	AAGTOTOTOT	STTOTATTC	CATGTGTATA	TOTOMOTOTO	TGTGTGTGTA	1560
	TGTGTGTGCG	TOTOTATOTA	OCCCTCATAA	ACAGGACTTG	MARCACTT	GOCTCAGAGA	1620
	COCMCTOCT	CAMOGEACA	MACCACTAD	TGAGAGAATC	TTTTOMOGG	ACTOMACCT	1680
	TTACAAGAAA	GGATOTTTC	TOCAGATTE	<b>OTATICITING</b>	ACCORCCATT	датадатала	1740
36	ancorre	grandicad	CAGCTTTCTG	TOTTICCE	OCHOCOLACCO	orchogrado orchogrado	1800
C	GAAAGGGGCA	TANGATOTT	TATTEGMCC	CTTTCTOTC	TCTTCTOLL	GTTTTCTAA	1960
	AATTCACAGG	GAGCTITIG	AGCAGGTCTC	MACTTANGA	TOTOTITIES	AGAAAAGGAG	1920
	AAAAAAGITG	TATIOTCE	TGCATAAGTA	ACTIVITAGE	GACTGAGAGA	CTCAGTCAGA	1980
	CCCTTTTAAT	gerocreard acrostreard	TATAATAT	GCANGTAGTA	AGNARCGANG	Grandward	2040
6	TACTOCTOO	CAGCGAGGTG	ATCATACCA	AAAGTAATCA	ACTITIOTOGG	TOCACACTTC	2100
્ર	TTTGTGAGAA	CTTGCATTAT	Trongrace	CCCTCATOTO	TAGGTAGAAC	ATTTCTTAAT	2160
	OCTOTOTACC	raccicracc	ACTOTATOTE	TT0TCTCT0DD	ATOCTAMAGE	TITICITION	2220
	CATGAAACCC	TOGANGACCT	ACTACADAM	ACTOTTOTT	TOGCCCCCAT	AGCAGGTGAA	2280
	CONTINUE.	COTTITALIA	GAAGACUA	TCCACCCAG	TAATATTOCC	CITACOTAGE	2340
30	TOTTTACCAT	TATTCANAGC	TCMANATAGA	ATTTOMAGEC	CHCCCCCC	ATCTOTOATT	2400
S	ATTTGCTTA	ATTAGAGETT	CTATOCOTOR	AGCCTACCTA	CCATAMACC	AGCCATATTA	2460
	CTCATACTOT	TCASTGCATT	TAGCCAGGAG	ACTIACOTT	TOWNTOWN	AGATCCAAGC	2920
	AGACCTOTTA	ANATCACCAC	TCCTOQACTO	DANTTANA	ATTONANDO	TAGACTACTT	2560

CONTINUED DE CONTI

detypood detypeada Augustana Augusta

55

8

8

2

73

င္ဆ

လ

CCAGCAGCTT

83

2	
-	
2	
7	
0	
23	
=	
٤	
Δ,	
	١

WO 02/086443

	2640 2700 2760	
	CACACCCAGT	Antenda
	TTCCATTITA TCCATCTTCC TOTTATTGAG	
	CTCTGTTTCT GTTCCTCCCC AATGATTTCT	W11110
•	TTTAGAGAAT CTTTAAAAAT TCACCAAGAC	
086443	TICTITITI TACICAMA ITTAGAGAT CICIOTICO TICGATITA MAACATAT TAGGATAA AGATAAGA CITTAAUAT GITCCICCC ICCATCITIC CICACCOG GACOGOAC GIATITICIO TEACAMACA ATRATITET IGENTIMA GEOTIGGII	W111W15
WO 02/086443	TANDATAT	1010000

Seq ID NO: 22 Protein sequence: Protein Accession B: NP\_003713

_		<b>=</b> -	<b>1</b> -	<b>1</b> -	÷_	15 –	
,	MEGSTOTHE?	LEPEVPOHIM DPLEDPICSV OPIDLAPVDE PSEDGATHKI	DPLEOPICSV	OPIDLAFVOR	PSEDGATHRI	BISHDCIRMO	•
	DSDLADPINE	OYTHIOLINS	850NDIOCOM	MOCOLONGS STRPYNTDHA	CNSVTAPBPY	AQPESTFOAL	Ξ
	SPSPAIPENT	DYPOPHSFDV	<b>SPQQSSTAKB</b>	SPOGSSTAKS ATMTYSTELK KLYCQIAKTC PIQIKVMIPP	KLYCOLAKTC	PIQIXVMIPP	=
	POGAVIRAND	POGAVIRAMP VYKKAEHVTE	WKRCPNHEL	BRBPNBOOTA	PPSHLIRVEG	NSHAQYVEDP	ň
_	ITCROSVLVP	TGROSVLVP YEPPGVGTBF	TALMENON	SSCVGCOURR	PILITATLET S	RDOGVLARRC	×
	PEARICACPO	RDRKADEDBI	RKQQVSDSTX	NODOTKRPPR	QNTHO LONTB	IKKRRSPDDB	36
	LLYLPVRGRE	LLYLPVRORE TYENGLKIKE	BLELMOYLPO	BLELMOYLPQ HISTYROOD OCCHORLLOK HLLSACPRINE	<b>COCHOHITOX</b>	HLLSACPRINE	Ş
	S. S. S. S. S. S. S. S. S. S. S. S. S. S	Court of the Administration of the special of the s	The state of the state of				

Beg ID NO: 23 DNA sequence Nucleic Acid Accession #: NM\_001944.1 Coding sequence: 84-3083

2		:	;	:		2	
ì	•	:_	<b>:</b> _	i	;_	i	
	TITICITAGA	CATTAACTBC	Адасодстад	CAGGATAGAA	осмосоостс	ACTTOGACTT	
	TTTCACCAGG	GAAATCAGAG	ACMATGATGG	00CTCTTCCC	CABACTACA	9009010190	-
ç	CCATCTTCGT	<b>AGTCGTCATA</b>	TTOOTTCATO	GAGAATTGCG	AATAGAGACT	AAAGGTCAAT	-
2	ATCATCAACA	AGAGATGACT	ATOCAACAG	CTAAAAGAAG	COMMACOT	<b>GAATGGGTGA</b>	ď
	MATTIGGGIA	ACCCTGCAGA	GANGGAGAAG	ATAACTCAAA	AAGAMCCCA	ATTOCCANGA	~
	TTACTTCAGA	TTACCAAGCA	ACCCAGAMA	TCACCTACCG	AATCTCTGGA	OTGOGAATCO	~
	ATCAGCCGCC	TITTGGAATC	Trorrorro	ACAMANGAC	TOGAGATATT	MCATAACAG	-
,	CTATAGTCGA	CCDOGAGGAA	ACTCCAAGCT	TCCTGATCAC	ATOTOGOGCT	CTAMATGCCC	7
સ	AAGGACTAGA	TOTAGAGAAA	CCACTTATAC	TAACOGTTAA	AATTTTOGAT	ATTANTGATA	un
	ATCCTCCA01	ATTECACA	CAMPITICA	TGGGTGAAT	TOMBOART	AGTGCCTCAA	Ψ
	ACTCACTOGT	GATGATACTA	ATTOCCACAO	ATGCAGATGA	ACCUMICCAC	TRUMATICIA	•
	MATTOCCTT	CAMATTOTC	TCTCAGGAAC	CAGCAGGCAC	ACCCATOTTC	CTCCTAAGCA	٢
	DAMACACTOD	GGAAGTCCGT	ACTITIOACCA	ATTCTCTTGA	CCCAGAGCAA	GCTAGCAGCT	-
9	ATCOTCT00T	TGTGAGTGGT	GCAGACAAAG	ATGGAGAAGG	ACTATCAACT	CANTOTOMY	æ
	STATATA	AGTGAAAGAT	<b>GTCAACGATA</b>	ACTTCCCAAT	<b>OTTTAGAGAC</b>	TCTCAGTATT	ō
	CABCACOTAT	TGAAGAAAT	TIDWITTIY	CTGAATTACT	TCCATTTCAA	<b>STACAGATT</b>	å
	TOCATGAAGA	<b>OTACACAGAT</b>	AATTOCCTTO	CAGTATATT	CTTTACCTCT	GOGAATGAAG	2
•	TTOOTTAWO	TGAAATACAA	ACTIGATICETA	GNACTAATGA	ACCCATCCTG	AAAGTGGTGA	2
3	AGGCTCTAGA	TTATGAACAA	CTACANAGCE	TGAAACTTAG	TATTGCTGTC	MAMACAMO	ä
	CTGAATTTCA	CCAATCAGTT	ATCTCTCGAT	ACCOMPTTCA	<b>GTCAACCCCA</b>	<b>STCACAATTC</b>	Ž
	AGGTAATAAA	TOTANGAGAA	CONATTOCAL	recorected	TTCCAAGACA	TITACTORGE	3
	AAAAAGGCAT	AAGTAGCAAA	AATTGGTOD	ATTATATCCT	COGAACATAT	CAROCCATOS	13
Ş	ATGAGGACAC	TACANGCE	CCCTCAAATG	TCAAATATOT	CATGGGACGT	ACCATOCTC	Ξ
2	DATACCTAAT	GATTGATTCA	AAAACTOCTO	MATCHATT	TOTCOMMAT	ATGAACCGAG	3
	ATTCTACTT	CATABITAAC	MANACAATCA	CAGCTCAGGT	TCTGGCCATA	GATGAATACA	5
	COGGIAMAC	TTCTACAGGC	ACCOUTATATO	TTAGAGTACC	COATTICAAT	GACAATTOTC	Š
	CAACAGCTGT	CCTCGAAAAA	GATGCAGTTT	<b>OCAGITICITIC</b>	ACCTICCOTO	ornarcreco	97
,	CTABACCT	GAATAATAGA	1ACACTGGCC	CCTATACATT	TOCACTOON	CATCAACCTO	5
3	TAMAGETGCC	TOCCOTATOO	AGTATCACAA	CCCTCAATGC	TACCTODGC	CTCCTCAGAG	1
	CCCAGGNACA	GATACCTCCT	<b>OGACTATACC</b>	ACATCTCCCT	GGTACTTACA	GACAGTCAGA	=
	ACAATCGGTG	TOACATOCCA	COCAGCTTGA	CACTGGAAGT	CHETCAGNOT	GACCACAGGG	2
	<b>GCATCTOTOG</b>	AACTTCTTAC	CCACCACA	<b>OCCCTGGGAC</b>	CAGGTATGGC	ADDCCCCCCT	5
5	CAGGGAGGCT	9606001600	OCCATCGGCC	recreater	TOOTCTCCTG	CHOCHOCHOT	5
3	100000001	TCTGCTGTTG	ACCTOTGACT	GTGGGGCAGG	TTCTACTOOG	OGNOTOACAG	2
	GIGGITTIAL	CCCAOTTCCT	GATGCCTCAG	AAGGAACAT	TCATCAGTOO	GGAATTGAAG	2
	CAGCCCATCC	TOMOGRACIAO	DANTCACA	ATATTTGTGT	<b>ACCTCCTOTA</b>	ACAGCCAATG	ä
	CACCCATTT	CATGGAAAGT	TCTOAAGTTT	GTACAAATAC	GTATGCCAGA	99000000	22
,	TGGAAGGCAC	TTCAGGAATG	GAAATGACCA	CTANGCTTGG	AGCAGCCACT	GAATCTGGAG	2
3	GTGCTGCAGO	CTTTBCAACA	GOGACAGTOT	CAGGAGCTGC	TICAGGATTC	GOAGCAGCCA	2
	CTCGAGTTGG	CATCHOTTCC	10,000,00	CTCCAACCAT	GACAACAAGG	Christian	~

Seq ID No. 24 Protein sequence: Protein Accession #: MP\_001915.1

H CHANGERGE MUTENATORE  PORTINE SELVICIA  PORTINE SELVICIA  I INSELLATO  I OSTILATO  I OST			CTTCCATCTO CCTTCAGAGT CTTCTTCTAC CAAGCCACAC	ATCTATACAT GATGGAGGA CATCCAACAC CAGATCCGAC GAGCTGTCCA	ACCTTCAACA CTGATCAAA AACATTCACC CTATTAGAAC	TOGANGCTCC AACTCCAGCC GATATAGTCC AAAGATCAGA ACCCTGGGCC		CATCTCCATO TTTCAAGGAA TGAGAAGTA AAAGGAACTA AAAGGAACTA	CTTGCAGGAA ACGCGGGTCA TAAATTACAG GAAAATGTTA AGAAGAGGGC	CTTGACCACT CAACATGOTG TCATACTOTG GGAAAATCAG	T TOCCOARD COACCTOC SO COLOGOOD TOCCCTTAG SO CONTINUO CTTACONA O CITTIFICE ACTITIONA A TITICATA TOATICATA A TITICATA TOATICATA		41   1 LA GOCGAVOFEED STACOOUPEED AN PEDSPALKEN SEGIOGATHR TO VINBESTHII GOTICOGOIL SENVILLELING GLOCESEUFTS SE HENAGOTAN LAVANIARS
индельтет функцевич индерерации для для для для для для для для для для	nce 4: Eos sequence 2					TOCANGATOC TOAGGAGGCC CCAGCACCA CCTCAACCAG TACACCTTCA GGGGGAAGGA TGGCTGGCTC AGAGGGCTGC ACATTAACAC CTCTCTACAC		GATATTGAAA ATGAAGCTGA GAGCCATGA AGACACTGCT CTCCGAGATG AAATTTGCAA AGTGAACATT TGGACACCCAATGCTGAG		COTCAMANCE TICATOMOS ACTOTOGERA ACCICAMAN ACTOTOGERA ACCICAMAN ACCICETTO CTOMOGRAFY AMOCECETTO GTACCAACCA	CCATTCTTC GAATTTACT CCTTATACC GAITCCTAG AMAGRACIA AGGESTORO ACCTCCTGA AGANTAGOT ATGCARACT CAGACATAG OTTOTTOTTO TITTITITITA TANGARATA ATTOTTCCA ATTATAMA GGGACAGAA	sequence: Eos sequence	11 
ALAIPVVILL ALAIPVVILL ALTIONERY BRIAFILVB CECHIVVEN BRIAFILVB TIOVINVRE BOOTVLIDB TIOVINVRE BOOTVLIDB TIOVINVRE BECHLUPA TIOVINVRE BECHLUPA BECHLUPA TICOVINVRE BECHLUPA BECHLUPA BECHLUPA TICOVINVRE BECHLUPA BEC	S DNA sequ Accession Ice: 56-16	11 	AMAGRATACT GOTTGTOTICC GCCCTGMGA ATCTTTRGGC	AAGGATGTAC AAAACCCACA CTGATCTTCA TCCAATGAGG	TACATCANA TCTATCANTC CCANCACTO TTTANANCTT	TGGATTCATO CAGAGCTTTG ATCAGGATCC CTCTGTGATC	CAMMACCAGE CAMMATTICE CCCTOTOCAT CAMMATCATT	CCTTGATGAT ACAGOTTGTG GGAGATGCAT ACAGGGGGTGCAT ACAGGGGGGTGCAT AAAACTAAAT	GOATGAAAAG CCATCAGCAA CTCCACCCAG CTCTACCACT GCCTTCACC	CAGCACTGGG ACAGGACCAG GAAGAAGGCA TTCTGCCAAA	AGGGAGANA AGACTGCAGC GCCTTTGGC TGGGTCAGCT TATATCCAGG TATGTATTT ACAGTTATAT CATTAAACA	- E	11   
MAGLERATOR  BENESORE  BENE	Seq ID NO: 2: Nucleic Acid Coding seque:	1 	CTOCTCTOTC GGAGATCAG GGAGATCAG GGACTCTTT CTTTCCCAG	DOMESTICATA  TAACTCAGGO  GPCCCTGGCG  GCCTTGCTC  GAAGAAGCTA	GAGGACTOTO TOGGCTCTCT ATOGGCACAG GATCTCATTC ACAGGGCAAG	AGATCTCNC TCGTAGAAC CATCTTCTCA CGAGCTGTCA ACGGTTGAAG	TOCCETTOR CAAGTTOACT CAATGTOAAT CATTGCTAGC ACTCGTTCAT	CAGACACAGG AGGAGCTCCT AGCTACAGCT AACAGCGGGA TGTATGAAGA	TTCAGGAGCG AGTCAGTGGC CAGCTTCTGC CAGAGCTAAA CCTCAGCCAAA	CTTOTTGCCA TCTTAATCAA TGAACCTTCG AAGGCCAGGT	ACACCACC AAACTCAAC TCAAATCTGG GGCCCTGAGG TATCAGGAAT TATAACCAC GCACCACAAA	Beg ID NO: 26 Prot Protein Accession	1 HSQGILSPPA SHEKVKVYLR PTPSQIPQPE PRELALIENS LKRSVYIESR
5 10 15	70	25	30	35	40	45	20	55	90	65	70	80	88

INIGPRIN ELITOLEPP SORNOUTA LCEDARDRY VIOLANINO DESENDLA GENERAGO PETITURES BESTEROITAL ACCOUNTE ISELACIA GENCHOCKS GENERAGOI PIETITURE LALACKOM REMUNIVER DELITAVO PYTORGECH IVANICASI YOSTIANAK SALACKOTA CATRATOLI MANIGOT

Seq 10 NO: 27 DMA sequence Rucleic Acid Accession #: Eos sequence Coding sequence: 13-1424

	•	
_		
9		
4		

WO 02/086443

TOTACAMENT (CONTROLLER, CENTRATED ACTUACAMENT INTERCACED SOUTHWATER TOTACAMEN CONCRUSION SOUTHWATER TOTACAMEN CONCRUSION SOUTHWATER AND SOUTHWATER TOTACAMEN CONTROLLER ANTHOGRACE ACCOUNTED TOTACAMEN CONCRUSION SOUTHWATER ANTHOGRACE ACTUACAMEN CONCRUSION SOUTHWATER AND ANTHORNOR TOTACAMEN STOREMENT OF ANTHOGRACE ANTHOGRACE ANTHOGRACE ANTHOGRACE ANTACAMENT STOREMENT OF ANTHOGRACE ANTACAMENT STOREMENT OF ANTI-CONTROL ORGANIZATION OF ANTI-COMENT TOTACAMENT STOREMENT OF ANTI-COMENT TOTACAMENT STOREMENT OF ANTI-COMENT TOTACAMENT STOREMENT OF ANTI-COMENT TOTACAMENT STOREMENT OF ANTI-COMENT TOTACAMENT STARAGAMENT STARAGAMENT STARAGAMENT ANTI-COMENT TOTACAMENT STARAGAMENT STARAGAMENT ANTI-COMENT TOTACAMENT STARAGAMENT STARAGAMENT ANTI-COMENT TOTACAMENT STARAGAMENT
---

3		;	;	;	;	;	
	<u>-</u>	<b>=</b> _	<b>=</b> –	<b>-</b>	<b>:</b> _	<b>4</b> –	
	act tcaccot	ACAGCTCCCC	COCACCACA	AGCCGGGCCT	GCAGCOCCTC	AGCACCOCTC	•
ć	COGGACACCC	-	CCAGGCGTGA	CCTGTCACA	GCACTTOGC	cororootoa	120
2	GAGACITAGA	AATCCAAGCG	THEATTAIT	TONGOCCAGO	CTAACTCGCT	TCAAAATGGA	240
	ACGAAGGCGT		CCATTCAGAG	CCGATACATC	ACCATCAGTO	TOTOGACAAG	8
	CCCACGGAGA	CTTOTOGAGC	TGCCAGGCA	олосстаста	AAGGATGAGG	CCCTGGCCAT	9
,	100000001	_	CCAGGGAGCT	CTTCCCGCCA	CTCTTCATOO	CAGCCTTTGA	<b>‡</b>
3	COGGAGACAC	_	TGAAGGCAAT	OCTGCA00CC	TGGCCCTTCA	ccroccrocc	9
	TCTGGGAGTG	CTGATGAAGG	GACCACATCT	TCACCTOGAG	ACCTTCAAAG	CTOTOCTTOA	9 5
	GGATTTACGG	ANGMETETE	ATCAGGACTT	CTOGACTOTA	TOOTCTGGAA	ACAGGGCCAG	9
9	TCTGTACTCA	•	CAGAAGCAGC	TCAGCCCATG	ACAMBRAGE	GAAAAGTAGA	52
20	TGGTTTTGAGC	ACAGAGGCAG	AGCAGCCCTT	CATTCCAGTA	GAGGTGCTCG	TAGACCTOTT	180
	CCTCAGGAA	gonoccaga	ATGAATTGTT	CTCCTACCTC	ATTGAGAAAG	TOARGOGANA	8
	GAAAAATGTA	_	GCTGTAAGAA	<b>GCTGAAGATT</b>	TTTOCALTOC	CCATGCAGGA	800
	TATCARGATO	-	TOGTGCAGCT	<b>GOACTCTATT</b>	GNAGATITTOO	MOTOACTTO	960
į	TACCTODANG	_	TOGGGDAANTT	TECTOCITAC	CTOGGGCAGA	TGATTAATCT	1020
3	<b>GCGTAGACTC</b>	_	ACATCCATGC	ATCTTCCTAC	ATTCCCC00	AGAAGGAAGA	1080
	GCAGTATATC	_	CCTCTCAGT	CCTCAGTCTO	CASTOCCTOC	AGGCTCTCTA	1140
	TOTOGACTET	•	TTAGAGGCCG	CCTOGATCAG	Tracreage	ACCTCATCAA	1200
	CCCCTTOGAA	ACCEPTED	TANCTAACTO	000000000000000000000000000000000000000	GAAGGGGATG	TGATGCATCT	1260
,	GTCCCAGAGT	CCCAGGGTCA	<b>STCAGCTANG</b>	TOTOCTOADT	CTAADTOOGG	TCATGCTGAC	1320
5	COATOTANGE	CCCCAAGCCCC	TOCAMOCTET	GCTGGAGAGA	<b>ACCITCAGECA</b>	<b>CCCTCCAOGA</b>	1380
	ocnoment.	_	GGATCACOGA	TOATCHOCTC	CTTGCCCTCC	recerrecer	140
	<b>GAGCCACTGC</b>	TOCONOCITA	CACCTTAGG	CTTCTAC000	AATTCCATCT	CCATATCTGC	1500
	CTTGCAGAGT	CTCCTGCAGC	ACCTCATOOG	OCTOACCAL	CTGACCCACG	TOCTOTATCC	1560
,	TOTOCOCCTO	_	AGGACATCCA	TOGTACCCTC	CACCTGGAGA	<b>GOCTTOCCTA</b>	1620
3	TCTCCATGCC	AGGCTCAGGG	AGTTOCTOTO	TOAUTTOOOD	COGCCCAOCA	TOORCTOOCT	1680
	TAGTOCCAC	COCTOTOCTC	ACTOTOGOGA	CADAACCTTC	TATGACCOO	AOCCCATCCT	1740
	Graccector	TTCATOCCTA	ACTAGCT000	TOCACATATC	<b>MATCHTC</b>	TTCTGCATAC	1800
	TTGGACACTA	_	STOCKTOCKT	CTTGAAGCAA	CAMAGGAGC	ACAGTTTCAG	7860
6	ACAMATGITIC		AGGAAAACAT	OTTCAOTOAG	GAMMAACAT	TCAGACAAT	1920
2	GTTCAGTGAG		CONTINUE	DATAGGCAGA	TOTTOACTTO	AGGAGTTAAT	1980
	GTGATCTTTG	GOGAGATACA	TCTTATAGAG	TTAGARATAG	AATCTGAATT	TCTAAAGGGA	2040
	GATTCTGGCT	TOCCANGTAC	ATGTAGGAGT	TAATCCCTOT	OTAGACTOTT	GTANGAAAC	2100
	TOTTOWNAT	AAAGAGAAGC	MIGIGAGE	AMAMAMA	AAAAAAA		

•							
09	н.	п.	<b>:</b> 2.	<b>:</b>	<b>;</b>		
	GCAGGTCTC	COTOTOGO		GCCCGCGTC	TOCTOCOCT	accondence	•
	COGNICACCO	COCCTGGGCC	CCGGCGCTCC		COOTCTOCCT		2
;	CTGACCCTCG	TGATCTTCAG	TCGTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTIVATOTA	8
65	CCTTCTAAAC	TAGAGGCAGA	CAAATAATT	GOCAGAGITTA	ATTTGGAAGA	GTOCTTCAGG	=
	TCTGCAGACC	TCATCOGGTC	<b>AAGTGATCCT</b>	GATTTCAGAG	TTCTANATOA	TOGGTCAGTG	2
	TACACAGCCA	GOCTOTTGC	CCTOTCTGAT	AAGAAAAAT	CATTACCAT	ATCCCTTTCT	7
	GACAAAAGGA	NACHORCACA	-	ACTOTOCTOC	TAGAACATCA	GAAGAAGGTA	÷
í	TCGAAGACAA	GACACACTAG	AGAAACTOTT	CTCAGGCGTG	CCANGADGAG	ATGGGCACCT	ŧ
2	ATTCCTTGCT	CTATGCAAGA	DAATTCCTTG	9900071100	CATTOTTICE	TCAACAGTT	š
	GAATCTGATG	CAGCACAGAA	CTATACTOTC	TICTACTOM	TAAGTOGACO	TOGAGITICAL	ŝ
	AAAGAACCTT	TAMATTERIT	TTATATAGAA	AGAGACACTO	GANATCTATT	TTGCACTCGG	÷
	CCTGTGGATC	<b>STOAMONATA</b>	TOATOTTE	CATTACATTAC	CTTATGOOTC	AACTGCAGAT	5
i	GGATATICAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGOG	TAGAGGATGA	MATGACAAC	2
?	CACCCTOTAT	TCACAGAAGC	AATTTATAAT	TITGAAGTIT	TOGMANOTAG	TAGACCTOOT	ž
	ACTACAGTOG	GGGTGGTTTG	TOCCACADAC	AGAGATGAAC	COGACACAAT	GCATACOCCOC	S
	CTGAAATACA	<b>OCATETIOCA</b>	GCAGACACCA	AGGTCACCTO	GOCTETTE	TOTOCATOC	š
	AGCACAGGG	TAATCACCAC	MOTOTOTOM	TATTTOGACA	GACAGGTTGT	AGACAAGTAC	2
	TCATTGATAA	TOWNSTACA	AGACATOGAT	<b>OCCAGTTT</b>	TYGGATTGAT	AGGCACATCA	5
ဆ္ဆ	ACTIOIATOR	TACAGTAAC	AGATTCAAAT	GATAATGCAC	CCACTITICAG	ACAAAATOCT	ä
	TATGAAGCAT	TTGTAGAGGA	AATGCATTC	AATOTOGAAA	TCTTACGAAT	ACCTATAGAA	22
	GATAAGGATT	TATTACAC	TOCCAATTOG	AGAGTCAATT	TTACCATTT	AAAGGGAAAT	2
	GAMATGGAC	ATTICAMAT	CAGCACAGAC	ANAGAACTA	ATGMOOTOT	rentrement	2
,	GTANAGCCAC	TONTTATOA	AGALANCOT	CARGITANCC	TOGMATTOG	AGTAMACAAT	=
S	GAAGCGCCAT	TTOCTAGAGA	TATTCCCAGA	GTGACAGCT	TOWACAGAGC	CTTOOTTACA	ž
	OTTCATOTO		TOOOOOCT	GAATOCACTC	CTOCAGCCCA	ATATOTOCOO	180

CTTCOLOUR CTCCTCOLOC ACTUCATOD GCTGAGCAI CTGACCOLO TOCTCTATCT  TETOCANCE CACTECACO ACTUCATO GCTGAGCAI CTCCTA  TETOCANCE CACTECACA ACTUCATOR TOCATCTA CACTECTA  TETOCANCE CACTECTAC ACTUCATOR TOCATCATO ACTOCTACT  TETOCANCE TETACACTA ACTUCATOR ACTUCATOR CANADACTO ACTOCANCE  TETOCANCATOR ANGENIAN ACTUCATOR CANADACA TOCATCANO  TETOCANCATOR ANGENIAN ACTUCATOR CANADACA TOCATCANO  OTTOCATOR CANADACTO GTATATOR ACTUCATOR ACTUCATOR  OTTOCATOR CANADACTO CATATOR ATTACACTOR TOCATCANO  ONTICTOCATOR CANADACTO ATTACACTOR TANCOCCTOR TOCANCETA  ONTICTOCATOR TANCOCCATOR ANAMANA  ANAMANA  MANAMANA  MANAMANA  MANAMANA	Seq ID NO: 10 Protein sequence: Protein Accession #: NP_06106.1	11 21 31 41 11 11 AAAGCTCCC COCAGCCTC GCAGGGCCTC	CACCOGCTTC CCAGGOTIAN COTGTCACA GCALCTTGGC GALANACCAT TITGATTATT ACTCTCAGAC GTGGDTGGCA ANTCCAAGCG TIGGAGGTCC TGAGGCCAGC CTAAGTCGCT	TYGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG CTTGTGGAGC TGGCAGGGC GAGGATGAGG GAGTTGCCGCCA CTCTTCATGG	COGGRADACHE NOCHARCEC TOMOGCANT OSTICHOGCE TOGCCCTTCA CCTOCCTCCC TCTCOGGRATO CTGATTAMAG GACANCATCT TCACCTTGAA ACTTCAMA CTGTCTTGAA TGGACTTGAT GGGCTCTTC CCCAGGRAGOT TCGCCCCAGA AGATGAAAAC TTCAAGTGCT CACATTCATAGA AGALACTCH CTGCAGATTGT CTGAATTTATA ATTCTCTGAAA AGATGACTGAA	TITCCADAGE CADAGEAGE TOAGECCHE ACADAGAGE ACAGAGEA ACAGECCH CATTCCATA GAGATGETO GGTGCCTOT CATTCCATA CAGAGAAG	CTACGCTOT GCTOTAAGAA GCTGAAGATT TTTOCAATGC ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTTOG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCGAGA	CYCCTCTCCC ACATCCATOC ATCTYCCTAC ATTYCCCOSO GCCCAGTYCA CCTCTCAGTCTO CATCACTOC TIATTYTTCC TYAGAGGCG CCTGGATCAG TYGCTCAGGC TYATTYTTCC TYAGAGGCG CCTGGATCAG TYGCTCAGGC		UNITEDATION CONTENSOR TENTONICAE CONTENSOR DE TROCATOR CONCENCOR CONCENCOR CONCENCOR CONTENSOR TENTOCONTO CONCENCOR TOCATOR TO	AGGACATICA TAGRACCITE CACCIGOADA AGITOCTOGO TAGATICAGO COGECCOGEA ACITAGAGO AGGAACCITE TATGACCOGO ACITAGAGO AGGARATE AAANGETITA	AUGUSCAGA GUCATGCA CTICAGOA CAAGCAGC AUGUSCAGA AGGAAACA GTICAGAGA GAAAAACA AAAAAAA GAAAAAAA GAAAAAAA GAAAAAAAA GAAAAAA	GOGGATACA TCTTATAGA TTAGAATAG AATCTGAAT TOGGAAGTAC ATGTAGGAGT TAATCCCTOT GTAGACTOTT AAAGAGAGG AATGTGAAGC AAAAAAAA AAAAAAA	ID NO. 11 DWA sequence	Nucleic Acid Accession 6: Eos sequence Coding sequence: 64-2754	11 21 31 41	GOGNISTRE GOTTUBBLA COCTICIONE GONOGRAFIC TECNOSCOTO BLONGOCATA COGATORICO COSTUBIOSCO COSTUBICATO PROGROBADA CONTINCATO BANTATORA CITALOCTOR TRAINTINGA TOTALANDE BANGOCTUBA MANDATUBA ACTIVATURA COTTICTAMO TANGOCRA, DAMINISTOR DISTANCIATO ATTALIANA STOCTUTORA PROGRESSIA DAMINISTOR STATUTINA STATUTINA STATUTINA STATUTINA	GOCYCTEC GETOTERA MANAMAI CATTACATA ANCIACACA GANAGOTT ACTOTOCT TANACATA ANCIACACA ANAMERIT ACTOTOCTO TANACATA CATOCAGA ANAMERIT ACTOTOCTO CANAGAGA CATOCAGA ANAMERIT TOMOGOTO CANAGAGA	CAGACADA CTATACTOTC TTCTACTOA TAAGTOGACO TAAATTOTT TTATATAGA AGAGACACTO GAAATCTATT GTGAAAAATA TGATGTTTT GATTTGATTO CTTATGOOTC	CCTCCCACTA CCCATCAGAS AATTTATAAT TTTGAAGTTT TGCCACAGAC AGAGATGAAC GCAGACACCA AGGTCACTG	TATCACCAC AGTOTOTOL TATTTOGACA GAGAGOTTOT TUMANTACA AGACTOMA GACCAGTITT TUGATTOLA TAKANGTAKE AGATECAAT GATAATOCAC CACCTITCAG THITMAGAGA AAATGCATC ANTOTOGAA TOTAACAA	TATTACAC TOCCATTOG AGACTCATT ATTCAAAT CAGCACAC ANGAACTA TGAATTATA AGANACCO CAATAAAC	TTGCTAGAGA TATTCCKAA GTOACAGACT TUAACAGAG GGGATCTGGA TGAGGGCCT GAATGCACTC CTGCAGCCCA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA
c ol	Beq Prol		20 8 5 8		3 2 2 2	30		2 2 885	6 8 E 8 S		24 at 1	20		55		1 – 09	65 5 5	2	5 <b>3</b> 8 1	2 2 2 3 2 3 2 3 4 5 6 7	80	5555	

HETLILLIO ANDROLPEA GESTELEDAN LAGENLARY VOLEHELPA TONTREGULA INTERPRETA TONTREGULA TONT

S

Seq ID NO: 28 Protein sequence: Protein Accession #: Ros sequence

8eq 1D NO: 29 DNA sequence Nucleic Acid Accession 8: NM 006115.1 Coding sequence: 236..1765

<del>\$</del>

iiii oigaringia Accordant Accordant III Acco

S

MATRIATION CONTESTED MOTIVATION MATRIATION CONTINUATION C

ន

WO 02/086443

TROUGUAND ANTIFORM ANTIFORM TRANSPARED TREATMENT TROUGUANTS AND ANTIFORMATION ANTIFORM

ဓ္က

승

S

CORROLOGO GROGOSTIC TOCCOLOGO A
CONTRACTO COMMENTO CONTRACTO
CONTRACTO COMMENTO CONTRACTO
CONTRACTO COMMENTO
CONTRACTO COMMENTO
CONTRACTO COMMENTO
CONTRACTO
Beg ID NO: 16 1 Protein Access 

9 2 5 5 6 9

Seg ID NO: 17 DNA sequence Mucleic Acid Accession 8: NM\_0168583 Coding sequence: 72-842 

ACCUGATE A

CTOCCOTTO
CTCCOTTO
CTCCOTTO
CTCCOTTO
CTCCOTTO
CTCCTOTTO
CTCTOTTO
CTCCTOTTO
CTCTOTTO

MAMORREN GANCIALLIA TUVIFSBORG KOROVILAND SICEDARIII GNUKLESCTRS 6
ADLIREBBOD FRUMDROSTY TRANCLARIER RESPITATOR SICEDARIII GNUKLESCTRS 6
ADLIREBBOD FRUMDROSTY TRANCLARIER RESPITATOR SURCENCTRY VILEBOROVE
TRITISTICAL BRACHAND DESPONDENCE MENOMETRY VILEBOROVE
TOUTIVENT LORGOVERSHOT TOUVICATOR BEDVERORY SEGULATION SURCENTES TO TOUTIVENT LORGOVERSHOT SICEDARIER SIC

Seq ID No. 34 Protein sequence: Protein Accession #: NP\_07741.

ATACCOGATA OTTGAGANGE ACTTCTGTOT ATGACATO ACATAGACA ATGTAGTOS CATATATATA

છ

Seq ID No: 35 DNA sequence Nucleic Acid Accession #: Coding sequence: 146-1273:

2 2 2 2 2

PCT/US02/12476

Ξ

· WO 02/086443 Seq ID NO: 38 Protein sequence: Protein Accession 8: NP\_057657 =

2	
Ç	
≏	
Ξ	
ĕ	
ജ	
≤	
5	

WO 02/086443

				•														
	.658	•		8	180	2228	5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	960000	11260	1500 1500 1620 1680	1980 1980 1980 2040	2220		2760 2760 2820 2880 2940		120	20000	660 660 660 660
Z	LTNALSNOLL TOPOLLEIGL ERIHLVIGDC	under the state of		S1   GACAAAAGGT	OCTCACAGOC ATCCACGCC	TATAGRATAT GATAATATAC CTACACCCTA	CAGGATACCCG CAGGATGCT GOTAAACAAT CCTCACTCTA	CCCCACCATT CCACGCCATT ATCCACCCAA CCAGCCCAT	TOCTOTAGC TAXTOGAGC TCTACTCAGT AMENTITAC CATTTCCCC	ACAGAGCTC ACAGAGCTC CAATAACTCA GCTGCCCAAG GCCTTCACC	CANTOTCACA ANACCOCAGT CCCCCAGAC TAACCCATATC	CTTGGCTACT TTCTCCTGGT TGCTCTGATA GCTTCTTCCT	CTCCTACTAA CTCGGGAGGC AGATCGCACC AAAAGAAGAC	OCKARAMA ANTOTETTOT CANTITIONIA TOOTEGETEE TTOCACAGIT		S1   VLLLVRNLPQ HIIQNDTGFY TQDATYLWW	LAVLY GPDAP WHYS CALLY COAN VLY GPDDPTI WEALYT COAN	TYLMWNGOS YGPOTPIISP GTYACEVSUL
<b>;</b> _	PLEPTGLAGS GLANI IDI KV ABILAVADKO	2000		41  - CAGCAGCCTT	AGACAGCAGA AGAGGCTCCT TCACTATTGA	ACCOTCAAAT OTOOTCGAGA ACACAGGATT		GCCCGGATGC ACCTCTCCTG CTTTCCAGCA CCTATACGTG	ACCATCACA GOTGOOTAAA GOACCCTCAC ACAACCACT ACCACCCCAC	AGCAACACAC AGCAACACAC CCTGCCAGGC TCTCTGCGGA AGGATGCTGT	TCACTCTATT CAGTGAGTGC CCATCACTTTC CCATCACTTTC ACTCGGCCTC ACACCACAGT	TTGTCTCTAA CATCTGGAAC TGGTTGGTTT		CCAAGATCA TGATTCTTTA ACTCTTACAG ACTCCTATAGAGA AATATAGTTA		41 	VBARREDSVI TQBLFIPNIT VALTCEPRIQ VDHSDPVILM ELFISHITER	PTCEPEAGNT REDPUTLOVL PLAKITENNE
	TLPLANMPAL LLGINTBVIP LRLANGOIT	Dana da	1.03	31  - CAGACAGTCA		CTGCATGGCA CCCGCATACA ATCCAGAATG		GANANTCTON GANANTCTON GTCANTGOON ANTAGTGOON	ACCECCATO ACCTACENT ANTOROMA TOTOGRATIC TATOGECAG	CTCAGCCTCT GGGACTCTATA ACAATCACAG GTGGAGGACA	AACAGAACE ATCCAGAACT CCGGACACCC CTCTCCTGCC		GCCAACATGG CGCACCTGTA CTCCAACATTG CTCCATCTCA GATACCACTG	AAACTGTCCA TGAGGATTGC TAAGCTATCC ATTTACATTT ATTGTATGGT		31   PTTAKLTIES PGPATSGREI SNNSKPVEDK	ABYRCETONP WPVNGTPQQB WGNPVEDEDA YECGIQNELS IDGNIQQBTQ	KPVEDICAVA CCICHBVEAN CIPQOHTOVL
	FOGUPVPLOQ GOTBGGLLGG VATPLVGABL	To the desired	ience   #: NM_004363.1  223	21.  -  -	TCCACAGAGG CAGATOCTGC CCCGCCCACC	AGOTGAAAGA TACCCCAGGG CCAGAACATC	TOTOMATGAA CTCCAGCAAC TCAGGCTGCAG CAGGCTGCAG				CACAACCTAC GICCAATGC TGTATGTOGA CCTCTATGGG GAACCTCAAC	TAACGGACC CAAGAGCATC COGCATCATG CTTCATTTCA	GACCATCCTA CTTGGTGGG AACCCGGGAG CAGAGCAAGA ACAAGTTTCT	CAGCTICATO AATGAACTAA TITTITICITY AAATTGAGAC GAATATTAT GTATAACAGA	sequence:	21   TASLLTFWNP GYVIGTQQAT YPELPKPSIS	TLINVTRNDT AAGNPPAQY8 BPPRPFITEN LGVTRNDVGP GNPPAQYSWL	PKPSIBENKE VTRNDARAYV PBPQYENRIN
<b>=</b> _	TOLLAGTING LPLIDITREG VTIPLGIRLO	OPVIRV	Seq ID NO: 19 DNA sequence Muchelc Acid Accession #: 1 Coding sequence: 115-5223	11 		CTCAACAAC CTCAACAACA	AGCCCTCAT. AGCCCTCAT. CCTGTGAACC		TCATCACCAG AACCTGAGAT GTCCCAGGCT ATGATGTAGG CAGTCATCCT	ATTACCOTCC AGTATTCTTG ACATCACTGA ACACCACCAC	Addencada Gectocader Cadadeceta Cectodator TTTCOGGAGE	CGCCAATAA ATTCCATAGT GGGCCACTGT GGTGTAGTTT	CAGAGATCGA ATGAGCTGGG GAATCGCTTG AGTCTGGCAA ACTCTTGAAT	AACTAACTA CATGGGACTA TCAGGAAACT TTGTGAACA AACTATTCAT TCTGCTCTTT	Geq ID NO: 40 Protein sequence: Protein Accession #: NP_004154.1	11 		VKTITVBABL NGNRTLTLFN LALGCHBASN
	NPQTOGLIVE BOGLIGILEN VQSPDGHRLY	DIVINGING	Seq ID NO: Nucleic Aci Coding sequ	1   CTCAGGGCAG	TCTCCTCGG TCTCCTCGG	TTTGGCTACA GTAATAGGAA GCCAATGCAT	CAOTICATAA GAGCTGCCCA GTGGCCTTCA CAGAGCCTCC	OCCAGOOCA TCCCTCTAA TCTAACCCAC		TCATACACCT CCACCTGCAC TTTATCTCCA GCCACTGGCC	TOTCANCETA ANANTORCS ANCCENDEN TOTCTTACC	GCCANATCA GGCGCAATA CTCTCAGCTG TAGCAGCCCT	AAATACAAAA TAAGGAGAA TGAGGAGGA	ACTITATO TAITATTT TECCAGATT AMENTACTT AGACTTOGGA TCAITAGAN	Seq ID HOr Protein Acc	1 MEEPEAPHR HLFOYSWYKG TLAVIKSDLV	NNQSLPVSPR TISPLATEYR AHMSDTGLAR QSLPVSPRLO SPEYTYRPO	LPVSPRLQLS PDSSYLBGAN
S	1	2	15		20	25	30	35	40	45	20	55	09	65	92	75	08	82

| CONTRICTOR CONCOURTS TOTALGOOD CONCOURTS TOTALGOOD AND ADDITIONS OF CONCOURTS TOTALGOOD AND ADDITIONS OF CONCOURTS AND ADDITIONS OF ADDITIONS OF CONCOURTS AND ADDITIONS OF ADDITI ANTECORACA ANTECORACA ACACTORAC TOTROGRACA TECCHOATTY 1
TOGALANTER ANTECORACA ACACTORAC TOTROGRACA TOCACTORY
TOGALANTER ANTECORACA ACACTORAC TOTROGRACA COGALICAR CATACTATOR
TOGALACTORA ATTORACAT STROGRACA TOGACTORY
TOTROGRACA CATACTARA CATACTARA ACACTORAC TOTROGRACI TATACACTAR
ANTANACATOC TITRAGANA TOGACTORAC ACACATORAC ATTORACAC
TOGALACATOC TICATARAC ANTECTARA OMOGRACA ACACATORACA
TOGALACATOR CATACTARA ANTECTARA OMOGRACA TOTROGRACA
TOGALACATOR ACACATORAC ACACATORAC ANTECTARA ACACATORAC
ANTECTARACA ACCATORAC ACACATORAC ACACATORAC ACACATORAC
ANTECTARACA ACACATORAC ACACATORAC ACACATORAC ACACATORAC
ANTECTARACA CATACTARA ACACATORAC ACACATORAC ACACATORAC
ANTECTARACA CATACTARAC ACACATORAC ACACATORAC ACACATORAC
ANTECTARACA CATACTARAC ACACATORAC TORAC ACACATORAC ACACATORAC ACACATORAC ACACATORAC ACACATORACACATORACA 11 21 11 41
WAKDINETYRE GROLLIFORM INCOCOLAIT ACTIFFYORD EBLYPLIGAT I GLIFOLGER DI SERVILLA YPILAITYR FEVAULTA I FLAGRERIN DISENDADO MONOGYTKIM DELALIZANCE OVADERDRA LANTHORE CONDEDING Y LEGIPOGRILA ELOFTRINLE THE ACTION OF STRINGOTE LIEGIPOGRILA ELOFTRINLE THE ACTION OF STRINGOTE LIEGIPOGRILA MALCHENILA THEYDRIEST. Seg ID NO: 43 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 83-2605 Seq ID NO: 41 DNA sequence Nucleic Acid Accession #: NM\_006952.1 Coding sequence: 11-793 Seq ID No: 42 Protein sequence: Protein Accession 8: NP\_008883.1 <del>4</del> 

9	
¥	
~	
=	
8	
×	
₽	
È	
65	
×	
_	

WO 02/086443

PCT/US02/12476

92929399

Seq ID NO: 48 DNA sequence: Nucleic Acid Accession N: CAT cluster

13

2

2880	300	3060	3180	3300	3360	3480	3540	3600	3660	3720	3780	3840	3900	3960	4020	4080	110	4200	4260	4320	4380	4410	
AGGAGGCTGA		AGTAACTCT	AATAAATTET GACCTGCCTT	ACAMATACAT	GGACACTAAA	TOCTTOWNC	TOGCTCACOG	<b>GTANAACCAT</b>	OCCUCTOOA	ATACCTACA	OCCITOCCIA	COCTATOTTA	TOGTOGGAIC	<b>OTTOCCAGC</b>	CTCAGGAAAT	ATGAATCGAA	CCAGAACTAA	GGAAAATCA	TTGGGAGTTC	ATTGAGACCC	CCTACCTACT	TGAGCTATGA	
ACAGTGACTC	OCTATOCTOC	TOOCCATAA	ATTOTTANT	AGGCATACAG		TTTGTAGTCT	TIBILITIONS	GCAGCAATTT	CTGCCACACA	TOCAGCAGGA	TOCATGAGAT	CATTGAAAAA	TACTITICAGO	ATGTTACAGG	CATACAAQAA	GCMACGAAG	MCTATAGGA	AAGTGAGGAA	TCCCAGAGCT	TATOCAACAC	TOCCTATTOR	GAGGITTACAG	The same of the sa
CACTOTAATC	AACTTAGCTO	CACTCCAGCC	TAGCCATOTO	TATCADATOT	TCCATAAA	CAGGCTGTAG	TITITIONAL	TANGCTTCCA	TOACACTOCA	TRECORCITE	AAAAGGATTC	AMGACATCT	TTCCTGGTTC	GAGGATTCAA	CACTITIONAL	ACCOUNTCCC	TCAGATGTTT	GTANATTETT	ACATCTATA	GAGACCAGCC	COSTOSTOCA	CCGAGAGTTT	0000000000
CAGTAGCTCA	AMMATTTA	CCAATCACTO	TACTTATAMA	TAGITITIOCA	TATTCTOTOT	ATTTATTCCA	GCAGGAGAAG	ACCAGGAGGG	AMGAAGCTGC	TOCCCCACCT	ONCAGENAC	AGTIGGATAC	CTAGGGAGTT	TATOTTOTAL	ATCCAACAA	CTACTAMAT	GCACTGTATA	AGACCACIAT	CCAGTGGCTC	AOCCAOTTIT	TAGCTGGGCA	TCACTTGAGC	1011000000
WO 02/086443 MATAMA TETECHAND	MAMMAN	CACATICACA	AATAAAAAA	GAATATTECA	ATATATTACA	AATAGGTCTC	GACTGATTAA	AGGCAGGTGA	TOGACTAAGG	OCTOCCTCCC	ACCOGCACCO	TCAMAMAGA	TCATAGOCTO	GANTITOTO	TCATGTATAA	<b>OTTOGAGAAT</b>	AMAGACTO	CTATTOCCAT	goodcchoor	DATCACTTOA	AAAAATAGAT		00.0000000000
WO 02/	CATTICITIES	TACAGTGAGC	CCAAGGGCT	TEATATOTAL	ANACCAATGA		AATAGAAACA	AATTATTAGA	GCCTTAGAAT	ADMANDED	GAATGCCCCC	ATTGCTGAAT	TATOCCCCTT	MINAGACCA	AACTATCAA	GTGAACCATT	ATTATATA	CATCTCCACA	DOMITCAMA	GADOCAGGAG	TATCTCTACA	GTOCHOCCTC ANGTACCAAA	-
		S			2	:				2				ć	2				č	3			

TRINCONCY GOACTCONGC CTGGGCNAN GNGUNANCC TTGTCTTT Beg ID NO: 44 Protein sequence: Protein Accession &: CASS276.3 30

20

Seq ID NO: 45 DNA sequence Nucleic Acid Accession N: NM\_005416.1 Coding sequence: 149..658

	9	120	180	240	300	360	<b>\$</b>	480	540	800	999	720	780	940	90	960	
ន-	CCCTGAGGAG	AGGATTCTTC	AGACCTITAC	CACCTCAGGA	CTOGALACAC	AGGTCCCTGA	CAGGCTGTAC	ADGICCCTOA	CAGGTGCCAT	AGCTACCAGA	AGAAGTAATT	TOTTCCCATC	CCCAAGCCAT	CACACACACT	TCTOSTCTTC	CTGCTCTTCC	
<b>\$</b> _	AGCAGATGAT	ADGAGCTTAG	CAGCAGAAGC	AGCCAGCCTC	GITCCACAC	GOCTOTACCA	OTCCCTGAGC	GOCTACACCA	TITICHTANC	GOCTACACAA	ANGACCAAGC AGAAGTAATT	CTOGACACCC	ACATTGTCAC	AGCT1TTGT?	TCATGGCTTT	TOCATOTITIC	
<b>a</b> -	TICTICTOCAC	TOCTTANTIC	GACTICITAC	GRANCHACCC	CCACTCAAG	CCCTGAGCCA	TTOTACCAAG	COCTAAGOCA	CTTCATCAG	TOCTOTOCCA	AGCTCAGCAG	CCACCAGATG	TOTAATCAGC	COTACTATA	CADAMAGTCT	TGAAAAGAAA	
	CACCTCGACC	TANGACTITIC	TYDOMOCAT	AGCAGCAGGT	AGGAGCCATG	STACCMOST	CTGAGCCAGG	DTACCAAGGT	CTGACCAAGG	ACACCAMOT	CTCCAOGCCC	GAGAAGCCAA	CTOTAGACCT	CCTAAAAATA	CTGAATTAAG	MOATTCGAA	TOCA
<b>a</b> -	AGAGGCTGAA	GAAAAGCCAC	TCCACGATCC .	CABCTTCAAC	CCCACAACCA	DAGCCAGGCT	ACCAAGOTCC	<b>GAGCCAGGTT</b>	ATCAGGTCC	GAGCAAGGAT	TCACGOTCA	ACAMICCETT (	TCTTAATTOT	TATTITUTE	CTGTAAGCCC	DOTTCATCTO	TGCTTTTAAT
	ACCAGATOCO	CTCAAGACCA	AAAAACTGTG	CCCACCACCT	MINITION	AMBATTCCA	<b>OCCADOCTOT</b>	CAROTTCCCT	ACCAGGCAGC	CAMOTICCI	OCCATOTOCT	TOOTGCACAG	TOTATA	AGTOTOTOTO	CTGAAGAATC	COCTOCTCAG	CTCATTAMT
55			5	3				,	S				ć	₹			

Seq 1D NO: 46 Protein sequence: Protein Accession #: NP\_005407.1 75

	KIPEPGCIK	GRIKVPDO	
<u>s</u> —	F	8	
	CHSKVPOPGI	VPEPGYTKVP	PAQOKTKOR
	EIFVPTTKEP	TXVPEPGCTK	
<b>z</b> _	VKQPSQPPRQ	OCTKVPRPOC	VPVPGYTKLP
=_	1000010441	RPDCTRVPRP	INVPEQUYTK
<b></b>	HSBYQQXQTP TP	VPEPGCTIVY	OFIKPPEPGA
8			

ខ្លួ

240 240 240 360 420 420 420 420		120	20223	20025		9 02 1	22002	5 6 6 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	96 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1260	1200	1680
B1 CTCACMAGT CACAGOGGA CACAMAGTTA GCOCACTTC CTCACATCC CTMACTTACA AMTTCTAACG COCTGGCA		51   CCTODECACT GACCOGTAAG GAGAGAACCC	GGGCGCCTC TTTTTTTTT CTTTATGCTT TGCTGCTTCA GCTGTATTCC	ACCTTGGATO ACCTTGGATO CCAACAACAAG		S1    -  - 	OTOTOOTTOO TOAGACTOOG CCATTCATT	AACACGGGGA AGATOTCCCC TCAAGGCAAG ACATCATTTT GCCAACCGGT	AGTGCCGAO GCCATTGCCT TAAGTCTCTG CTAAAGGCAA GCAATATCTT	AGGCCATGGGA ANTITICCCCC CATTIANTCC TRACTTANCC	CANATAGAT GACTTGCTCA GGACAAGCAG CANAACCATA	ATOTCCTCA OOTAGGAAGG GCTCCTCCTC
41		41   	ATTTTTTTT ATTTTTTTT TACCCAACC ATTTTTTTC	TTCTGTCACA GCTGCCAGC GCTGTGGCAC GCTGTGGCACA CGAGTGTACA		4.1  -  - 	AAGGGTAAAG GGGAGGAAGG GGAATTGGA TATAATCAGT CCACCTCAGC	AACAGGACTC CACCCCTCCC TAGGCCATTG	ATGAMACAG AAGCCAGCTG GTATACCAGG TAGAMATTAG AGAGAATAGT	TIGITCAAT TIGITCAAT OTAACACTOC CICTACTORO CICTACTORO CCTAACOTAC	AAVTGAAATG ACTTTTGGGA AGGGGTATTT AGACCAGAAG	TOCODACCTE AGOTOCCTTO TOCCTTTA AAATGTAATG
11	cluster	31  - GTGCTCTTCT GGGGGGGGG AGCGGTCGC	CATCACCATA CACCCCAAA AATACAAAGA CAGCACTCCC TTATGGTAGC	COGRECANDA GITCCATTOC OTGANGCTCA ATTITICCA CCACCTACT		31   	ACCAGTOAGA ACCAGTCAGG GTAGTTTAAT ACAAGGGGTC CAAGGGGGCC	AAGAAGCCC GOCAAGCTC GCCTGCTGCT CAGTGAAAAT GTGTTCATCA	CAGGTGAGGA CATCTTATAA ATTCTGCTCC TTTTCATTAT AATGGGAGAT	AAAGGACCTT CTGGAGAAGA AGCACTCTCA TTAGATGGAT	ATATATAAAT AGGGCTGTGC GCTATGATGG GTGTAAGCAC	AGACCTATA ACCAGAGATA OCAGAGAAA TITCATTIT
11		21   TOPCTOTOCT CTTCTCTOAT	CCTGGAACNG CTTTTTAGGG ATTTATATTA TTTTCTTTGA	OCCTTOGCAG CCCATCCTCG ATATATCCGG GGGACCTAGT CCTGCAGCAT	DNA sequence Accession #: LOS187 nce: 19912260	21   	GAMAGTCCCT CAGATTAGCA CTGAATGTGT GGACTCTGAG	TCATGTGTGC GACAGCAGGT CCTCCATGAA ATGAGGGTGG ATATCAGGTG	TCATGTGTGA AGGGCTCATT CACACAGCC CTAGTGTACT CCAGGGTTTC	ACTOGGAGTE ACTOGGAGTE CTCAGGECAG ITTTAATTTA	TOOGCAGAGA AGTGATOTGA GCAAGOGACT	ATTTCCAA ATAAATGGA ATAAAATGGA ATCCAAGCTTA
11	Seq ID NO: 49 DNA sequence Nucleic Acid Accession R: CAT	11    -  - 	GACCAGITIT OTGITIAAAA AAACICIAAI ICIOIGICIT CAIGGGAAIC	OTOCACTOCA OTOCAGCAGC GAOCTOGTCT CCTOGCCCG		11    GCAGGTAGAA  GGAAAAGGCC	ATTAGCCCT CAGGTTTTCC GTAATTATT GCAAGGTCTT	CAATGACAAG CAATGACAAG CTCATGAAAC GAGTCTGAGG	OTACTTOAGGC CCCAAGGGAC ACTOGCAATT GCAGGTTAAT	TAMATTACAG TAGTCATTGA AGAACTAGAA TTTATAGAAA	CTAGCAGAA NTCACGGAGA TAGGOTGTCA MANAGCATTT	OTCTOATGCC TTAGTAGGC GAGAACTCCA CTGAAAATTA
TECCANTT TTTAGTAN TCCANTTA TCCANTACT CCCANGCO CCCANGCO ATTTGCAGA ATTTGCAGCA ACTTGCC CGACTGGC CGACTGGC CGACGGC CGACGGC CGACGGC CGACGCC CGACCC GACCC CGCACCC CCCACCC CCCCCC	Seq ID NO: Nucleic Act	1 CTTTCTTCT CCTGCGIACC	DACACATOCA CCCAACCAAA TTCATTTAAA CTTTCTCTOA	GAGACACAT GAGACACAT GAGACACAT GAGACACAT GAGACACAT		) CTGCAGGGAG TCAGAAAGGA	CAGAAGAAG TGAAGAAAG AGAATCATA GGAAATGGA	CCCCTCCTT ACAACCATCT CCAGGGTTAA CCCTGCACCT CAGCCAGCTA	OATGAGGATG AGCTTCTATT TCACACCAA ATTGCAACAA ATATGTGTAA	TATTTAMOT CCTCAOTAGA AGTTCATAGC TGACAAGATA ATTTAAGGCA	ACTANTEGE ACTANTEGE ACTANTEGE ACATGOGAG	
20	30	35	40	. 45	20	55	99	65	6	75	80	. 82

<sup>8</sup>eq ID NO: 47 DNA sequence Muclaic Acid Accession #: Eos sequence 82

25

2

2

2

30

35

PCT/US02/12476

PCT/US02/12476

Seq ID NO: 59 Protein sequence

1 11 11 11 11 11 11 11 11 11 11 11 11 1	ANTICITY TOATTOCA AMITOCITY TOATTOCA ENG ID NO. 57 Protain sequence. Protain Accession 8: NP. 203114	20 1 11 21 31 41 51 1 51 1 61 1 51 1 61 1 51 1 61 1 6	осилод верыпов ( 17-2300 ) 11 (1 ) 11	MARIATECHOS GENERASIS GENOSOGOS MARIATECHOS GENERATIONA MARIATECH TEOTROCAS TEOTROCAS GENERASIS MARIATECHOS MECCHETA GENERATION MARIATECHOS GENERASIS MARIATECHOS GENERASIS	COMPUTED CONTRICTORY TO CONTRICTORY TATAYNDRIC ORTHOLOGORY, GOOD INCOPTORY ACCORDING MORE ACCORDING MORE ACCORDING MORE ACCORDING MORE ACCORDING MORE ACCORDING ACCORD	GALANDERIC ALGORATES TRECENTAIN AND GALANDERS CONCETTING CENTRACES TRECENTAIN AND GENERALIST GENERA	TICHOGOCIA GARGOTETE CARGETETE GATTECCOC TITUCADA METATOREM CARACTORE CRANCAGO STRUCTICE TRACETTE GARGOTETO CRANCAGO TITUCTICE TRACETTE GARGOTETO MOCUMENT TRAMANO TRACETORA METATOREM ENTONOMINA TRACETCO AMONTANA ETTETORIO ENTONOMINA PERTATORA AMONTANO TRACETETO CONTICUE PERTATORA CHANTENO TRACETORA CONTICUE TRACETCO AMONTANO CRANTENTE CANANTOCIA TRACETCO CRANTENCE CRANTECIA CONTICUE TRACETCO CRANTENCE CRANTENCE CONTICUENTANA AMONTANA AMONTANA ANTORICHA ANTORICHA AMONTANA ANTORICHA AMONTANI ANTORICHA AMONTANI ANTORICHA AMONTANI ANTORICHA AMONTANI ANTORICHA AMONTANI ANTORICHA AMONTANI AMONTA
1200 1200 1200 1210 1210 1210 1210 1210			60 120 120 130 130 140 140 150 150 150 150 150 150 150 150 150 15	59	120 120 120 130 130 130 140 140 140 140 140 140 140 140 140 14	600 660 730 900 900 1140	99 170
TOTATION CHITTETTAL TITULANDO PRESIDENT STATES BANAMACO ACTITUMOS TRANSPIRES TO PRESIDENT STATES BANAMACO ACTITUMOS TRANSPIRES ACCORDED ACTITUMOS TRANSPIRES ACCORDED ACTITUMOS TRANSPIRES ACCORDED ACTITUMOS TRANSPIRES ACCORDED ACCORDED ACTITUMOS CHITAGAN CHITAGAN ACTITUMOS CHITAGAN CHITAGAN ACTITUMOS ACCORDED ACTITUMOS ACCORDED ACTITUMOS ACTITUM	Seq 1D NO: 51 Protein Accession Bi-MACT6518	BPC65TVIPA PAGGKTRGK 22 DRA sequence 1 Accesion 8: NM_002639.1 ince: 120-473	WATACHET MAGNATIAT CECTUTIAN TACACHAIC COCCUETAS OCUAGOCON OTTOMACHE AND CONTROL CANACHAE CONCUETA CONTROL CONTROL CONTROL CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE CANACHAE AND AND AND AND CONTROL CANACHAE CANACHAE CANACHAE AND AND AND CANACHAE CANACHAE CANACHAE AND AND CANACHAE CANACHA	Seq 1D NO1 53 Protein aequance:  1	13 11 11 11 11 11 11 11 11 11 11 11 11 1	COMMITCAIN CONCECTED AND AND AND AND AND AND AND AND AND AN	9 Protein sequence: seion s. NP_062564  1 21 1 1 1  23 1 1 20  24 1 CTTIND. NOWTHOOD GODFILGION NEWCONTRY NOSTICALS SUNAPPRY ASSOCIATE LISELACETH

45

<del></del>\$

20

ဇ္ပ

65

2

Beg ID NO: 56 DNA sequence Nucleic Acid Accession #: NM\_003135 Coding sequence: 65-334

85

73

PCT/US02/12476

translation recurrence concernant secretarian systems and concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant recurrence concernant concernation concernant concer

	CT/US																																																			
	Ā																										٠																									-
•																																															•					
	7560	7680	7800	1920	8040	1160	8280	8340	9	8520	6640	8700	8620	9880	9000	0906	9180				9	120	2 5	8	420	9	9 9	220	5	5 6	960	000	1200	1260	1380	140	1360	1680	5	1800	1920	1980	2100	2220	2280	2340	2460	2580	2640	2760	2880	2940
	200000000	ATCCT0000C	AAGGGAGAGC			COAGGCTTTG	GOCCACCTO	COADOTICCC	CTGACCCAGG	CAGGGCCAGT	GTACCCCTG	ОАСССТОАЛО	CACCCTTTTG	TOCGAGCGCC	ACCOUNT	<b>STCCOTTAIT</b>	AGCGCATOTO ATTCTGGGGG			16.	RENTREVREP	STREETHE	STEAPROLVL	BVRLRGLRPL	ARTDABVEOT	LDGLQPGTBY	VRREPETPLA	DITCLOPOTT	TAPEPVORVS	I ROLEGGVBY PRACOPILIHM	RTESPRIVER	ATRRULERLY	GNINLGTAVVŢ	CPKOOKGEPG	GPEGGPPGPRG	SPGPGGPVGP	GPROEKCEVG	PPGEKGDPGR	ОРКООРОСРО	GPSGPNGAAG	PKGDRGETGS	LPVPERRRGP GLAGEPGR PG	GPKVSVDBPG	NPGLPGERGN ETGPPGERGLT	RUSPGVPGSP	DRULPGPRGE	PGASGLKGDK	KOSAGLPOLR	KGACGLDGEK	RVVGAPGVPG	BOSRPLPSYA DSDDPCSLPL	PRVVQSQQTO
٠	TOAAGATGGC	CTCAGCTOTO	CAAGGGCAGC	ADGLANGGAT	AGACAAGGA	CAAGGOTGAC		GAAGGGTGAG		CTOTOCCTOC	. 6	GOACTACCAG	AGAGGCCTGT		TOTCAGCAGA	ОСОМОТОСАС	OTOGGCAOTO CATGGTGCTG			· <b>5</b> .	PLIDGSSSIG	GDVIRAIREL	CVPVTRPPDD		RSUCPATSLA	VLPSDVTRYO	PRECEASULT	OTLPPOSTAT SUTITIFIEDD	DGPPASVVR	ILPGNTD9AB HSLRLRWBPV	GEOPBAEVTA	ATQUIRABLEAS	I REMPYNED S CASGLAVVML	OPRPERCEVY	POLEGREGEP		DPAVVQPAVA	GRAGPPGDSG		SCILDCKPGAA NGXNGBPGDP		LOTROPSOSP 1	POTPGPPGPP	GENGPROODG	RDGASGRDGD	PPGPPGVKGD	dDASDddDdd	DXCSXCBPCD	PROLEGERGY	OKCIERCPPCE	HCACQOQFIA ESTQDPEAPW	TREACERRCP
	GCATCCOOG	ACANGGGAGA TGGGTGAACG	ACCCTOOTGA	COCCATCCCC		TOATCOOTCC	<b>&gt;</b> <	TICKGGGGCA	. 6	TGAOTCAGCA	ATOCAGAGGA	ATTCTOTOGA	CAGGCAGCAC	GTTTTOOGAC	GGAGTCGGG	ACCITCIAGCCT	DOUTOOCT TOTOATOA	<b>á</b> .		ı.	- CTRLYANDIV	BPGLDALGSG	VSRRVCTTAG	MASATIADOTO	YEVTVETLEG	ETGLEP PORV	YTVRVBARVG		VHVRAHVAGV	REGGENRAG	RVRLEVLOPA		CDIPSPIREA	TALCOASPTT	APGGVIOGEG	POPOECOIAP		PGDRGP1GLT PGKAGERGLR	TOPGAREKGE	DRGPPGLDGR	LPGPVGPPGQ	PEPOCEPOLA	EOGROOPPGE	RGVPG1KGDR	CETGKPGAPG	POVOVPOBRO	GREGI PGPLA	GPRODIGOPG	GEKGDVGFMG GN SGYEGI. 10	GPRGPEGLGG	RGFVRQEMSQ EYBEYSETSV	OCOCHANIE PO
	GGGGAGCCAG	CTAAAGGGTG	GOGTTGCCAG	CCTOOTGACC	GGCCTTGATG	AAGGAGGGC		CCCGAAGGAC	оотсстсала	COCCAGAGA	Ö	TACTCCOAGT	) Ç	MTGCCAACC	ATCCCTGGA	осттототос	CTCACTOTOO	AAAGGCAAAA	n sequence: NP_000085.1	12.	URACHRERVT	TVQYSDDPRT	PSILRTLIPL	OYKVQYTPLT	LLRDLRPOTO	ARGYRLEMR	DLDDVQAGLE	VPGASGFR18	DGLEPDTEYT	TTPPBAPPAL TTPPBAPPAL		SVTGTPVCPR	RPSPLFFLNG	BLDGAVEGLA	OPROPXGEPG	DKGDRGERGP		DEGPPGDPGC		GVRGPAGERG		NVDRLLETAG PROLKODROD	GERGEKGERG	GNODOGPROD	QGSPGLPGQV	AVVGLPGAKG APGPKGFKGD	BUERGLAGPP	ROPROLIDOR	POKOGVPOIR		GRALTEDOI	
	WO 02/086443 GOCCCG AGGCAGGGT	GAGTGCAGGA ACGGGGTGCC	ACCTCOGOGA	AGCAGGGATC	COCCACCTOT	0000000	₹ 6	TOCCADAGGC		GCGCTTTCTC	. 0	GTACTCTOMA	CTCOTACCAT	CTOTGGAGGG	GAGATTCAGC	<b>QOTOCTAGAG</b>		racrommer	63 Protein	<b>1</b> .	- CAGILABAPR	AASAQGVRPA	TEDEPPENNO	CHTABGEVT	DELCPOOGSV	ILLSMILVPE	LVLPGSOTAP			VERITHWOVT REGIEVAIV	VLOPELSSYH	VLDGVRGPEA	VOVGLLSYSH	OTFFAVDDGP	POPRODEGER	POLPOTAMKG PDCA PGL BOD	VAGNEGAKGE	GGERGPPGLV	GPKCDRGBPG	RCPPGPGGDP	DOPKGERGAP	GURGEPGSVP	VOEAGREGER	GLKGAKGEPG	PPGPEGLVGP	COPGEDGONG	РЯСБИООРОР	PRCAKCIONGE	AAGI PODPOS			
	WO 02	CTCCAGGCC	CTOGTOACA	AACCTOOTOC	GOGGAGTGA	OCCUSTODO	TTOGGGCTT	COCACACACAC	AGGGGGGGCC	ATGACATCCO	TCCATGCTGT	AOGATGATGA	ACACCCTGGG	TCTATGGTGG	ATAATOAGCT	COCTCCCCTT	CCTOCCACCC	3	Seq ID NO: 63 Protein		MERCEVAND	DESTANTANT	ESLICRYASOP	SEPSECULAY	RVLSGGPTQQ	LRPVILGPTS	VRSTOGVERT	VPGLRVVVBD	SAHGPEKSQL	SVRVTALVED	QPEGGGRGSR FLEVERTEIN	CVSYIPSLTP	AHRYMLAPDA	RRLAPGEDSV	APGLEGSPOL	PLCDPGPRGP	OPACIBROLPO	PAGPAGATGV	DCRMGSPGSS	APGERGIEGP KACDPGRDGL	DSGASGREGR	KCDSQLPGER	I POL PORAGO	PGLEGEOGOPP	CPTGAVGLPG	KGEAGRAGEP	GWGPPGGTG	DBAVILGPPG	OLUGBOOPO DECEMBER	DENOTPOID	APGERGEGGR ADTAGEQLEA	DEGSCTATTL
			n		9			15	١٠		6	2			25		ç	2		35			9			45	2		9	5.		3	3		5	9			65			20			75	2		ć	2		;	82

	51  -   GTGCCCACO   ACCACCAAO   GACACCTTCC	S1   QOKYPPVTPS		51 		AACACCTOR AACACCOCAA ATTTCTTCT AACATCTOTC		GCCTOGATOC GCCCTOGATOG GTGTGGATOG ACAGCCTGG	TTCATGGCTG GCCTTCATCG CTCTTCTTCT TTCATCACCG ATCTCTGTGG GGCGGGATTT TGGCGGCT GACGACTTC TGGCGGCT GACGACTTC TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGCT TGGCGGCT TGGCGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGGCT TGGCGCGCT TGGCGCCT TGGCGCGCT TGGCGCCT TGGCCCT TGGCGCCT TGGCCCT TGGC	CTOSTETACA GCCTOTCCT OGCACCATOS GAGTACCOAG AGCACCAGO	CTTTCCCTGA CACTAAACA TAGATGCTC CCCCCACCA CCAGGAGAAA GCTTGGGAAA GGAGGCAGGG CCCAATGGCCG	OGAGAGINIA TCTOSOCANA TGCTTOTATA CCCTTOTANA CCCTTOTANA ACTTCATA	CTOSOTOTE CCCAOQAAGO CACCTCCAOT
	41 	000404040C   11		41 { cccaaaaaca caccacaca caccaccac toorridea accaacaca		AACACCCGGC CATCATOTCG OTGCTACAA AOGAATCCCC CAATOTCTGC		GTACTTCACT GCTGCCTGGC GTCCCCTCAG GOGGCCCTC	CATECTORIC GEOGRAPH CTODOCTOC TOTODOCTOC TOTODOCTOC CCAMODON GEOGRAPH CONCECTORIC CONCECTO	CTACCACCCC CTACCACCTTC CACCACCTTC ACTOTCCCAC			ATATTCOTC GGGGCACACC GCACTTCCCG
<b>5</b> .	31  - cccrdccadc AAGTGCCTG CAGCAGAAT AGCAAGTAA	31      CPEPCPPPK	629.1	33 ccocococo cccoAdcoc occAdcoco octcoadco	GOOGCCCOOL TOACTGOOC GOCGCCCCCC CCCCCCCCCC CCCCCCCCCT CCCCCCCCT CCCCCC		ACCTOSTCAA CTCCCSACTO TCACCTOTOA TCTTGAGGCT	GAAAGATGGT GTGGAGTGGT CAAAGCTGGG CCATTGGCCT ACAAGAAGGC	TOTICITETE CARATEROS TOSCOCACT WATTETRAS ACTECOTTT ATCTCTCAT CCAGGGGCA	ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACCEPTODE A ACC	CACCCTCCA BAGAAGCAC ATATCACAAC AGGCCCGCC CCCCACCCCCT CCCCAGAGAG AGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA		ACCCTOTAC CACCCTOTAC TAAGOTOGAT
equence ion #: NM_006945 219	21 	NP_008876 21   RECPEPCEPP	ience 1 N: 2M_005629.1	21 	CAGGAGCCTC GGACTGCTTC CCCCGGGCCCC CCCCGGGCCC GGACTGCTTC GTGGGGCCG GTGGGGCCGAAAA	AAGGCCCCC TGGACGCCC OTOTGGCGCT OTCCTGATCG	ACCTOGRACA CTOOCCACC GAGAACAAAG GTGACCTTT	AACAACTOCT		TTCATCTTCA TOGTOGOGTO ACCCAGGCCA GGCCTGACCA ATGTGACAAC	AGCCCACCS OGGAGGAGG AACGCCAAA AGCTGGTCCT CCCTGCCACG CCCTGCCACG CAGCAGGAT CAATATTC AGCCACAT AGCCACACAT AGCCACACAT AGCCACACAT AGCCACACAT AGCCACACAT AGCCCACACAT AGCCCACCACACAT AGCCCACACAT T AGCCCACACACAT AGCCCACACACAT AGCCCACACACAT AGCCCACACACAT AGCCCACACACAT AGCCCACACACACACACACACACACACACACACACACAC	TTOGOTICAL CAMGOTIAN TTTATATAMA CCCAMCCAT CTAGCCAGG TGTGCGTGT	TOTOGOGO CA TOTOGOGO CA TOTOGOGOTO COTOCOAGO CT
86443 1 DNA e Access	11 	ession \$1 ) 11 PCOPPPUCET	66 DNA sequence d Accession #: 1 ience: 639-2546	11 daggagaga daggagaga caccoccac gagagagaga	GNGCCGCCG GNCGCCGCC AGTGCTTCGT CCGCCCGTC CTCCCCGGTG CGGCCCGGCC TAGCGTGTCC	OCCAAGGC CTTGGGAAC CTTGGGAAC TATTCCTAC GCTGGGCAG	OCTOOCCTOO ATOTOOCCAC CAATOCCAG CAACTOOGAG	GAAGGGGGC CCTGCTCAAG CCAGATTTC CCGCTCAAC	CAGCTTCTTT COTECACATO GOTTOTTOGT COTCCTCCO TOCCTCTGC GOTTOTTOGA COTGTTTGAC	CATGOCATC COTOCACCO COTOCACCO GOACACCTO ACATOTCACO	CCCCTGCTTC OTCTGCTGG OTCTGCTGC CTGCTGCTGGGG GAACGAGGG		CCAGACTOGA TOCCACAAOT CCTGGCCTGC ACGGCTCCCA
WO 02/03 Seq ID NO: 64 Nucleic Acid Coding sequer	ATUTETTATE CCANAGEOCE TOTOCHAGE CCACCETACO	Seq ID NO: Protein Acc 1 1 HEYQQQCXQ	Seq ID NO: 66   Mucleic Acid A Coding sequenc	1 TACTECOGAGE CCGCCCCCGG CCGCCCCCCGG CCGCCCCCCCCCC	DOCCOCCCC OCCOGNOCCC CTCACTTCA COTCOGNOCC CCTCOGNOCC ACCCCACACC		ACATCATGOT CCTOGOCCAC AAGACTOTOC CCCCTOTCAT CAOOGOCCT	TCTOTGTCTG CCTACGTGGT GCACGTTTA ATGCGGGGC GCAGCTACAA	ACMINISTRACIO CAMACACAC CCTACCACA TCATACTATT GCTCCTCOA ACONCTTCCA	COCTOOTCO ACAGOCTA CCATGCTOTO CTOAGOCTO CTCAGOACCT	CACTTTTGGA CACTTTTGGA ACTTTTCCA TCCCCTCCA CANTACTGCA CANTACTGCA CATTTTGGAAGGA GAGGGGAAGGC TTATAGAAGGC	CCAGTATCA TATAGACTTOT GGAGGCTTOT TTTCTAMAA CCTACCTTAC GCAGACANA	GCCCCCCTT GCGCTGCTAA GACCCTTGAAC
	s . 01	15	20	30	35	40	45	20	55	65	70	80	88

CTICHOTA'S GENOTITIA CONCENTIVA TOTATONOTI COURTOCOS BIODECTUA 1980 TRACCIOLAS AMAGENTOS CONCENCIOS BIOLOGOTI COLOGOTICA CONTENTA 1910 CONTROLAGO CATACTACTO TOCTAMANA COACTICAGA CATACTACTO TOCTAMANA COACTICAGA CATACTACA 1910 AMAGENTO ATTITICA

WO 02/086443

Seq ID MO: 67 Protein sequence: Protein Accession 8: NP\_005620.1

MAKKSAENGI )

13

20

10

Seg ID NO: 68 DNA sequence Mucleic Acid Accession #: NM\_011953.1 Coding sequence: 178-2469

22

30

33

49

S

45

55

S

65

2

75

8

83

WO 02/086443

Seq ID NO: 69 Protein sequence: Protein Accession #: NP\_068772.1

•	<b>.</b> -	<b>:</b> -	- 31	<b>:</b> -	5_	<b>1</b> –	
	MASPREDI	LKRRRLPLPV	CHAPSETERE	BPKRBPAQCB	SUCATABREV	AESNGCKPPA	8
5	LRPOTOTSYD	AXRTBYTLET	LOPKPAARDV	MLPRPPGALC	EQKRETCADO	RANGCTINNS	8
2	YNAMIOFAIN	BEDGLOSKBI	DIVINIEDHE	PYFICH LAKED	EPERPBASMO WICHSTRIBULS	LADALVRETS	2 5
	ANGKVEPNTI	HPGANRYLTL	DOVPRELAPOR		COKREWPELA		9
	DEVITA BENT	ADLOGACION	ATSOMMANDI ATSOMMANDI	LQPSVRVPLP ept.t.cvrrrre	LAABLASSEL	ARHERENTIA DELLABOTETE	7 7
15	SPPLEMPSP	APSTKEESSH	BWEDSEQUPT	PRPKKBYBGL	REPTROVEEN	LVIQHRERRE	2
	RERERRIGHT	LPPCVDBPEL	LPSECPSTER	WAAELPPPAD	BEDPASQLEY	BOEVGOPPET	009
	TIPLOSAPPL	ESPORTLESS	PESWELTPPA PLOLI SVPFG	WOODLONG WAS A WOODLONG WOODLONG WAS A WAY A WOODLONG WAS A WALL WAS A WOODLONG W	GTSGGASDPL KPGSPRPOVS	GLAANRELTE	120
00	GLVLDTNenDS	LSKILLDISP	POLDEDPLAD	DNINWSOPIP	3		
3							
	Beq ID NO.	Seq ID NO: 70 DNA sequence	ence	,			
	Ording and	d Accession	424 BC00652	1.6			
25	has ferrom		;				
	<u>.</u> .	1	<b>~</b>	<b>.</b>	₽.		
	-	CONCLUSION.	amendana 	1			
ć	CCAGGTTGGA	GGAGCCCGGA	CCCCCCTTC	DOMOCTACOO	CCTAACOGCO		130
3		<b><i><u>adtechenet</u></i></b>	TOTOATTCTC	AATOGAGAGT	GAMAACGCAG	ATTCATAATO	190
	MANCTAGCC	cccarcage	ACTUATTICTO	ANANGACOGA	DOCTOCCCT		240
	ANTOCCCCAA	GTGAMACATC	AGAGGAGGAA	CCTANGAGAT	CCCCTGCCCA	ACAGGAGTET	9 5
,	ATCAAGATTA	TTAACCACC	CACCATGCCC	AACACGCAAG	TAGTOGCCAT	CCCCAACAT	200
35	GCTAATATTC	ACAGCATCAT	CACAGCACTO		GAAAAGAGAG		480
	OGGCCCAACA	AATTCATCCT	CATCAGCTOT	ОООООЛОССС	CACTCAGC	TCCAGGACTC	540
	CCCCTCAAA	CCCAMCCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	OGAGACCTTO	9
	CARCLARAGE	MARCHAETAN	SCATOTOAAT	CTICCIAGAC	CACC TOURGE	CLITTOCHA	9 6
4	TCCACATCC	AGTGGCTTCG		TCTGATGGAC		CACCATCAG	2
	CAAGAGATGG	AGGAAAAGGA		CTGGAGCAGC		OCTTOACGAG	840
	CCTTCGAGAC		CTOGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATGA		CATCAACAGC	ACTGAGAGGA	ACCOCATGAC	TTTGAMAGAC	9
45	ANCIATAGGI	GGATTGAGGA		TACTITIANGE	ACATTOCCAS	GCCAGGCTGG	020
ì	AATOGCAAGO		DACCATTOAC	CCCAGTOCCA	ACCOCTACT	GACATTOGAC	1140
	CAGGTGTTTA			CCAGAGCTCC	GCCOGAACAT	GACCATCAM	1300
-	ACCGAACTCC	CCCTGGGCGC		ATGAAGCCAC	TOCTACCACG		1260
6	TACCTOGTAC	CTATCCAGTT		CASTCACTOS	TOTTOCADCE		1320
3	OTOCCATIVE OTOCOCATIVE		TICKTICATE OF THE PERSON OF TH	AUCTORORGE	THECCOCCA	TAUCAMOCCA	1380
	GGACCAGOGA		ACTOCHUTT	GGAGNAGGGT	TITICICETE	OCTECAOTT	1500
	CAGACTATCA	AGGAGGAAGA		GOGGAGGAAA		AGCOAGACCC	1860
**	ATCAMOTOD	AGAGCCCTCC		raccocrece	COUCCCCATC	TTTCAAAAA	1620
3	SATCATCTC	ACTCCTGGGA	GGATTCOTCC	CATCTCCCA		CAGGGGGGG	1680
	GAGAGGAGG	AGAGGAGCCG	OTCTCGGAGG	ANACAGCATC	TACTOCTCC	CTOTOTOGAT	1800
	GAGCCGGAGC	TOCTOTACE	AGAGGGGCC	AGTACTTCCC		AGAGCTCCCG	1860
9	TTCCCAGCAG		מכבופנכוכנ	CAGCTCAGCT		AGTGGGAGGA	1920
2	CCTTTTAGA	CACCCATTAN	OGANACECTE OGANACECTE	CCCATCTCC	CCACCCCAAG	CAMPETOTO	1980
	TTCAGCCCAG	TACAAACCCC	CCAGGGGGCC	TOTAGE	TOCTOROCT	CCTOGGGTG	2100
	ATGGATCTCA		CTTGCAAAGT	ОСТССССССС		GCALAGGETC	2160
39	CTCAOTTCAG			OTCCCCT TTO	<b>GCARCTCTTC</b>	TCCCTCAGAT	2220
3	TCTCTGACAG	AAGGCCTGGT	CCTOGACACA	ATOMATOACA	CCTCACCA	GATCCTCCTG	2 5
	GACATCAGCT	TTCCTOGCCT		CCACTOGGCC		CAACTGGTCC	2400
	ATTENTACE	CTGAGCTACA	CARROCAL	CASCOTTGOCC	ACTOR COLCAR	SCHOOL STORY	2 5
20	ACTOTICIOC	TCCTCATAGC	TCCCTGCTGC	CTGATTATOC	AVAQTAGCA	OTCACACCCT.	2580
	AGCCACTGCT	GGGACCTTGT	OTTCCCCAAG	AGTATCTOAT	recretocra	тесетасска	2640
	GAGCTGAAGG	GTGGGACA	CLANGGCIAT	COTTONAMON	CATTAGGAC	CCCCCAGCT	2700
ì	ANATAGIATA	MITCHOOM				TICCITAGAT	2820
C	CATTATCCAG	AGACTOCCAG	AAGGTGGGTA	GGATGACCTG	GOGTTTCAAT	TOACTICION	2880
	rectroctary	TAGETTECAT	AGNAGOGANG	ACCTGCAGTG	CACCOUNTECT	TOCAGGCTGA	2 2
	OTCCTTTTO	CCCCTCCCTG					2000
08	AAATCCTGGT	TAMMANOTO	TETTOTATO		TOATTTOO		3130
3	ATGTCCCCAA	TCATACCAGG	CHOCOTOCCC CACACTGGCA	TTGACGAGAA	CTCAGGGGGA	OCCUTCACATA	1260
	опссаммая	ОСССТВАСС	TOCCTOOCT	CCTTAGCTTG		TTGCAAAGAG	200
6	ATAMAAGGA	CCCCAGCTGA	ANAMANAAA	ANAMAN	TTGAGAACAC	TAACTACTCA	3360
Co		1					
	Protein Accession	į	AAKO6529.1				

PCT/US02/12476

PCT/US02/12476

2

13

Seg ID NO: 74 DNA sequence Nucleic Acid Accession #: Coding sequence: 111-416

8

Seq ID NO: 72 DNA sequence Nucleic Acid Accession #: U74612.1 Coding sequence: 178-2581

20

ဓ္က

23

승

33.

S

5

S

25

15

2

3

53

GOODAGAGE AGGCTGGCC THYTAMGGA CTGCTCTTTG TCCAMCIOLA TOCKTCATTG AGGCTGGCC TGGGTTTT GAMGGAMA TCCAGGTG AGGCTGTT GAMGGAMA TCCAGGTG AGGCTGCC TGGGTTTT GAMGGAMA ANGGCCC TGGGTTTT GAMGGAMA TTGGGCCG AGCTGCCCC AGGCTGCCCC AGGCTGCCC AGGCTGCCC AGGCTGCCC AGGCTGCCC AGGCTGCCC AGGCTGCC AGGCTGCCC AGGCTGCC CTGCTGCGC CGGGTGCC CTGCTGCCC AGGCTGCC CTGCTGCCA CGGGTGCC CTGCTGCC AGGCTGCC CTGCTGCCA CGGGTGCC CTGCTGCCC AGGCTGCC AGGCTCCC  AGGCTCCC AGGCTC

Seq ID NO: 75 Protein sequence Protein Accession %: Bos seque

35

<del>5</del>

Sed ID NO: 76 DNA sequence Nucleic Acid Accession #: Coding sequence: 111-416

45

TENTACED AGGETERAD TRANSPAR CHGETETTS TECHNACAC, COGGNAGAGE ATTACHAGAS TRACESTES AGGGNAGA TENCATETT GAMAGANA TENCATETTS ANADESTES AGGGNAGA TENCATETT GAMAGANA TENCATETA CANTACTAR CHGETETTS ANADESTES AGGGNAGAT TENCATETTS TENCATED AGGGNAGAT TENCATETTS ANADESTES AGGGNAGAT TENCATETAT AGGGNAGAT TENCATETAT AGGGNAGA GAMAGAT GATTETTAT AGGGNAGAT CHGETETTAN ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT ANADESTES AGGGNAGAT CHGAGAT AGGGNAGAT CHGAGAT AGGGNAGAT CHGAGAT AGGGNAGAT AGGGNAGAT CHGAGAT AGGGNAGAT 20

55

250555

Seq 1D NO: 77 Protein sequence Protein Accession #: XP\_048124

8

8

Beq ID NO: 78 DNA sequence Nucleic Acid Accession #: 273678.1 Coding sequence: 253-2433

2

2

23

8

8

73

8

decorration Accessed III

CONTRACTOR INTERCENT

CONTRACTOR INTERCENT

CONTRACTOR CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTOR

CONTRACTO

82

217

Sed ID No: 73 Protein Protein Accession #: A

WO 02/086443

CCCNTCTC GOAGNGG RATIONAL TRANSPORT OF ANTERCRICA ANTERCRICA CONCAVAGE CONCA

ಜ

220 CUTTOMONE MECHANISM CONDUCTOR ORGANISM CONTROLLED STATEMENT OF THE CONTROLLED STAT

Seg ID No: 82 DNA sequence Nucleic Acid Accession &: BC001291 Coding sequence: 44-541 MEDSENCING EMMANGAN LA LITURASED YEGGUATER PR GRICOLMPILL SITERALLO CI GOSHICARE OMERCINILE LIPHESTICE NATORNIA PE PROSPILATE PARTIFIER UN EMPISIONO QU

MANSPLKTAL AYECFODODN ST TLEHENROGN TOGLADATAT OT SQNEDWISHY PROSONTICA GS OMYSTYSTC SOGNAIKKEP VR ECSOLITIPA VYTLSSODEN YO GYNYQQAAQA LHULVFRSTI NK

Bed ID NO:

S

21 11 41 crecross Acceptages coccostrates and acceptages | | 000000000 | 000000000 | 000000000

PCT/US02/12476															•											•				•				
				•																														
180 240	2 2 2 2 4 7 8 3	9 9 9	780	2 2 2	1020	1140 1200 1260	1320 .		120			9 2 2	2 8	9 29	240	99	280	000	1020	1140	1320	1500	1560	1740	1860	1980	2160	2220 2280	240	2520	2580 2640	2760	2820	3 5 4 0 3 0 0 0
OTCATOTTTO ENGAGECATA	AGCAGTGCTC TCCTOGAAGA TAGAGGGGCC GCTGTGGTGG	OCCTOTOTO GACCOTTOTC CCAGGOTOTT	TTTCTCTTTG	TO A TO A TO A TO A TO A TO A TO A TO A	DECACACOTT TCAACCTTTC	ANCATETONA ANCATETONA ANGATOCAGE	ACAAGGGGAC AAA		51     TPECQNPRRC   PYLKCCKIRY		<b>a</b> _	TCATCTTCCC	OTCTOBCOGC TCTTOAAGCC	GOATCATGAC	DOATAAGCCA	TTCTGCACAT	GCATOGTTT	TCCTTCCCAG	CACTECECCC	GCGGTTGAAT GCTGGCAGGG	TCCTCTGCAA	CCAGAAGCCC	COCOCTCAAG	CGAGGAGGAG	COCCCTACCC	CAGGGACACT	OCTOCTOGOC OTTCGACCTO	ATCOCCTTT	ACCOCCCCCO	GAGAAGCCAC	GAGTAGCAAG	ATGGCACAGT	AGCCCCACTC	TOANTOCATO
ADANTOTOGE TOCAAATOGA	AAGCGGTTGCAATT TACTGCAATT	ACTOBACTICA ACTOBATCA TITTORACTIC	TOACAGOT	TACCACTOAT	COGCANTOC	ANGAMETTA GTGTGTGTTC	AAAAAAAAA		41 VNCHVCBREN RFLLEEPHPF GLSLS		٥	CTCCCACAT	AGCCCACCAT	CTCCAGAAGG	COTOGAGOT	CCTCCCCTCG	CATTCACCAG	OTGCAGAATG	OCTTICCACC GCATAGAGCG		CCCCCTCCC		CCGACGACGG	ADGAAGAGA		ACCATOCOCA ACCATOCOCA		AGTGGCTCGC						TCTCACCOTT
CCAAGAAT	ACCITITITIC DCCAGAGGAG TAAATTCGC TGCTGGGAGC	CTCCATTGCA COGAGCATGG TACCTCTTG	DOCTOTTANC	NOGCCTANG CAGGAACAC	CTCAGCATGG	ATTCCCACAC	AAAAAAAAAA		31 60RTDECIONR AMENPRPEER 1LLLLASIAN	93.1	ā-	CATGACGGCT	COGCOCCOC	TECCATTOG	CTCTGCTTAG SCATCCAATC	MOGGGCCTCTA	TGCAAACAGC	TCAGGACTAG	GENGANGOGC	TTCTCTAGGA	CTOGGGACGC	CACCAGGCGCA	TTGGTGGGCA	GAZGAAGAGG		CTGGCCGAGG GACCGCATAG		AGCTTCGGAG	GOCACOCOGA	CONTCTCA	TGCAACTATG			CCAGCACAC
GAACCEACEA	AAATATTTCC AGAGACCCAA TCAAGTGTTG TCAAAGAATA	TOCTOCTOCC CTGAOCCTTC TTCTOTTGA	NGGTGCAGTT ICTCCTGAGT	CATGGGGAGG	TOAAGGACTC	ADATTCATAA ATCAGGGTAA	ATCAGACTCA	AAH01291	21  - LTARQRDPED VAKQCEAGCA GBSCGGLMLA	ence 8: NM_022893 726	<b>5</b> -	AMAMAMAGE	GCCCCCCCC	AGACCACOGC CCAGATGAAC	CAATGGCAGC	TCTOCACTOO	ATGTACAACT	TOOTATCCCT	Treesdeerd	CCATCACCOS	OCCUCCATION OF THE PROPERTY OF	CCTGGTGGTG	CACCACATO	CGAGGAAGAG	COCCOOTCOTO	GCGCGACTCG	CTTCTCTANG	TCCCTTCCTT	CTCGCAGAAC					oractiones, trititium
086443 averecease Avexettres	DODGCCOTOA DCAGCGATGC TTCTTTACC TCATCAGTGT	OCCATOCTOC FIGOCOACAGA TOTAVACTTOT	илосоалтс зилотесиа	TICOGACC	ATCCCTOOAG	CCAGGAGGCA ACAGGTGCAC AGTAGAGAGC	GACCTGAGAA	1) Proteir	11   Alpruytdan Aukipprppm Buykeyagsm	84 DNA sequence d Accession 8: N ence: 229-2726	#-	THUTHTGCTT	AACCCCAGCA	ATGATGACC	CACCAATCOA	AAGATGACGA	GCAGCTACAC	CCCCCCCCCCC	CACCACCGAG	COCTOGCCAC	CAGGTAGCA	TTCAGAGCAA	TOCACALATC	AGGAGGACGA	AGGCATGCT	AGAAGCATAA	CCCCGGGCGA	AGCTCAAAGA	COCHOCACTC					TTTTCCTT
WO 02/086443 AGATECKAND AGATECKAND ACCURATE TOAGAGAMA AACUETT	COCHOCITATA COCHOCITOR GCCCATGCCC ACCTATCACC	ACCTOTOCCTO ACCTOTTOCA	ACATTCAGAG	OCTOTANGO TOCTOAGATO		ACCAGETOC ACTINGGES	CATCCATGOO	Sed ID NO: Protein Acc	MALLALLLÝV MATEPYCVIA CALEGEPINS	Beq ID NO: 84 Nucleic Acid A Coding sequenc		TOCOCCATC	ANGCANGGA		CCTTCCCCTT	GTCACGCCAG	GATTAGCCCA	AGTCCCCTGA	GOATCAGTAT	CCATGGCTA	CCATTCCAGC	ACOTTCOART	ANGACGCACA			GTCCTGGGCG	AGCCCACT				ACOGOCCIAN CTCACCAGGC 1			ACGMAGCTAA TICTITITIC
	ν.		<b>-</b>		^		9	S			,	c	,		0		0		S				v	,		_		S					S	

v	TATTTTAAAT		TOTTICTOR	ACCATOCTOC			3240
1	AGACAGAATA	GATAGCACTO	AACGTGAGGA	TCTATGAGCT		CTCTANGOO	2 2
	CAGAACAAGT	CAATTOGAAA TTATTCTATC	ATTTOSTET	ABOCCTTGAA		ACAGAMAA	35
10	TAATAMOCT		CATATAATAC	ACTTOTACCT TATATTOTAT		PTGGGTAGG AATGGCTAGC	1500
	TAMAMAGATO	ACCCATTATO	TOCTAGETAA	ACTITIOCICC		TANTITATA	3660
	TROOCTETT	TGCCCAAGT			ATTANATEDA		3780
23	TOCTTANTA	ATGICTITE		CENCENNAGE			200
	AGAGGCTGAC	TOGACATCA	AATGATAAAC GACAGAGGGG	AACAGAAGAA	ANTANTATOR	ATTAITAGGA	1960
	CACCITOGIA	CTATTTOCCA		GAACAGGTAT			4080
2	GAGAAAGAAT	TTAMANTA	GCAGTATATA GCAGTATA		CCCTAAAAGT	TOTACTTCAT	420
	THEFT	TACACTOTOT	CTATTION	TTANCATOGA	CTGCCCCAGT	TOTTTTAL	426
	ATAGCACTTO	АСТСТОССТО	TOATATCTO		TAATCAGAGA	TACAGAGGTT	3
22	TACAGGICTA	TACATAGG	MANGTTOCA		AAAAAAATTO	ACACASTC	1200
	CATTGAGGAG	CATTITITAL	MACTAMAA	AAAAAAAACT		TTTACTTOAC	4560
	TTACATAGA	AATGAATGAT				TTOTACAMA	2
ဓ	CTTTTTTAAA	TATAMATAT	TCCATTGTCT		ACAGACTTCAT	TATOTATAGO	2 2
	AAAAATGOTA	GTGGUAATTC		ATACACACO	CTCTTCAGGT	TOTANAAAA	4860
	AAAACATAC	ATTCCTATGC	TAMATACAT	TATATAGIZAC		TTCTAGNATO	1920
35	GTATTTGAAT	TAMATGETICA	TCTAGTOTTA	GOCACTATAG			5040
3	MANAGACA	GOTTOCOLCA			AGGATAATAT	ACTOCAATT	5160
	GANGCCATAT	TTCAAAAAA	AAAAAAAGAG	MONANCANA	AAGTOTGACA	TTACAGATGA	5220
\$	GOOGTTGTAC	ATATOCTTT			CATACTOTAT	GCAGTACTGC	5340
9	AAGCTAATAA	COTTOGETTO	CATATOTAGE	1001111101	CCCTTTCCTT	CTATCACCCT	\$400
	AAAAAAAAC	CAATOTTTO	CASTITITI	CATTGOCIAA	AACTAAATOO	TOCTTTATAT	2520
	ACTITITION	AAATOGCAAT	DCAGAATATT	ATATTAMON	CONTROLA	TTTAGTCAT	550
45	AAACTUTT		GAMITITAL		OGGAGTCACT		5700
	TATETETE		TOACCAAAGG	TCATTACAC	CTCCCTTTTT	ATTOTATE	5820
	TTICTOUTCE		CTATTOGAAA		TOTOTOTA		5880
20	CIGCATIANC A				GAMMATAA	AMMANTAN	9840
	Seq ID NO.	85 Protei	n sequence:				
34			•				
S	<b></b>	=_	<b>1</b> –	<b>=</b> _	<b>;</b> _	<b>5</b> –	
	MSRRKQGKPQ	HLSYNEPSPE CNOSTCLERA	PLEATLTDDE	POHCPLCAPE	GENERALTON	COMMPEGDI	9 5
Ş	CPKQEHIADK	LLHWRGLESP	RBANDALIPT	POMBABYAPO	AICKOEP86Y	TCTTCKQPPT	3
3	LR I PG SVSRB	NTIMER LYES ASOLAEORPP	PTPPLFSPPP	NOI PEOLGAB RHHLDPHRIS	CPEOPPLEOI	HIADHNPPHL THHPBAPDRV	2 2
	PPLOGAPPE	PAYOPERRIR OPPVKSKSCE	ELAGNT8SPP PCGKTFKFQ8	LEPGR PSPMQ NLVVHRREHT	RELEGPICING	KPPFLATPPL DHACTQASKL	2 3
. 59	KRHMKTHMHK	SSPATVKEDD	GLETABSPEP	OTSDLVGSAB VDYGFGLSLS	SALKSVVAKP	KSENDPELIP	\$ \$
	RALPDVADGA	VLSSMQHPBE	APHQVLGBICH	KRCHLAEAEG	HRDTCDEDSV	AGESDRIDDO	9
	AGYAASROLK	DPPLSPGD6R	CSPFASSEN	SENGSLAFE	TPPGBLDGGI	BORSOTOSOO	2 2
20	STPH I SCPCT QSSKLTRFFCK	GRP8SKEGRR THGQVGKDVY	KCB1CKMPP9	PRICENTAL	RRSHTGERPY Kwhedrvlan	KCELCHTACA DIKTE	780
	on at	200					
75	Nucleto Adi	ld Accession	ong in not as Day Baguanca Mucleic Acid Accession \$1 XM_015292.2 Coding sequence: \$3-1576				
		<b>:</b> -	17-	<b>:</b> -	<b>;</b> _	121	
õ	acteactes	CCGCGGCTCC	coordracc	Aggecegge	OGTOCOCAGA		8
3	CONDANGATO	CTGGCGGCA	AGAGCGCGGA	000CTC0000	CCOGCAGOCO	AGGCCIAGOG	
	TATCGGCTCG	GOCATCTTCS	TOACOCCOAC	gocoracte	AAGGAGGCAG	acroscono por concordo	2 2
82	COCCOMOCTC	GGCACCACCA	TCTCCAATC	GOCCOCCO	TACGCCTACA	TOCTOONOOT	2 2 3
	ATCCCAGTAC	Атсотовосс	Tagrerrose	CACCTACCTO	CTCAAGCCGC	TOTTOCOCAC	940

œ
7
7
~
=
ñ
~
S
<b>=</b>
5
-
u
Ξ.
_

	WO 02/086413		
	CTRCCCOOTO CCCRADORAG CAGCCAAGCT COTICCCTOC CTCTOCOTOC TOCTGCTCAC	009	
	ODCCOTOMIC TOCTACHACO TOMAGOCOC CACCODOTIC CAGGATOCCT TTGCCGCCGC	960	
	כאפכדנכדו פכנכדוספכלכ זמאלכאולכד פכדנספכדוכ מזככאמאולם פמאוסמסדמי	720	
	TOTOTICIAL CHARACCCA ACTICIONTI TGAAGGCACC AAACTGGATG TOGGGAACAT	780	
^	TOTOCTODES TINIACADED DECTETITOE CTATEBAGGA TOGRATIACT TGANTITED	840	
	CACADADDA ATDATCACC CCTACADAM CCTOCCCCTO OCCATCATCA TCTCCCTOC	006	
	CATOSTOACO CTOSTACO TÓCTGACCAA CCTROCCTAC TTCACCACCC TGTCCACCO	096	
	GCAGATOCTO TCOTCCGAGO CCOTGGCCOT GGACTTCGGG AACTATCACC TGGGCGTCAI	1020	
•	מדכנוסמאוכ אוכנכנסוכו ונטומסמכנו מוכנומנוזו ממנוכנטונא אומסטוכנכו	1080	
2	OFFICIALISC INCRODUTOR TOTALOSTODO OFFICIADORA OSCURICADO CONTRATO	1140	
	CHECATGATE CACECACAGE TECTICACECE COTOCEOTEC CTOMOTTEN COTOTOTAL	1200	
	GACGOTOCHE TACGOCHTET CEAAGGACAT CTTCTCCGTC ATCAACHTET TCAGCTTCH	1260	
	CAACTGOCTC TOCOTGGCCC TOCCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC	1320	
:	TOAGCTTOAD COOCCCATCA ADDTOAACCT DOCCCTOCCT OPOTICITICA TCCTGGCCTO	1380	
2	COTOTICCTO ATCOCCOTOT COTTOTICA (ACACCOCOTO GAGTOTICA) TOGGOTTOAC	1440	
	CATCATCCTC AGCOGGCTGC CCOTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA	1500	•
	מדספרוכבוכ כאסספגובד זכרכנאכלאכ נסוככוסוסו כאפאסכוכא זסכאפסוסמו	1560	
	CECECHODAD ACATACECAD DAGDECDADT OGETOCECON GOAGCATGE		

Beq ID NO: 87 Protein sequence: Protein Accession #: XP\_015292.3 

		<b>=</b> _	<b>#</b> _	<b>-</b>	<b>\$</b> _	- 13	
MAGAGPERRA LAAPAASEKE EARENGLAAK BADGSAPAGS GEGVTLORNI TILMGVAIIV		AAPAASEKE	BARETONIAAK	BADGSAPAGE	GEGVTLORNI	TELMOVALIV	8
OTITOSOIFV TPTOVLKEAG SPOLALWWA ACOVFSIVOA LCYABLOTTI	۲	PTOVLKEAG	SPOLALWWA	ACCUFBIUGA	LCYABLGTT!	BKBGGDYAYM	120
LEVYGELPAF LKLMIELLII RPSSQYIVAL VPATYLLKPL PPTCPVPEEA AKLVACLCVL	3	KLWIELLII	RPSSQYIVAL	VPATYLLKPL	PPTCPVPEBA	AKLVACLCVL	180
ILTAVNCYBV KAATRVQDAP AAKLIALAL IILLOFVQIG KODVENLDPN PSPECITKLDV	2	LATRYODAP	MAKELMIAE	IILLOFVQIG	KODVENLOPN	PEPEGTKLDV	340
CHIVLALYBO LPAYOGNNYL NPVTEEMINP YRMLPLAIII BLPIVTLVYV LTNLAYPTTL	3	AYOOMNYL	NPVTEEMINP	YRNUPLAIII	BLPIVTLVYV	LINIAYPITL	300
STEGNISSEA VAVDPONYHL GVMSMIIPVF VGLSCPGSVN GSLPTBSRLF	5	VDPGNYHL	<b>CUMBNIIDAY</b>	VGLSCPOSVN	<b>GBLPTBSRLP</b>	PVGSREGHLP	360
SILENIHPOL LIPVPSLVPT CVMTLLYAFS KDIPSVINFF	5	TAVIBAVY:	CVMTLLYAFS	MANIABATON	BPPTWLCVAL	SPERMLCVAL ALIGMINIRH	420
REPELERPIK UNLALPVPFI LACLFLIAVB PWKTPVECGI OPTIILSGLP VYPPGVMWKN	5	TALPUPPI	LACLFLIAVE	PWKTPVECGI	OPTITLEGLP	VYPPGVWWXX	9
KPKWLLOGIY STIVICHKLM OVVPORT	ь	TVLCOKLM	OVVPORT				

Seq ID NO: 88 DNA sequence Nucleic Acid Accession #: NH\_005269.1 Coding sequence: 168-989

•							
_		=-	<b>17</b> -	11.	<b>‡</b> .	15-	
	7344440744			1	1	-	5
	TCTGGATATG		TO CONTROLLED		Carried		200
	ACCCCTGAGG	AGTAGTCACT			GTCCACCATG		180
_	TCTTTCAGGG	ACTCCTGAGT					240
	TOTOTOTO	CITCATCTTC	COCOTOCTO				300
	GTGATGACCA	CAAGGACTTC	GACTOCAATA		CCOCTOCTCC	AACGTCTOCT	360
	TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC			ATCCTOOTGA	420
	CATGCCCCTC	ACTOCTCOTO	STCATECAGE STCATECAGE	TOGCCTACCG	GCAGOTTCAG	GAGAAGAGGC	9
_	ACCANGANGO	CCATGGGGAG		AACAGTOGGC GCCTCTACCT	GAACCCCOGC	AAGAAGCOOG	240
	graddered	<b>OTCOACATAT</b>		GTCTGCAGCC TAGTGTTCAA	OCCGAOCOTO	GACATCGCCT	9
	TECTOTATOT	OTTCCACTCA		TICTACCCCA AATATATCCT	cccrccrora	<b>GTCAAGTGCC</b>	9
	ACCCAGATCC	ATGTCCCAAT	ATAGTGGACT	OCTTCATCTC	CARGOCCTCA	GAGAAGAACA	720
	TTTCACCCT	CTTCATGGTG	OCCACAGCTG	CCATCTGCAT	CCTGCTCMC	CTCCTOGAGC	780
_	TCATCTACCT	OCTOACCAAG	AGATGCCACG	AGTGCCTGC	AGCAAGGAAA	<b>GCTCAAGCCA</b>	9
	TOTOCACAGO	TCATCACCCC	CACOGTACCA	CACGGTACCA CCTCTTCCTG	CAMCAGAC	GACCTCCTTT	900
	COGOTOACCT	CATCTTTCTG	OCCTCAGACA	OGCICAGACA GICAICCICC	TCTCTTACCA	GACCGCCCC	960
	GAGACCATOT	GANGANAACC		ATCTTOTIONS GOGCTOCCTO	CACTGGTCTG	OCAGOTTOGG	1020
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TOAGAGTGGG	GONGCTANGC	1080
2	CATGAGGTAG	GGGCAGGCAA	GACAGAGGAT	TCAGACGCTC	TOGGAGCCAG	TECTAGICC	1140
	TCAACTCCAG		CCACCTGCCC CAGCTCGACG	GCACTGGGCC	AGITCCCCCT	CTGCTCTGCA	1200
	CTCCCTTC	CTTTTCTAGA	ATCOLARTAG	CTITICIANA ANGONANTAO TOAGOGICAA TOC	700		

Seq ID NO: 89 Protein sequence: Protein Accession 8: NP\_005159.1 

	ŝ	120	180	350	
2 —	PDCATROPOC	ENSORLYLNP	NIVOCFISKP	PHOTTSSCKO	
<b>≠</b> _	KRVMSDDHKD	<b>QEKRHREAHG</b>	VVKCHADPCP 1	KAQAMCTGHH	
ā_	FRVLVYLVTA	VVMHVAYREV	BPYPKYILPP	NEVELIYEVS KRCHECLAAR I	TIL
II _	GRIMLBLVFI	LILVICPSLL	VDIAPLYVFH	NEVELIYEVS	PDRPRDHVKK
<b>:</b> _	CWRIFEGLE GOVARYSTAP GRIMLSLUPI FRULVYLVTA ERVMSDOHKO P	VSHVRLWALQ LILVICPSIL VVMPVAYREV QEKRHREAHG	YVCSLVPKAS VDIAFLYVPH SPYPKYILPP V	EXMIPTERM VATABLETEL !	DELLECTRIF LGSDSHPPLL PORPRDHVKK TIL
<b></b>	HOW STREET	GNVCFDRPPP	GKKROOLMIT	SEXMIPTLEM	DOLLSCOLIF
	ć	?			

Beq ID NO: 90 DNA sequence Nucleic Acid Accession 8: NM\_002391.1 Coding sequence: 26-457

4 4 8 9 8 4 L 2 2 3 3 5 6 C 2 3 5 5 6 C 2 5 6 C 2 6 C 2 7 C 2 7 C 2 C 2 C 2 C 2 C 2 C 2 C 2 C 2 C 2 C 2	120	1100	8 4 8 0 9 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	120 120 180	750 750 750 750 750 750 750 750 750 750	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1200
	S1 DCGVGFREOT RYNAGCORT I	S1 	ACATCHOTA AACCAGAT AACAGAGA CAGTGAGAA TCCTCAGAT AAGATGTT TTTTOTOTT TTTTOTOTT CAGCATGTA AAATGAGCA AAATGAGCA ACTCTGGGGA	S1 KSRPGWGRP VYWGVABIL RESIKGKSTT DT 8C	51 CCAAGAGGCC CCAAGAGGCC CCAAGAGAGC CCAAGAGAGG ACCACAAGA TOOOCAGGG GGCGACCCAT	MACKACCOT GOALGOCOL COALGOCOL GOALGOCOL COALGOCOL COALGOCOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL MACAGOTOL	TOCTCANTOT TCATTGAGAG ACAGCTTCGG
	41 	41 	TCACAGAMA OUTTECCA AGGAGAGA TCTAGCCTAG TCACCTTA	41 	41 CCACTCCCTO AGCCCAGAA AGCCCAGAA ACCCAGAGC ACCCAGAGC AATGAGTGGC AATGAGTGGC	GENGCANAN TACACCOCCA TACACCOCCA TACACCOCCA TACACCACACC	AAGGACGACC AGCCGTAACT AACTACACGA
	31 	31 CACTECCACT CACTECCACT CACTECTOTO CACTETOTO CACTETOTO CACTETOTO CACTETOTO	GANTCTGGGG GACCACCCC GACCACCCC GAGCACCCC GAGCTCTCT ANGAGANCO TCTCTACAOT TCTTCTACAOT TCTTCTACAOT TCTTCTACAOT TCTTCTACAOT TCTTCTACAOT TCTTCTACAOT TCTTCTACAOT	31 LHSKYWSEDK BFSCVFAGNP VBSTLFGNTK LEFCGSTWSS		CCAGATORS  GOGGAACHG  GOGGAACHG  GOGGAACHG  GOAGACHG  GOACACHG  GO	AGGCAACTTC GGCGGACCTG CTATGTGAAC
CCNCCCOOT CCTGCCCAC TOTAMOT TOTAMOT TOTAMOT TOTAMOTOCCA ATAMOTOCCA	11 1 ALIALTS VAKKONYKK OPPOPOWKK OPPOWKK OPPOWKK OPPOWKK OPPOWKK OPPOWKK OPPOWK  21 decreeart Aresectate Testercas Testercas Searcas Areses	MASTROCCOS AMCCAGAGA TATTROGAM AGGCANGA CAGAGACTTO AMTARAGACTA AMTATTAM TYGGAGATTO TYGGAGATTO AMTATTAM TYGGAGATTO TYGGAGATTO	HP_005121.1 21 21 21 31 31 31 31 31 31 31 31 31 31 31 31 31	21 Anticrosts CTGACCCCA CTTGACCCCA CTTGACCCCA GTGCCAGAA GTGCCAGAA GGAGGCCCCT GGAGGCCCCT GGAGGCCCCT GGAGGCCCCT GGAGGCCCCT GGAGCCCCT GGAGGCCCCT  GGAGGCCCCT GGAGGCCCCCT GGAGGCCCCT GGAGGCCCCCT GGAGCCCCCT GGAGGCCCCCT GGAGGCCCCCT GGAGGCCCCCT GGAGGCCCCCT GGAGGCCCCT GGAGGCCCCCT  GGAGGCCCCCCT GGAGGCCCCCCCCCC	ACCENCIAGE ACCENCACIO OCURACECCA CONCECTICA CONCECTICA CONCECTICA CONCECTICA CONCECTICA ANAMANA  GACAGTCACT AGATGTGCAA GTGACCATCG		
086443 roccadada roccadada roccatoroc roccaccera Acadacar Acadacar Rocatoroc	11 LIALLALTSA RVPCWRKEF RAKAKAKKK RAKAKAKKK 92 DNA SEQUI	11 11 12 13 14 15 16 17 18 18 19 19 19 19 19 19 19 19 19 19 19 19 19	ACACTOTA ACACTOTA ACCAMBETE ACCAMBETE ACCAMBETE ACCAMBETE ACOTOTA ACOTOTOTA ACOTOTA ACOTOTA ACOTOTA ACOTOTA AC	ession 8: 111 111 ATEQUED ATEQUED ATEQUED ATEQUED BY STANKENCE ATEQUED BY STANKENCE	4-00064306	AGTOGOCH GRANAGGGG GROTCHAF GCOTCHAF GCOTCHAF GCOTAGGGG GCOTAGGGG GTOGAGGGG ATTGAGTAG ATTGAGTAG ACCCOGAGGGG ATTGATAGGGGGGGGGGGGGGGGGGGGGGGGG	GAGGACCTGG CACCTTGAGA GAGAACGGTG
WO 02 ANTGETCAA ANGGETAAA CCCCTTGET ANGGETCTCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCC GAGCETCCCC GAGCETCCCC GAGCETCCCC GAGCETCCCC GAGCETCCCC GAGCETCCCC GAGCETCCCCC GAGCETCCCCC GAGCETCCCCC GAGCETCCCCC GAGCETCCCCC GAGCETCCCCCC ANTAT ANTA	11 11 11 11 11 11 11 11 11 11 11 11 11	1 	TOMAGAOTC ATATTCCANO THACTAOTC GTCCCCCAO GACTACTC GACTACTC GACTACTC TOTCCTANT	Seq ID NO: 91  1	5888888F	TACTTORO  OUTSTTORO  OUTSTTORO  OUTSTTORO  OUTSTTORO  OUTSTAND  OU	OCTOGAGGGG ATGCATGCGC GAACCACATG
\$ 10	15	30	35	55 50	9 % %	5 2 2 2	6

Seq ID NO: 97 Protein sequence: Protein Accession 8: MP\_542399.1

9225

ve
~
7
~
_
ñ
0
Ü
=
=
-
Ł.
$\overline{}$
-

WO 02/086443

Sag ID NO: 95 Protein sequence: Protein Accession #: NP\_036233.1

30

9	120	202	2 8	240
S1   	LGAAKKPPVT VLCDSCIGNK	TWELFCQTDQ KWQKEKDRIK DEBAKULHED	NEWDOLLANC	BBIQNSDNDL PVVQQBSSFB GIGSNEAP
11 11 21 31 41 51  WANTENDORDA ATTENDORDA ATTENDORDA AND AND AND AND AND AND AND AND AND A	GKREPYAGIQ LGAAKKPPVT PERSKEGSEE VLCDSCIGNK	EARKCPVHGK TWELFCQTDQ KIIEIEDEAE KWQKEKDRIK DOUNCIWDAL DERAKVIHED	DENOTORIES PRICETALE CONTROL HENDELANC HARMCHARY VINYTHERD EMBARDTHIR YEMYLTPKGG	BRICHBDNDL
31    -     NGTKADGKDA	OPVERDOOM BNYFSMOSNE BIMEPGETRR NSYPRADTGL	PHIEGAAFED HQLIEPIEDS EBAKAEKETE LSIQKEQIQI CONTESTION ALEGGEDIAN	DALMSNYBLP PPLPTYHVLL I	NYTERVWEYB YR PPYVNKGN
21	OFVESCIOORS SIMEPOETRR	PHLEGAAPRD EBAKAEKETE	GALMSNY8LP HNENGGDHRY	NFNNLYGTKG Kegkotmleh
11	POEGRALI AGRESHRPI GPVBSGDORN SNYTSMOSHE (POEGRANA SNYTSMOSHE I PSESHKPIV SIMEPGETAR NSYPRADIGL			
	KPGEGRBALF	OKAVKBCLVC TCICYLCMPO	KOTRECLASI	VRTBYQP8SP LKGYPSLARB
	35		40	

Seq ID NO: 96 DNA esquence Nucleic Acid Accession #: NM\_080668.1 Coding sequence: 83-841

45

1.   1.   1.   1.   1.   1.   1.   1.		ACGAGG	<b>:</b> _	<b>1</b> .	:-	1.	:-	
CONTRACTOR CETTOCOCCUS TREASCUCES CORROCADE CONSIGNATOR CONTRACTOR	280 280 280 280 280 280 280 280 280 280	ACGAGG		_				
COLONGOCCO CUTTOCTOR GUAGOCTOR GUAGOTTOR GUAGOTTOR COLONGOCTOR COLONGOCTOR GUAGOTTOR GUAGOTTOR GUAGOTTOR COLONGOCTOR COLONGOCTOR GUAGOTTOR GUAGOTTOR COLONGOCTOR COLONGOCTOR GUAGOTTOR GUAGOTTOR GUAGOTTOR GUAGOTTOR COLONGOCTOR COLONGOCTOR GUAGOTTOR	0000 0000 0000 0000 0000 0000 0000 0000 0000	CTCGAGA	CAGCGAGTGG	cerreceast	TOCCOCCCC	COGOGCOCC	одсастадуа	8
CENCORDER STETCHER MANCTICE GRANDARY STROGGICE CECCATORY TANADARY CONDECTES METAGOLICA CECCATORY CECCATORY CONTROLLED METAGOLICA MET	000 000 000 000 000 000 000 000 000 00		COGAGCCTAG	TTATOTCT00	GAGGGGAACG	COSTCCOGAG	<b>GAGCCGCTCA</b>	130
CECCOGETE TANAMAGA GORGECCA GARGAGA ANACACA GISCOGETE CECCAGGAT CE	200 000 000 000 000 000 000 000 000 000	Crococa	CCAAGGGCCC	CATCTCCTAC	TANGCCTCTG	COGNOCITICS	AGCOGRAATC	180
CCCATORTE PANAGANE CORRECTED AGAINAMA ACAGGOCTET COCCATOR COCONGRADOR CORRECTED AGAINAMA ACAGGOCTET COCCOAGUS COCCATOR COCCAGO ACCOCATOR COCCAGO ACCOCATOR COCCAGO ACCOCAGO ACCOCACO ACCOCAGO ACCOCACO AC	2000 000 000 000 000 000 000 000 000 00	ACTOR	CTCCCGAGCA	TOCTOCCTGA	MICTOCCO	ANGACACCCA	отосостос	2
CECOLOGICA MONACCETTE CATACTETTE GARANAMA ACRACCECCE CELOCADA CETTACTADA MONACCETO CATACTETTE CATACTETTE CATACTETTE CATACTET CATA	2000 000 000 000 000 000 000 000 000 00	CAGAAAG	CCCATCOTCT	TAAAGAGGAT	COTOOCCCAT	GCTGTAGAGG	TCCCAGCTGT	300
CHINCHAMA AGAINTER DANALOLA NOTICIONE CHINCHAMA MANTERIA MANATCIA CICCIACTICA MANATCIA CATTORICA MODIZITA MATERIA MANATCIA CATTORICA MODIZITA MATERIA MODIZITA MATERIA MODIZITA MANATCIA MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZICALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZITALI MODIZINA MODIZITALI MODIZITALI MODIZINA MODIZICALI MODIZINA MODIZINA MODIZINA MODIZI	55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	TCACC	CHCAOGAGCC	CTAGGATTEC	CTTTTTTTG	GACAAAGAAA	ACGAGCCCC	360
GONANTICES ACCURATED GOTTICES AND AGENCING MARGENCING AND AGENCING ACCURAGE ACCURACY ACCURATE ACCURACY AND AGENCING ACCURACY ACCU	250 750 250 250 250 250 250 250 250 250 250 2	CAGGGAG	CTTACTAGG	AGGACCTTT	CAGACACAC	ADCORCCCTO	CCACCCCCAC	62
OMMETICAL ADMANTED ACCITECTED ACCIDENT ALCOCATION ACCIDENT ACCIDEN	2556488855555855556885555555555555555555	100	GTGCCGAACC	CTGAGGCCGA	STCCAGCTCC	AAGGAAGGAG	AGCTCCACCC	9
ACTIONATE CHORONOMIC ACCURATE CONTRIBUTE OF CHORONOMIC CONTRIBUTE OF CHORONOMIC CHORONOM	E664846646846646466	AOACTT	CANATOTOTA	AGAAAGTCAG	ACCUTACTAC	AOCCOGCTOG	AGACCCTGGG	540
TITITICOGGIA TITITICICA MATTICA CONCECCIO MATTICACCO MATTICACCO CONCECCIO MATTICACO DE MATTICACO CONCECCIO MATTICACO DE MATTICACO CONCECCIO MATTICACO DE MATTICACO CONTINUATO DE MATTICACO CONTINUATO DE MATTICACO CONTINUATO DE MATTICACO CONTINUATO DE MATTICACO DE MATTICACO DE MATTICACO DE MATTICACIO MATTICA CICIANCIO CONTINUATIVA CARRIADA MATTICATICA MATTICACIO MATTICACIO MATTICACIO MATTICA CICIANCIA MATTICATICA M	264845545345548455	1000	ACCTOCACCC	CAGOCCOCCO	precraema	DOCTTCGAGG	00017001000	9
ANOCITIONE CENTRANCE ANANCERIC DOMINICE CICCICCOM CUTTUALADA ALANATICE ANANCERIC DOMINICACIC CICCICCANA MINATECCI DECETTORA ETECONICE DETECTATOR INCOLUCIO BIOLICITIO GOTTECCECC CETETATORA ETECONICE DETECTATOR DETECTATOR MONCECCHIO GOTTECCECC CETETATORA DISCUSTANCE DISCUSTANCE COCCUCIONA ACCURIONA COTTECCANA DISCUSTANCE DISCUSTANCE COCCUCIONA ACCURIONA COTTECCANA DISCUSSA ETECTATORA TRECTICO PROTOCOL TETATATORA COTOCOLO ETECTATORA TRECTICO PROTOCOL TETATATORA COTOCOLO ETECTATORA TRECTICO PROTOCOL TETATATORA COTOCOLO ATRICATORA TRECTICO PROTOCOL TETATATORA COLOGICA CETETATORA TRECTICO COTTETATORA COTOCOLO ETECTATORA TRECTICO PROTOCOL TETATORA TOTOCOLO ETECTATORA TRECTICO PROTOCOL TETATORA COLOGICA CETETATORA TRECTICO PROTOCOL DISCUSTANO COLOGICA ETECTATORA COLOGICA DE LEGISLA ETECTATORA COLOGICA COLOGICA TETATARA CETATORA ETECTATORA COLOGICA COLOGICA TETATARA CETATORA COLOGICA COLOGICA COLOGICA TETATARA CETATORA COLOGICA COLOGICA ALANCATORA TATANANCE CECATORA COLOGICA CALCITATORA ANOCITICA COLOGICA COLOGICA CALCITATORA ANOCITICA COLOGICA CALCITATORA ALANCATORA ANOCITICA COLOGICA CETATORA CALCIDARIO ATTORATA ANOCITICA GORANTIA COCCUCIA CALCIDARIO ATTORATA ANOCITICA GORANTIA COCCUCIA CALCIDARIO ATTORATA ANOCITICA GORANTIA COCCUCIA CALCIDARIO ATTORATA ANOCITICA COLOGICA CETATORA CALCIDARIO ATTORATA	\$3\$\$£\$£\$£\$£\$£\$£\$	AGAAGAC	TIGICCOGAG	TCTCGCCAGT	COTOTOCTCC	MACTCACO	AGGTCCCCAG	999
COTAMANDA ALAMANDOS DADORTOS MANDATOS DE ANTONOCOS TOTATANOS DE ANTONOCOS TOTATANOS DE ANTONOCOS TOTATANOS DE ANTONOCOS DE	######################################	TEGECA	AAGCCCTGGG	CCCCAGACAT	GACTCTCCCT	DOMATCTCC	CACCACCCCOA	720
AND ATTACKT DETITIONAL TREATMENT STRUCKTORY INTOCCACTOR ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE ORGANIZATION TO CONTINUATE CONTINUATION TO CONTINUATE CONTINUATION TO CONTINUATE CONTINUATION TO CONTINUATION CONTINUATION TO CONTINUATION	84554536848465	ACADAMA	COTTAGAMAA	AGAAAATOCC	AGAGATETTO	AAACGGAGC	TOCATCACTO	780
AGACATTA GITCCCTCA CITUATTA ACCUTATA ACCUCTC AGACATTA GITCCCTCA CITUATTA TACCUTATA TACCUTATA AGACATTA GITCCCTCA CITUATTA TACCUTATA TACCUTATA TECCOLADA ACTACACA GITCCCANA GITCCCANA CITUATA ACCUTATA TO AGACACA ACTACACA A ACTACACA A ACTACACA A ACTACACA ACTACACA ACTACACA ACTACACA ACTACACA ACTACACACA	\$5555555555555555555555555555555555555	TOCOGCC		AGTITIONAGE	TOCTOROCAG	TITGARCTCC	TOOTTOALTO	940
GORGOGICH GENTRAGE GETTRAGE AND AGAINTER GENERATED STANDARD GETTRAGE AND AGAINTER GENTRAGE AND AGAINTER GENTRAGE AND AGAINTER GENTRAGE AND AGAINTER GENERATE AND AGAINTER GENERATE AND AGAINTER GENERATE CONCENTR INAUGUST TREATED AGAINTER GENERATE AGAINTER GENERATE AGAINTER GENERATE AGAINTER GENERATE AGAINTER GENERATE AGAINTER GENERATE AGAINTER AGAINTER GENERATE AGAINTER AGAINTER GENERATE AGAINTER GENERATE AGAINTER AGAINTER GENERATE AGAINTER AGAINTER AGAINTER GENERATE AGAINTER	664636843466	TOCAGIG	_	CTGGCCAGAC	TCTCCCTCCT	STCCTSTACA	TAGCCACCTC	90
AGRECOCCTO GECTRANTA GETTAGOGGG GEOGGGAGE CANCETRATI DECENDARIA EXCLINACIÓN GETTAGOGGA GEOGGGAGA TECCHANA ACCULACO ATTCAGOGA GEOGGGAGA TECCHANA ACCULAGOS ATTCAGOGA GEOGGGAGA TOGGGGAGA GETTANATA GEOCGGAGA CENCACTAGO TOGGGTACA TETTAGOGA GEOGGAGA TOGGGTAGA TETTAGOGA GEOGGAGA TOGGGTAGA TETTAGOGA GEOGGAGA TOGGGTAGA TEGGGAGA TEGGGAGA TETTAGOGA GEOGGAGA TEGGGAGA TEGGAGA TEGGGAGA TEGGAGA TEGGGAGA	64636843466	OTCCAGA	_	GOTCCCCTCC	CCTOOTCTTO	TTACCTOTOT	Gronocrage	960
GEOGRACIA GEOGRACIA CONCECCIÓN TOTATORNO RECOLOGA MATRANACIO CITACONTO MATRICADO CONCECCIÓN CONCECCIÓN TOTATORNO RECOLOGA MATRANACIO CITACONTO MATRICADO CONCECCIÓN TOTATORNO RECOLOCIÓN MATRANACIO CICAGONO ROCALITADO CONTENENTE CINAMACIÓN TOTATORNO RECOLOCIÓN DE TENENTE CONCECCIÓN TOTATORNO RECOLOCIÓN DE TENENTE CONCECCIÓN MATRICADO RETALACIÓN DE TENENTE CONCECCIÓN CONTENENTE CONTENENTE CICAGONO RETALACIÓN RECOLOCIÓN TOTATORNO RETALACIÓN RECOLOCIÓN TENENTE RETALACIÓN RECOLOCIÓN RECOL	£63£8£3£65	CCCATG		OCCITIONO	GCTTGGGCAG	CAGCGGCAGC	CATCTTOOTT	1020
TECCENCIONA ACUTANGO STITUCIONA GORGOLOIA CTGGGGGGG CCCAGCODA ATTANGO CTOMOSTITO AUTRIANAO CACCITUTO TO CCCAGCODA TOTOTOGAT TETATITA COCACCITUTO TANAGAGAT TEGOTITICO CTITUATES GIANNAIS COLOLADA TEGOTICO CTGGTITICO CTITUATES GIANNAIS COLOLADA TEGOTICO CTGGTITO TEGOTICO GIANNAIS COLOLADA TEGOTICO TEGOTITICO CTITUATES GIANNAIS COLOLADA TAGOTICO TEGOTICO CTITUATES GIANNAIS COLOLADA TAGOTICO TEGOTICO CTITUATES TEGOTICO CTAGOTICO TAGOTICO TEGOTICO CTITUATO EGOTICO CTAGOTICO TANAGATA CTUDAGATO CECTUTO COCACACO CTGATACTA INAGATICO TAGOTICO COCACACA CACCACA CAGOTICO CAGOTICO TAGOTICO COCACACA CAGOTICO CAGOTICO CAGOTICO TAGOTICO CAGOTICO CAGOTICO CAGOTICO CAGOTICO TAGOTICO CAGOTICO CAGOTICO CAGOTICO CAGOTICO TAGOTICO CAGOTICO CAGOTICO CAGOTICO CAGOTICO TAGOTICO CAGOTICO CAGOTICO CAGOTICO CAGOTICO TAGOTICO CAGOTICO CAGOTI	636863866	COAMATO	_	GCCCAGCCAC	TCACTGGTGT	CCTOTCTCTT	proprocesor	1080
COCCIOCOCIO AFTINADO CINDOCIOTO BATTACIO COCCIOCOCTO TTOCTICO TOTODANA OCCOLOGOS CICICOCIO COCCIOCOCTO TTOCTICO TOTODANA OCCOLOGOS CICICOCIO TANAGOST TOCOTICO TOTODANA OCCOLOGOS CICICOS CICI	36863366	TCCTATC	•	ACCATAGOCA	GITTCCAGAT	OGGCCACAGA	CTGGGGAGGA	1140
CONTROLLE TRANSMENT GORGANISM STREAMS CONCURS TANABAGIT TRACETTES TRANSMENT STREAMS CONCURS TANABAGIT TRACETTES TRANSMENT STREAMS CONCURS TANABAGIT CONTROLLE CENTERING CONCURS TO CONCURS TO CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONCURS TRACETTES CONCURS CONC	£853466	TCAGTGG	_	AGTTAAAGGG	CTOAGGCTTG	AGGTGAGAGG	CACCITICACT	1300
TROCTITICO FOTTUBATE COLOMORA TICOTROCA CONTROLLO TENDESCETO TAMBOTAT COLOMORA TICOTROCA CONTROLLO TENDESCETO GOLOMORA TICOTROCA CONTROLA TICOTROCA CONTROLA TICOTROCA CONTROLA COLOMORA TICOTROCA CONTROLA COLOMORA TICOTROCA CONTROLA COLOMORA TICOTROCA CONTROLA COLOMORA COLO	8593665	OFTIGODA	_	CTTOGAAATA	goccovcggg	CTCTGCCAGC	CTCGGCCTCT	1260
TOTATION CONTINUES COMMON TICOTROS  CONSCIENTO TOTATION CONTINUES CONTINUES  COMMON TICOTROS  COMMON CONTINUES  COMMON CONTINUES  COMMON CONTINUES  CONTIN	£33555	TCCTUMO	•	TTOOTOOTT	TCTTCTTGAA	OCCACCTOTO	TAAAGAGGTT	1320
CONTECTION GAMAGIC GROWING CITTURE CENTRACTOR CANAGETY ELEGISTED STATEMENT GENERAL STATEMENT CONTROLL GAMAGICA TETRIALAN THEORINA CENCRITIA LAGGECTOR GAMAGICA CETTRIALAN THEORINA CENCRITIA LAGGECTOR GAMAGICA CETTRICA CENTRACO HICTORIA MINISTRA CANAGICA CETTRICA CENTRACO HICTORIA MINISTRA CHARGANIC CETTRICA CENTRACO HICTORIA MINISTRA CHARGANIC CONCENTE CENTRACON CONCROTO GOGGOGICA THATATATO CECCENTA TETETRICAT CONTROL ONTECNITO CHARGANIT CETTRICATO CHARGANIC CANAGITA CHARGANIT CETTRICATO CHARGANIC CANAGITA ANAGINECTO GOGGOGICA PETRICATOR CHARGANITA CONTROLLA PETRICATA CHARGANITA CONTROLLA CHARGANITA	33666	AGTTCCO	•	CTTTGATTCT	GTAAATAGTC	CCACACACAA	TICOTOGOCT	1380
CONTRIBUTED ADCIDITARY GENERALES COMMUNICATES TETERATECH PETERALAN TETERALAN GENOGRACIA COLMANDARIO CHITTAGANA TETERALAN TAGORDOCCA COLMANDARIO CHITAGANA TETERALAN ATTACTARI COLMANDARIO CECTUROCA COLORACTA CALCATECTO CHITAGACCA CANONANO TENANDARIO COLANCTAR FAGALITATO TATAMATICA CECTUROCA CECTUROCA CALCATECTO TAGATITATO CATECTOCATA CATACTARIO CATACTARIO TAGATITATO CATACTARIO CATACTARIO CATACTARIO TAGATITATO CATACTARIO CATACTARIO CATACTARIO TAGATARIO CATACTARIO CATACTARIO TAGATARIO	3666	OCCANT	_	CONTRACT	DONCATTCAG	CCTOTOGAGT	CTGAGTTTG	1440
TECHNOCITIC ENTITIONAL THEORYMAN GENOMICATION AND CONCINCION COMMONINA CONTRICTOR ACCURTOCATION AND CONTRICTOR MATTERIOR CONTRICTOR CONTRICTOR MANUFACTION AND AND CONCINCION CONTRICTOR MANUFACTION CONTRICTOR CONCINCION AND AND CONCINCION CONCINCION CONTRICTOR CONT	666	CATGIAG	_	TTGGGTCTCA	DACCATAAGT	<b>STOTACTACA</b>	CAGAAGCTOT	1500
COMMONIO CUTTORIONO TRADOCCIOCA CARGINATATA MOTICATORI TUTORICTO IN CECTATOCA CONDOCCONO TRADACTA ANTANTAL CANADARCO CENTETTATO CONTACO TRETATALA ANTANTAL CANADARTE CENTECATA CENTROCA TRETATALO ANTANTAL TANANTEC TEGRAMATA TECTEGOTA CONCACTO CONCACTO TANANTEC CONCACTA CENTROCATA DANACTOR CONCATORI TECTATORICA CONCACTO TECTATORIA CONCACTOR TECTATORICA TECTATORIA CONTACTORIA CONCACTOR TECTATORIA CONCACTORIA TECTATORIA TANANTAL CATALOGRAPIA TONANTAL CONCACTORIA TANANTAL CATALOGRAPIA TONANTAL TANANTAL CATALOGRAPIA TANANTAL	8 8	TICTAGE	-	TOTTOAGATO	TITOCIANAT	<b>GCCAGGTTGA</b>	TAGOGGGCTG	1560
TETRAGETAD TECETIFICAC MODICACIO CERUTATA ALMAGINAC CHAGOTINGOC CETETIFICA CECURICOS TETETIFICADA MINIMETRA CHAGOTINGOC COCATATOR TETRAGOCAN COMBODO GORGINETO TOTAMONTE TOGOMANTI TETRAGOCAN COMBODO GORGINETO TOTAMONTE TOGOMANTI TETRAGOCAN COMBODO GORGINETO TOTAMONTE TOGOMANTI TETRAGOCAN DAMACHOS CONTRATO AMOCHOCO COCCOLNET TETETICETI CONTROTO GUITAMAN AMOCHOCO COCCOLNET TETETICETIC CONTROTO GUITAMAN CARGOMANTI CONTROTOS TOGOMANTI TOGATURA CATOGOMAN CARGOMANTI CANTEGORO DAGOCATA TOGATURA TAMAMANC CETRICOLOS TETRICORAN COMBODOCE TAMAMANC CETRICOLOS TETRICOLOS TETRICOLOS TAMAMANC CETRICOLOS TETRICOLOS TAMAMANC TAMAMANC TAM	E	CCTTCGA	_	CATTICAGGG	TOTOGOCACC	ACCTGCTOTG	AGTETICIONG	1620
ANADROCC CENTERIOR CCONTROCO THETATACA MINATAC CITUDOCCIA ANADRAMOT ECHANCERA TAGANCERA TAGANTER MATTHER CENCENTRE CENCECTA COLACIDO CORROGICA TAGANATER CENCENTRE CETCHOLAN DALACHOE CONTROLADA ANADROCCE (DECONTRE) TECHNOTICA CONTROLADA ANADRATICOS GANATAGA CETURASTA DALACHOE CATTONIA ANADRATICOS GANATAGA CETURASTA TRANSCE CATTONIA ANADRATICOS GANATAGA CETURASTA TRANSCE CATTONIA TAMANAC CETTACAGA TETERDANT CONDUCATO	֡	CATOOCC	•	TCCCTTOCAC	AGOGCCCACG	CTCCACTCT	ACCACTCTGC	1680
CTTCGCCCTA GANGGAAG TOUANGATE CONACCTAC TAGGATTTC TOTAMGNEC TCGGAAGT TCCTCGCTA CCAGAGG GCGGGGGT TAGTTTTG CTCCCCATT CTCTCTCTT CANCGATTC CTCGATGAT CTCGAGAATT TCCTCTCTT CANCGATTG GATGATGATA AGGCTACC TCCCCCATAC TTCCTCTCGC CANCGATGATAC AGGCTACC GGAGTAGAC GCTCAGGTG CAGAGGAC TOTACGATA CAGCTACCT GGAGTAGAC CCTCGGGTG CAGAGGAC TOTACGATA TAGTAAGC TCTCCCCAG TCTCGGGATT TGATGATAC GTCGGATAA	5	AGGGGTG	_	CTCTTOTCA	CCCATACCCA	TITCITACA	MIMOTIAC	1740
TOTAL AND ACCUPACION TECTORORIO PORMODO GOSGOGICTO MATTITUTO CONTRATOR TOTAL CONTRATOR	ğ	GAGTETA	_	GANGAGAAG	TTOANGAGTC	CCAGACCTAC	TAGGATTITIG	1800
HARTHTHOS CETCCTATE CETCHICATO ARACICEDE CETGATECHT CRUSAMATT TECCHOSTET TECHTICATE CATTORNOS GATTORNEO ALACITICAT GOAGGIAGE TETCHTOCOS CALCECTOS CATTORNEO AGAICITICAT GOAGGIAGE GETUROSTOT GOAGGIAGE TÓTICBATIA CACACITICAT GOAGGIAGE CETUROSTOT TORNIAME GITUGOGEC TARRAMACE CETUROSTOS TEMBRATAT TORNIAME GITUGOGEC	3	CTATOCT	-	TCGGAAAGTT	TCCTCGCGTA	CCACACAGC	000000000	1860
CTOGRAPHY TECCOLNETT ITELETETT CONCURTOR ONTOWING ALTOWARD AMOUNTED CONCERNING CONTROLLED CONCURTOR CONCURTOR CONCURTOR CONCURTOR TO CONCURTOR CONCURTOR TO CONCURTOR CONCURTOR TO THE CONCURTOR CONCURTOR TO THE CONCURTOR CONCUR	24	11700	TAGETTEROS	CCTCCCTATC	CTCTCACATO	AGAACACTOC	CTOGATGCAT	1920
мовствесе тасесства тетествеся смесетове смятитмест маметует вометумые сетиолят восможное тоотвали е сметьме тетестве тетестве стетестве тетестве стетестве тытамме стетестве	Ğ	ATGATCT	CTOGAGAATT	TOCCCATOTT	TETETICITY	CCATCOTOTO	GATTCAATAG	1980
AGAAGTICOT GGAAGTAGAC GCTGAGGTOT GCAGAGGAGC TOTTGATAAAAA CAGTGAGGGTACT TOATGAAAAA GATGAGGC GTTGAGGTAACT TOATGAAAAA GATGAGGC GTGAGGC TCTGGCAGC TCTGGCAGC TCTGGAAGT CGAGGCATTC TOGTGAAGC TCTGAGAAGAAAAAAAAAAAAAAAAAAAAAAA	E	COLUMN	7	TOCCCCCOAC	TOTOCHOOO	CACCCCTOOC	CATTOTACCT	2040
CAGGGAGAT GACTOCTOGG TCAGGGTACT TGCATGAAAC GGTGCAGGCC TAATAAAACC CTCTGCCAGG TCTGGGAGTC CCAGGCCATC TGCTCAACGC	E	CATOTT	_	GGAAGTAGAC	OCTOAGOTOT	GCAGAGGAGC		2100
TANTAAAACC CTCTGCCAGG TCTGGCAGTC CCAGGCCATC TGCTCAACGC	č	CALABOA	_	CACTOCTOGG	TCAGGGTACT	TOGATGAAAC	-	2160
	5			CTCCCAGG	TCTGGGAGTC	CCAGGCCATC		2220

•		٠	i				
53 24	1 MEGRITEGO KRIVAHAVEV EAESSEKGOE SPVVCSKLIE FEAAEQPDIL	111 	21   BPTNPLRREO RISPPLEKEN KVRREYSRLE PDMTLPOIGP	31     RKBGSELPS1   BPPGRELTKE   TLGSASTSTP   PPEKUKKKK	41 LPEIMPKTPS DLFKTHSVPA GRRSCPGFEG KMPEILKTEL	51 	
20	Seq ID MO: 98 Nucleic Acid Coding sequen	Acces	Kos	หลานจกต่อ			
		=_		<b>ä</b> _	₹		
22	GCGGCATTTC		CCGAGCGGGC		<b>GAGCGGGACT</b> TGCAGGAGAC		
	TECOTECTOA		CGCGOTOCTO TOTCCOGAAG	CATCANCTON GCATTACAGA TCACTCAACA	CATCTTTAGT GTATTGAATT	TTTTTCCAGA TCGTGAATGT	
8	AGAGAAGAAA CCTTACTCTO AAATGTAAAA	TCCTAAAGTT TTGAAATTAA TTCCAGCCCT	TTTATOTATT GAACACTTOT GGACCTTCTT	FTCTTAGAAA ACCAGTGTTT ATTAAGTTAC	AAATGGGCCA ATACAAAAGA TTCAGACTTT	GAAGATCGCA TAGAAGTTCT TAGAAGTTCT	-
	TTGAMAAAA	ATGAATTTAA	TACAGITITA	TATTTAGTA	ATGAGCTCCT	AGAACTTGCA	
35	GGATCTCTCA	AGGCTTOTC AGGCTTOTC CAAGGGAGAT	GACATCAGCA	GTANGAGAGC TOCANCTTCA	CCANCTACC	TOTTCTOGCA OGAAGAAGAT	
40	TTTAGCACCT GCCCACACAA	ATGCTOTGCC GCCTTCTOGA ATGTAGAATT	CTCAGCTGGC CAACTACGTG GAAAAAAGCT	TTGCGCCTAT TCTCTATTTG GCACTTTCAG	AMOTETTOTT CECTOGAATE	TOCATCTCAG AAAGTGGTGT CTTTCTGAAA	
	CAGGITTICTA ATGGAGCAGT GCTATCCGTG	ATATOGROOC TTTATGOAAT GATATGGACT	GAAAAATGCA CATCAGAAAT TTTTGCAGGA	GAAATGCATA GTGGATTCGA CCGTGCAAGG	AMATAAACT ACAACAAGA TTATAAACCC	OCTATCTATT OTTATCTATT	
45	ACTOSTICATOT ACTOSTICACO CTISTACCTTO			TOCANOCAGA AGCTTCCTCC	AGTECTENC AGTETOTTOC TOGAGOCACET	AAGCOTCTTO COTGOTGATO	
	CAGATAGACA			AAATGCAGC	TCACCAATTO	CAGAGCCATA	
20	OAGTCTGAAT CCCACATACA	CTGAAGACCA	COGNATATOT	TCTAAACCAG GGGGAAGTCA AGACATCTCC	DOTCCTTCC GAACTGGCAA TGAGCTCTGA	ATGGAAGGTG	
	CATTTACTT		AGCATTTTC TOTAMATCC	TCTOTOAATT	CCTCCAGTGA	AAGTCTGAAT	
22	ACACTTGAAA ATGATCCCAA GCTTTCATTA	TACAGACTOT CTTCAGATOC ACCTGGTGGA	TOGGGAACAA AGCGGCTAAC ATTTTGCAGA	DAGAATOGAO TTOCATCCAO GAGATTCTCC	ATGAGGGGCC CTAAACCTAA CTGAGAAACA	AGAGAATTT	
			ATTECATAT	DAATTACAGTAA		ANGOTTGCCC	
9		CTTTATTIOT TTTTGGCCTC	GAAATTTOGC TTTTTTGACC COTTCCTGCA	AAAGAGGTGG AAAGAGGTGG TTTCTTCTGT CTGCAGATGG	CAGTTAMAT	GAAGCAGTAC CAACATCATT GGGCCTGAGC	
65			AGCCTGAAT TTACAAAGAC GACCAAGAAT AGTGGTGTTA	ATTCTCCCT AACTOGGAAG AACTOGGAAG	AATGGTCAAT GCCTGGATGG TGTCAGCTCT AGAAGACAAA	ATACTICANO TTCTCOGOCT GAACCTTTCA	
;	000		AGAAGAAATA AAATCTTCTG AGAGAAGGGG	ACAGTCACGT CTGAGCTTTG	TAGTACAAT CCTCAGATGA CAGTGCCTT	GCTTGGATCT GATGATGAAG	., ., .,
2	AAACCTOTCA AOTGACAGAC TTOOCCAAAG TATAAGGGA	AAACTAAAGT CCACGCAGAT CCACGCAGAT		CCTCGAGTCA GAACTTTTAC GGACAGGGAG	CAGAATTAGC ATAGCATGOT CCCCACCCAT ATGTTGATCA	OCTCACAGEC TATOTTTATO OTACCAGETE	
75	CAACTOTATO GAAAGTCAGG GACAGTACTT AAGCAATAA CGACTTTATA	AGCACTAOT ATACTOTTOC TAGGAGATT CACCACAGCA GCCTTGCGCT		ATTCACTOOT CCTATATTOO TOTATTCOAD AGTCCAOTAA GCTTTCAAGA	ATOGAATTOT AATTCCTTA ACACCAATC	CAAGAATTT GGACCCTGTT ATGGTCCATT GCTTTTCAAG	
80	CATACATTC CATACA		ATTCAGGGAA GGAGAGTCTG TGATGCCATT AAAGAAAGGA	GCCTTAGCAC GATCACCTAT COTTTGCCCC	ATOCACATOR GCCCCATCA GAGGATTTCC ATTOTGGGAG	GAAGTCCTTA GAAGTCCTTA TGAAAAGAAG ACCTTCGGCA	
82		ACAAATCCAT ATTTOTGOCT AGGGGGGTGG GGGGGCCATT	GAAGATOTT CTGTGGCCAG CAGCCTGCAG	CTCAAGGAAG CCCTCGGGCA GCCACGCTAT		OCCAGGCAC TTTTCTCATC OCCGCCCTC CCTGCTCCTG	~~~

v	
2	
<u>-</u>	
•	
Ň	
⋝	
~	
9	
-	
•	
8	
_	
È	
٠.	
_	
=	
2	

PCT/US02/12476

13 13 13 13 13 13 13 13 13 13 13 13 13 1	4 4 9 2 9 2 9 2 9 2 9 2 9 2 9 2 9 2 9 2	65100 65100	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
OCTCCAGTC AGAMGCATT AGAMGCATT AGTANCOGA OCTCGGAACA TCTGAGAGA TCTGA	TETCAMATOT TETCAMATOT TETCAMATOT ACTOCCAC COTTCCCAC COTTCCCAC COTTCCCAC TEMPTORA TOMICOO TOMIC	TANTOTOTO CCCTAGATO CCCTAGATO CCCTACAGA CCTACAGA CCTACAGA CCTACAGA CCTACAGA CCTACAGA CANTOTOTO CATACAGA TOLOGOG	
CTOTAGGAGC CTTTCTTCTT CTGGGGGGGGGGGGGGGGGGG	MACHINECTOR MACHINE CONTRIBUTION CONTRIBUTIO	CONTROL IN CONTROL IN	TAGETTANE CONTITUES CONTIT
AMAGCAGNA AMAGCAGNA TACACGNA TACACGNA TACACGNA ATGGTCA TE AMAGNA TACACGNA T	AMEGICANA ATTIKACIA AMEGICALA MEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICA AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICA AMEGICAL AMEGICA AMEGICA AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICA AMEGICA AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICAL AMEGICA AM	DESTRUCCES CHARGESTER ANTEGRADAS ANTEGRADAS ANTEGRADAS GENERACIONES GE	OTROCTTITI  OTROCATOR  OTROCAGO  OTROCAGO  OTROCAGO  OTROCAGO  OTROCAGO  OTROCAGO  OTROCAGO  ANDIAGO
CACOTTCATT TECACTITIO AGGRAMA AGGRAMACA AGGRAM	ACTORIGATION ACTORIGATION ACTORIGATION ACTORIGAMATE ACTORIGAMATICAL ACTORIGAMATI	ACROMICACION ACCONTRACTOR ACCON	HARATAN AN ANALOSA AN ANALOSA AN ANALOSA AN ANALOSA AN ANALOSA
(186443) ANTECTACIA ANTECTACIA ANTECTACIA ANTECTACIA ANTECTACIA CONTRACTOR ANTECTACIA ANTECTACIA ANTECTACIA ANTANTANT CONTRACTACIA ANTANTANT CONTRACTACIA ANTANTANT CONTRACTACIA ANTANTANT CONTRACTACIA ANTANTANT ANTANT ANTANTANT ANTANT	TECHORAGE MISTERIAL MISTER	OTTITOGRA MARCAGAMA MARCAGAMA TENTOGRA	THE CASE OF THE CA
WO 01/2 cccccorror ccccccrrcar cccrrcar ACAGGCCA ACAGGCAC	AMANTOGOM  AMANTOGOM  AMANTOGOM  CONTROLOM  CONTROLOM  TOTOMOM  TO	ANCORTOR ANCORTOR ANCORTOR ANCORTOR ANCORTOR ANCORTOR ANTORITOR AN	

	GAGAACCCC	CAGACCTAAA	TAMATCHE	ACTORACCAT	TITATOROGA		::
	CCTTACATER	TCCGCAGCAA		CTOCTCCAGO	<b>GAGAGGCTGA</b>		Š
S	TACAGECATETA	ACCIDAGREE	TATGCACCGG	CTOCAAGATO	ATCTTCACAG	AGCCAAATAT	2 2
	TACATTCALA	ATGOCATTCA		CAGAATTATT	CTAGTATTGA		2
	CACCAMOTA	GACTCACCA	ATTGCAGTCT	OTACAGGCTT TCATCTCARG		TCAGGAGTTC GAGACTTCTG	2 2
,	ACACCTOOA	CAACAGATA	TCCAGATOCT	AAATGGACC		CTGGGATGAC	2 2
2	ATCATCACAA	ATCOATOTT	CTTTCTCAGC	AAAATAGAGG	AGAAGCTTAC	<b>CCCTCTTCCA</b>	986
	GAGCAGGAAG	DIATERATOR	CHECKAGAT	AGGRACECECA	DTOACAGGAT	CALANTIGAAG	972
	ATGATAGACA	GTGCCCGGAA		TOCATTO	CTATGAMCT	ACTGAAGGAG	9
21	CTGCATAAAG		DAT	TOOCTOGTOA		GAGCTACTOC	99
3	COCCTOAGCC	ACTOCCOGAO	COORTCOCAG	OCCTGCTCTG	AGCAGGTGCT	CACTGROCTG	966
	GCTTTCCGTO			ACACTTACA	CCATCATAGC	GAATGCTCTC	8
	AGCAGTGAGC	CAGCCTGCCT	Ş	GAGGAGGACA	AGGCTAGAAG	AATCTTAGAG	101
20	CTTTCTGGAT	CCAGTTCAGA	GCATTCAGAG	AAGGTGATCG	COORTCIOTA	CCAGAGAGCA	200
3	AGENCACA	TETETOAGGE	TOTAL STORY	GCTTACATOA	MUCCLANCE		1032
	CACAGAGCTGC		AGAGNATOCA	TCAGTTATTO	ATTCTCCACA		2
	TATCCAGCAC		GAMATOTTO	AAAGCTTTAA	ATTAATTC	CAATGAAGCC	Š
36	AGATTGAAGT		ACTTCAGATT	ATAGAACOGT	ATCCAGAGGA	CACTTTCAGC	1030
3	CTCATGACAA	MARKATCTC	TOCOTIOCC	TOCTOBONOT	TCATCAGCTG	GATCAGCCAC	1056
	ACTGATAACT	ACCCOCAGGC	TATTOLITAL		TANGCAGCGA	AAGCTATTCC	106
	TTCAAGGATA	CTTCTACTOO	TCATAAGAAT			TAMANGTANG	1074
6	TTGGATCAAG	GAGGAGTGAT	TCAAGATTTT	ATTAATOC	TAGATCAGCT	CTCTAATCCT	1080
3	GAACTGCTCT	TTAAGGATTG	GAGCAATGAT	GTAAGAGCTG	AACTAGCAAA	AACCCCTGTA	1086
	ANTANAMA	ACATTORAGA	TACTATORA	ACARTOTATO	CACCITAGO	TOACLEMON	
	AACATTTTO	GGAAAGGAGG		CTGAGAATGA			100
į	ATTACCAACA		AAAAATGAAC	ANAGACTOM	AGCCCCCTOO		=======================================
ç	GAATOTTCAC	CCTGGATGAG	COACTICAM	OTGGAGTTCC		OCTOGAGATT	9111
	eccounce of		CATTOON			CATCACCOCO	1122
	GGCCATGAGG	AGAGGGAACA	COLUMNICA	OTGAAGGGTG		GCGCAGGAC	i
:	CAGCGCGTGG	AGCAGCTCTT			TOCCCAAGA	crececerae	3
40	AGCCAGAGGG			<b>АВСОТТОТОС</b>	CCATGACCTC	CAGGITAGGA	116
	TINATTONOT	GGCTTGAAAA	TACTOTTACC	TTCAAGGACC	TTCTTTTGAA	CACCATOTCC	1152
	TOTAL	ABGCCCCTTA	AAAACATGAT	OCCAGGGGGCAC	ACCOUNTED A	GTATAAGGG	
:	GCTAATCGTA	CTGAMACAGT	CACATCTATA	-	AAAGTAAAGT		::
45	CTCTTANAGC	aggetttegt			AGGCTTTCCT	0000000000	1176
	TOCCACTTOO		COCTCTGATA		ACTOGATOCT	COCCATTOCA	=======================================
	CACAGACATC	TOMCACTT	TATOGRACE	ATGGARACTO	TCCTCACTT	CATOOTTO	
;	CCGCTAACTC		CAATCTGATO		AAGAAACOOG	CCTTATOTAC	200
20	ACCATCATOO	TACACGCACT		COCTCAGACC	CTOOCCTOCT	CACCAACACC	1206
	ATOGATOTOT	TTGTCMGGA			ATTTTOMCA	GALALATACTO	122
	CACABABTAT	COLCAIGUA		acadatacta	ATCCAGCAGT	CATTACTION	122
;	GATGAGCTAC	TOCTOGOTCA			GAGACTATOT		ŝ
25	CGAGGAAGCA	AAGATCACAA			AGAGTGGCT	TTCAGAAGAG	1236
	ACTICARGITAR	AGTGCCTGAT	OGACCAGGCA		ACATCCTTOO		2
	GAAGGATGGG	AGCCCTOGAT		TOGGRESS CTO	GAGATAGAAA		7
;	CTAMBABAA						136
9	TOAGTAAATG	TOTATOGGTT		TARGOTTATA	STACATOM		1266
	AGOTTTATAG	AAAGATAGAT		ACCAMOTAT	TANGTCANGA	ATATAATATO	1272
	TORGODAAT	GTGGGGAAGC	CTTOOATOC	COLLEGION	CTGGCACATT	GONANGCACA	1284
,	CTCAGAAGGC	TTCATCACCA	AGATTTTOO		TANGTATAGE	TGATOTAACA	1290
6	TTGTAGAAGC	AGCATAGGAA	CAATAAGAAC		<b>GCTATAATTA</b>	TOOCTTATAT	1296
	TAGAMATCA	CICCALLICA		ATTRICTE	TAGAAGGAAA		100
	TAGGAGGGCA	AAAATTTOO	TCATAGGATT		ATTCCATCT		ä
5	GATACATAVA	•	ATTAMATTIG		AAAATCCCA		3320
?	TAGGGATAGT	ACTAMOCATT TOCACOTARA	TCAGTTCCAG	CACATANA	ACARONTOCIA		
	ACANANGTEG		TOTOCHOTOC	CTOTOCOCCC	COCCAOTO	TOCACACCCA	1
	AACTOTTICT	GATTGGCTTT	TAGCTTTTTO	TITITION	THECTICS		114
75	CCAAAAGTA		TTTCAGAAGT	ATACTCTTGA	GTGTTTAATA		5
	Protein Act	occession & . 1	NP_008835.5				
80		11	12	11	7	91	
	_	_	-	-	_	_	•
	RDPGLLVFVR	KGLMBIEFRE	CREETLKFLC	I PLEKNOOK!	APYBVEINT	CTEVYTKORA	2
\$8	AKCKIPALDL	LIKLLOTPRB	SRLADSPK10	BLPOKPYGEL Averpklpvl	ALKICKI POTV ACCLKGL881.	LERVYELLOL	2 2
;	DPQTGREIFN		DEKRYAVPSA	GLRLPALHAB	QP STCLLONY	VSLPEVLLKY	2
	CARTHVELKK	AALGALEGFL	KOVBNWAJCK	AEMHONIZQY	PMEQPYOILE	NVDSINNKELB	ä

WO 02/086443

2

15

ຊ

23

30

33

各

5

20

25

S

AAAAAATTT AAGATTTAAA AAAATGACAA CATCTGAAAT	ACCEPTANT ANIMONAL ACCEPTAND ANACOTACA ACCAGENCE TECNOTATA DESTRUCTOR OF THEMSELE ANACOTATE THEMSELE TECNITATE CANATACTO TECCATORIO CANATACTO	CATTITICAA TATOOOTACA AATACTOSAI TOATACAGTA TTAATAAAAA		11 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CKBAGABRII HLETMIDALA LVTBFLAKIO	763.1	31 41   1   2   2   2   2   2   2   2   2	TTCOTCTGCA OTOTCCCACA OTOCCCATGC	AAGAGGGAATG TCGCTGTGGGT ATGGAGGGGGT	TTTACCATTT TGCTACCTGC CACCCCATC AGTGGTCAAA		11   1 FEVMILIANA OBVMEDEGED VANGVALYNH ETTEKPROB NYVPFFLYNG YHLMVLACG	411	31  - GGCGGGATAA CCTTTGGTGC	ATTOCOGNEY ATTOCAMACA OF ATTOC	CONCOLOR		n
GOACGCACAT CCATTTAAA OTCCTGAGGT TTCCCTGGG	TRANSCATE TRANSCACED TTGATTCACE TTGATTCA TATTCACA TATTCACA TATTCACA TAGACATT COCRETACE CONTRACT TTGATCACA TATTCACA TATCACA	AMAGATTAA GAAACTGAAA TTAGAAAATA ACTTATCATA GTOCTTAGTA	Seq ID NO: 101 Protein sequence. Protein Accession 8: NP_006664	1 11 21 HATAGENIK PRIBETENA KAPULANDAN PRIBETENA KAPULANDAN VITYRODNY GULADOTIRP TCKORPVHHP MOTSEPTETT	GANKTOKYK POSTCYVPGL GOVGLEVING IBPDSTKPI SEVLSENTON NVOTTPEVIO LITYDPHILIFT GRENKGCVPG GIKERDEVPK LIMBOGSIRT VLIF	8eq ID NO: 102 DNA sequence Nucleic Acid Accession \$: IM_006783 Coding sequence: 1786	1 11 21 11 21   1   1   1   1   1   1	GGGGGGACGA GGGGTGACGA GCTATGACCA TCTCCACCCC	GAAACACTC GCAAGTTCAA GCAAGAAGA ATTAAAAAGC ACAAGATTCA GATAAAGGGCTTT TTTTCCQAA TCATCTTTAA AGCAGCTTT TACCACTTC CCTGGTTGTT GAAATTGG	GGCCACAGA TGCTTAACGT GAGCACAGAC TGAATGAGCT	Seq ID NO: 103 Protein sequence: Protein Accession #: NP_006774.1	11 21 21 CONTRACTOR OF THE STATE OF THE STAT	Seq ID NO: 104 DNA sequence Nucleic Acid Accession #: NM_020411 Coding sequence: 86-526	11   AGGAGCATAG GGAACCTCAC	ACINACIONE TICCOATON CENCTIONES GOGGACTOS OFFICENCIAS ACONACIOS CONTECENA GANCAGIGA AACOAGIGA CONTECENA GANCAGIGA CTGANAGITOS GGATOCTICA ACAGETOAGA TECENGIGGE GGACATGGAN	ACCOGGATA ANTERGATT TODOTTECKS ACACTOTALA ATOCCAGANG CAGOTGANGA ANCALGGGA AGENGATITT ATATTAGATA CAGETITECAC CHANANANA ADAMAA	Seq 1D NO: 105 Protein sequence: Protein Accession 8: NP_065144.1	1 11 21
vn •		15	20	25	30	35	. 40		45		55	09	9	70	75	80	85	

\*\*\*\*\*

S1 DHVIXOTAVB LCIREDITOR LIGCOFFICY KANAVGATEC VVGVPPEAIN

922**2** .

FVCNTLQPGC KRNDPKDIED IDPCPNLVDC HPWRALKESK

CANOTICAL CITOTICS CATORICS CATORICS CATORICS AND CATORICS AND CATORICS AND CATORICS AND CATORICS CATO

85

8eq ID NO: 100 DNA sequence Nucleic Acid Accession #: NM\_000673 Coding sequence: 101-1225

\$

ATOTOMAGOS AS OTSTANDATES AS AGAGITOS S TOTOMAS S AGAGITOS S TOTOMAGOS S TOTOM

72

8

2

S

င္ပ

PCT/US02/12476		·		
120	11120 11120 1120 1120 1120 1120 1120 11	130	56 1120 120 120 120 120 120 120 120 120 12	60 120 180
нтотоннт АВ Отроз И. О. С.	1   CONCENSE CADACCAACA COCACCAACA TOCACTATAGO ANGTATAGO CTCTOCTOOTO ANGTATAGO CTCTOCTOOTO ANGTAGO AN	51 EDMLEIVLER TTPIGEMICA	18.  Oleanaucto, Arroccuca Arroccuca Controller Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Arroccuca Controller Controll	s1   vvgogranr addreskuyy Glalafsvyh Tadnageego
LEPLIREDO PTOTOHETAS MKVICKECIS GTPGIMILDIO	Accorded Galerian Control Co	41 	41   Landacchin canadachin canada	41 
 BPATRVPEUM RIQLÆSDCAT	11 CCGCAGCCC CCCCAGCCC CCTGCACT TCCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCAGCA TATCCAGCAGCA TATCCAGCAGCAGCA TATCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	31: UNTLKAPLR BATILLOTOYD LOLXQMEEPC TURNOE	11  Interpreted Agencia Agenci	11 EKGESTEGER EKGOVODIVL YQEADISK DSTYDSTLIN
LAP SPYMOTERSC. TOT LHIGSRGIKI AG ENGPOV SEQUENCE SEQUENCE 1597		107 Protesin sequences 111 21 11 21 11 21 11 ELPLACTHE SULPHINITY VARIATION KWKINTYVAN BINGOPTIAN RULPHINITY 108 DNA sequence 108 DNA sequence 108 DNA sequence	11 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	equence: 006133.1. AAPMKGAV BYREKVBT I I DBARBA ADLHTLSE
186443 CCLOVYPRAP CCLOVYPRAP ESHCROPEAG 106 DWA se d Accessio ence: 99-5	11		11	109 Protein 11
WO 02/( HLAMCPPQCA PREPVHEST GOVNWIIPH SEQ ID NO: Nucleic Aci	1 CATCCCTCT TCACCCTCTOS ACACCTCOS CACCCCCTOS ACACCACA ACACCACA ACACCACA ACACCACA ACACCAC	Seq ID NO.  I MULL MENDER SEQ ID NO.  NUCLULA COLUMB SEQ ID NO.	TCCSAGCEA TCCTAAAAG TCTTAAAAG TCATAAAG TCATACAAA TCATACAAA TCCTATAA TCCCAAAG TCCCCAAAG TCCCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAG TCCCAAAAG TCCCAAAAG TCCCAAAAG T	Sag ID NO. Protein Acc  1 1 HERABLIQVA VLB9IEQKSN VLB9IEQKSN YEIANGDYYRY YEIANGPEEA

					2CT 1320 CCGG 1380 CCCT 1460 CCCT 1560 AGG 1850						77VL 240 JERT 300				TOAT 720	
7	NTGA AGGATUMAC NAGG AACCETTTOO CTGG TGCTCCTGGT		MACT GCGACCCCCA CAGA CCTGCGTGGC CCCG CCCTGCAGAG CTGG GCCCATCAT	COCCO TOCCCATTOO TOO ACUTOCAGGA ATCO TOAACOTOCA CTOO OCCTUTACGC		CAGO CTCAGGTTGC AGOT CTTGCTTCTA CAGO TGTCCTCACT TOGC CAGGCCCACT AGOG CATCAGCCT   AGOG CATCAGCCCT AGOG CATCAGCCCT AGOG CATCAGCCCT AGOG CATCAGCCCCT AGOG CATCAGCCCT AGOG CATCAGCCCCT AGOG CATCAGCCCCT AGOG CATCAGCCCT	CACT CACCACACACACACACACACACACACACACACACA	DGGG CACATAGAAG CTGC ATGTAAGACC CCAG ATGAGCTGCA TCCT GCGATCAGCT CCTT TAAAACGTTC TCAT AGCCCAGATA		51     CLPA CNCVUKPSE 18PR VGKIVMTAAT DYVL CSPEMQERUL	DSNR SDRYIAI SHSR QVVNQM CLLA PSQLEKI	4-		MATTERATOR AND TETRATOR AND TETRATOR AND TETRATOR AND TETRATOR AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND COORDINATE AND TECHNOLOGICAL AND TECHNOLOGICA AND TECHNOLOGICAL AND TECHNOLOGICA AND TECHNOLOGICAL AND TECHNOLOGICA AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICAL AND TECHNOLOGICA AND TECHNOLOGICA AND TECHNOLOGICA AND TECHNOLOGICA AND TECHNOLOGICA AND TECHNOLOGICA AND TECHNOLO	ATT TECTTERATE THE ADACTACA THE TECTTERATE THE TECT	TECT CACCEGAGE SECT TCCCAGAGA NTAC AGACACTCAT NGA AGAGAGAAA CAT AAAGATCAAA
DOCK GACATATCHO		TOCK ANOTHORICS TOCK ANOTHORICS TOCK GEORGEANCE	CUNT OCCOPODA CANT OCCOPODA GAGO CTOCTOCCCO	CACO TECROCOROS CACO OTECTOOTOS CATO CTGCCCATCS GOAG AAGCCCTOS	OGAG COCACCAGO OTCC GTGCCATTCO CTTC GACACCTTCT 'AAAG GACATCCGCT 'GGGC TCCCAGAGCT GAAA CCTGAGTCTA	KANDA ETOCOCCAGO KETAG ANAGEMAGOT KOMA ACATOCCAGO COOT CAGOTTOGO TTACC TTCTTAGOOG	CCTC CCCCAGGAT CCGC ACCCTGCACT TCCA CTGCACAGTG TTCC TTATGTGAAA	ATTCC ANGOCACT  TOTAL ACTOROGOGO  CATO ACTOROCOTO  COTO COCNETICO  TOTAL	41 	LGCO RVA 1000SNR OCKP LALYAPSNSR TPDT PSHHRTCLLA	<b>.</b> \$-	COCO COCOACOMO TOTT COCOSAAGOS COMO CTOATGAAGT GANA TCTTAAACCA	CAMO TCATCCCATT TICTC CCCTACACA ATGG GAGATGAAT TATGG GAAAGTACA TTGG TGAATGCCCT TTGG TGAATGCCCT TTGG TGAATGCCCT	CCAC CTCGGAATT CCAC CTCGGAATT GGGG CACTTCCTCC GGGG AGCAAGCT TGCT TCCTACGCT GGGG AGCAAGCT TGCT TCCTACGTC GGTC TAGAACAACAC	TTTO CTOCTGCTCT AND GAOGACCOCT GANT CAMOGATAC GATA AMGAGAMA TGTC AMGAGAMA	
	ACCEPTION CHACTERIA TUNGETICAN CECNITIONS CETTANACTA CECNITIONS	TOCTOCCCO, OTACCTORAC CAGOGCACT OCTAGACAC GCAGATTOT CATGACTOCT	GCAGGACCC CTGCTACGTG CCTGGTTCTG CTACTTCAAT GCCCCGAGAT GCAGGAGAG GCGACGACCC CCAGAGCTCC	COOCC ATTACTORGE TACAT COCCCCACO INTETT COOCCCATC ATCAA CCOCCAGAG	TTOTOMACCA GATGCTOGAG CCTACATATC TCTGCTOTC ACCACGAGA GATCACCTC CCGGCCTGG GAAATTAAAG TOTTAGGCTG GGGCATGGG GAGGGTCA CACAGAGAAA	ATCTTCCTCC ADACCOCADA ATCCTTCCTTO CCAGGGCTTC AGACCCTGTA CACCCCCACA CAGACCTTTA CCTCTCGGT CGAAAATACA CTCCCTCCC		CCMACTETA ATAMAGA TALCAGGETT TATCACCMO AGCIGGECT CANABACTET OTTICCACA GIAMACCATE TAMAGCTOC TTACATOGAC TAMAGCTOC TATCATOGAC			LGRIINGKOP GRENALLGCO IVNVQSVDBA IKTINKQEKP FOGVGHBGNG KYHGKFTFDT. BCTLL	H_004456		CTTGGATTTT CCACACAG CATAATGTAT TCTTGGTCTC ACTAACAT CCTATATGG ACTATAAAA AATTATGATG TGAATTTTT GTGGAGTTGG		
ě.		CTCCTAGGA TITAL CTCCTAGGA TOCTO CCCCTAGGA CAGG	AACCOCTOO GCAAO AACCOCTOO CCTOO GTCTTGTOCA GCCCC COTTTCTATO GCAC	CAUTTCCAGC GGCTG AACGAGAGCG ATCGC GTGATGCAGG AGGAG GAGGCCATCA AGTTC	ACCAGACAGO TTOTO GAGGGCTTCA CCTAC ATOGGCCGGT ACCAC CTCGCCCCT CCGGC AACCAGCAGC TOTTA CACCGGCTC CAGG	ACATCACA TTOTT ACATCACTOC ATCCT ACATCACTOC AACA TCCCCAATTC CAGC GTOTCACCCC ACATCACTOC AC	GCCCATCCC ACTO TCTCTGCACC ACCCC ACTOGGAAA CTGCG GTCCCTTGAC TTCTC	OTCACTTATO CCAM CACATOCCO TAACA COTATOGAAA AGCAC TACCACOGCC TAAAA AACCTTOTT TAAAA TOGCCCTCT TOTT	Protein sequ	11 21 	YGDDPQSPN LGRII QEEIPGPILP IVNVQ PTYISLLSVP FGGVG QLLRWGM03Q BCTLL	100 00 00 00 00 00 00 00 00 00 00 00 00	CANCECEGE AACH GENAANNTC TEAGA AACTEAAAC ACTEX ATCOTCAAN AATTT			CCCCACTT GGAGG CCCCACAAA AGTC CCAGCACCC CACCA GGACTGAAAC GGGGG CGAGCTGAAAC GGGGG
=		AGAGAAGOTC CTOG OCTGOOCOGA CCC CACAGGGAGC CCTC	TOTCACCCTO GAOC GACCOTOOCC AACC CCCTOACTAC GTCC CACCATCACC COTT		CTTCTCCAAC AGON TOUNGOCAAT GAGO CCACAGTOGO ATGG CACCTGCCTG CTCG TACCGACTGG AACC OTGAGGGTCC CACC	OCTANGET CON TOUGHTO ACAT TOTOGOGIAC GETS CACCEACE FEEC CACAGOGICA OFFE	TTCCACCTCT GCCC CCCACACTGG TCTC AGCTCCATCC ACTG CTGGGGGCAA GTCC		U	1 	PALQSTITRF YGDDQGS VDVQSTEPVM QEEIPGP SSGSFCONEG PTYISLLA RYPPYIDMG QLLRWGM Sec ID NO. 112 DNA	letc Act	DANTTCCOGO CGAC GOCCAGACTO GGAA GAGTACATOC GACT TTTAGTTCCA ATCO	AATOCAOTICO TAIC OTGOANDATO AAAC AATOTACTI TCAT GAATOTOCOTI TTAI	MANATTORNO ATCH MANATTORNO AGGE GRANATATA ANGA CCCANCATA ATCH CATACOCTT TCTO	CCACATTT ACCA COGATAAAA ACTAGCAGGC CCAG AGGGAAGCAG AATGAAACTT CGAG GATGAAACTT CGAG
8	F 28 3		2 2	2888	336843 70	25 25 25 25 25 25 25 25 25 25 25 25 25	2884		04		50 PAK VUV 5508 87791 55 668				25 25 25 25 25 25 25 25 25 25 25 25 25	8 8 5 8 8

CACAATTOO T CACAACTTOO O CACACTOCO O CACACTOCOO O

Seq ID NO: 110 DWA sequence Pucleic Acid Accession N: DM\_000695 Coding sequence: 407-1564

2	
፰	
7	i
8	
2	
Ç	
-	•

Seq ID NO: 117 DNA sequence Mucleic Acid Accession #: BC012178.1 Coding sequence: 204-2285

PCT													
	•											•	
11111111111111111111111111111111111111	. 3820	120	7 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		120 180 240	6 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		9		, 52,000	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	250	960 1020 1060 1140
MOCHANAT COCATACTOR MANTOTOR MENTOTOR METANOTOR CECAGANIC CECAGANIC METANOTOR METANOTO	AAAAA	51     ERTEILNGEW YEWBLOONF   PVELVMALOO   PPOEKTTAERL	KYDCPLAIPPH GGRRRGILPH NBRGTPINM VKESBIIAPA DBBCPCVIAQ ADMDBRWVB ADRRGIVYPK PAKRAIQIGE		81 	COTCOANTCT COTCOANTCT COCCOCCACTT CCACTCACTT	5	ВІДМУНУНІЯ		51 	CTGCATTTGA TTGGGAGGCC ACAGAGAGAA	AGCGAGAGAA AGCGAGAGAA GACCTCTGGA TCTGTGTTGC	CONTRACTOR  ANTAGENET
CTTOTOTOTO TOCOCTITICO TOCOCTOCO TOCOCTOCO ATANTICAT GOLANOTOTO GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA GCTATOCAA	AMMANAMA	41   MFSSNROKIL LNAVASVPIN RECOFINDSI	ENTIFECTORY BRITIPERS BRITIPERS BRITIPERS BRITIPERS BROCHPROPC DPOLCLTCCA YCGBISGOB WYRCDHRIGI		41 	ATCTGGGGAT AGTGAATACT CACAGGAACA AAAAGTTCTT CTTTTGTTCA	=	BENRRIGV00		41 	CCCCACATOC GOCAGGAGCT TACCACACT CCTGGGCATG	GOCTGGAGC TGGGCAAAA AGAATAAAA CGAGAAATAG	TOCTOCTACT ACCACACCT TOTTTACTC ANTAGAATCT GCAGCCTTGG
AUTHORICA CONTICTION CONTICTION CONTICTION AUGUSTITION OTCHANA ONTICIONAL ONT	талсттал	31 	SURFICHE SURPOSELIS AKEPAALLA ENDKEEEK PCAIARLIGT DOSSNHVINY CPCYLAVRGC PVQKNEFISE VNPNCYAKW		11 	AATGAAGTTT GOTAGTATTC CTGTATTCTT TGTTTAAGAT	=	QVPKTHLMSE	cluster	11 	TTAGCADAC CCTCTTBAGA ATGCCTATAA TCAAGACTAG	CACTCCAGCA CACTCCAGCC CTTATTTTOO ACGTTTACAC	OTTACTIC AGGGCTTTCT TCAGCMTTC ACTTAGGTCA 19101TGCAA
CCTTOTICA CAAGCATTCA CAAGCATTGC CAAGCACTCCAA CAAABATCCT CTTATACAA CTATTCOOTA CAGTATTTT CAGCCAGCT CTCCCAGCA	ANGANTACT ANGANTACT sequence: P_004447	21 	TPHIDDRNAK GPOCYOHLED DREAGTETGG DREAGTETGG AHCREIGLK AHCREIGLK RCKAQCNTKO VACHGIFTICO GNKIRPANHS RENBIP	(4 DNA sequence Accession B: NM_001827 nce: 96-135	21 Crosscrass Crosscrass Crosscrass Crosscrass	CATTACALUA GATCAACAA GAGATATAA TOTGCATUAG TACTGTAAGA GAGTTTACTG	In sequence: NP_001818	KYPDEHYEYR HVMLPRELGX RPLPKDQQX	5	21   	ACCAGANGT GGCTGGACCA ATGGTGCCTC GCCAGGAGT	DGAGOCTOAG TACCCCACTO TAATAATAAT GAAAGAAAAG	CTTOTOOMA AGOAACCA ACCTTTOTA AOTTAACAC CCAGTGTTTO
086443 ATCCACACA ANTITITION ANTITITION ANTITITION ANTITITION ANTITICACA CONTITION ANTITICACA ANTITICACA ANTICACACA A ANTICACACACA ANTICACACACA ANTICACACACA ANTICACACACA ANTICACACACA ANTICACACACA ANTICACACACACA ANTICACACACACA ANTICACACACACA ANTICACACACACACACA ANTICACACACACACACACACACACACACACACACACACACA	CACCTGCAA AACTTGAAT 113 Proteir	11 	QUPCALPPEC TETALDNKPP NVLESKOTDS ENSGAEASP KKKRKHRIMA SECONRPPC KKHLLIAPED NDFVVDATRK	114 DWA secid Accession	11 	ECTECAMA INTERTATA CATCCATACC GCAAGTAGOT GTGCCTOTTT TTAMMANA	S Prote	KYPDEHYEYR RPLPKDQQK	d Accession	11 	ACCTOSCTCA TITISCTOAGC GATCTTTAA	CAGCTACCCA GAACTGTGAT ATAATAATAA CATTTGGGTA	OCCUPATOR OCCUPATOR TOTCHARATI
WO 02/ CCCTOTANT TITTUTOMA TITTUTOMA TITTUTOMA MANACTOCA ACMANTE ACMANTE OTTANTO ACMANTE OTTANTOMA ACM	Seq ID NO:	1 	ATPATTARED ATPATTARED HIGGRESTPTI KRHIEDPERV PAEDVOTPPR NFCEKCOCS CROCSIOROS HACSFLPHLM ELFVDYRYSO	Seq ID NO: 114 DW Nucleic Acid Accel Coding sequence:	ASTETICEDAE COSTETICATA COGACAGTA	TAGAGACC TITICAMIT ACAMICTIT AMIGCACT TITICICITAM	Seq 1D NO: Protein Act	MAHADITYSD EPEPHILLFR	Mucleic Acid Acces	TCAGACCTCA GCATCTGGAC AGAGCTGTGT GCAGCCAACA	CCTTGGAAGG TCAAGAATTC AGTGTGGGAA	CCTGTAGTTC AGCTGCAAT CCTGTCTCAA TTTGAGGTGC	CATACOCA CACATCCCC CCCCTCCCA CACCOCATA FCCTCCTCCO
<b>s</b> 0	<u> </u>	\$3	۵ <u>۶</u>	9	45	02 : 53	3	S	22	2	22	00	82

TITUTICE GEGGGCTG GECCOGGCT CONCENTRATION OF CONCENTRATIO

လ

Seg ID NO: 119 DNA sequence Nucleic Acid Accession #: NM\_006500.1 Coding sequence: 27..1967 

S

2

13

ຊ

25

30

35

6

5

S

55

•	ē	ς.		•																																																									
												•										Ī																																							
		300	9					2	999	130	780	840	900		2	1020	1080	1160	1260	1260					1200	1560	1620	1680	1740	1800	9			1980	2040	2100	2160	2220	2280	2140			100	25.20	2007							9	22	3190	3240	3300	3360	3420	3480	3540	
		Ļ	,	{ }	3 6	5 5	3 (	5	Ę	ę	ş	5	¢	1 6					ü		:	: 1	:			8			8								_	_	_	_										_										ğ	
		משתשתשת	DO TO TO TO					MAIN	MOGGACAG	CTOCCCACTO	ACAGMAAAA	GAAATCAGGT	CONTRACTOR	į		ATATEMETIC	9	AGTAGCCAGG	COCCIOIGO	J. Contraction of the Contractio				ACCOUNTS OF	ACCCCCGGAGG	SC GG GG TC	ACCACTOOCC	GAGAGAAAGC	ATCCTOOLC	TOTAL PROPERTY.		STATE OF THE PERSON		COMMICACIT	200000	CCTTTCAGAG	TCAGGGACCA	CCCCAOTCTC	TATOGCTOT	TOCTOCCC			5	מבוברותום	TACGIGCOM		CIACING AND	ALI LOOMAGE	201000000000000000000000000000000000000	TANKSANANS TANKSANANS		ATATATATATATATATATATATATATATATATATATAT	CCAAATGAG	prototoro	AATTTGCAA	TATGAAAAT	OTACCACAGO	AGTTOGCAGC	GAGCAGACAG	CCTOCCAGGC	
					_			_	•	_	ភ្ន	3	Ę	į		Y	ě	Ž	9		į		į	3	Ų	ğ	ğ	8	ATC	į	į	;	3	8	ខ្ព	Ê	ភ្ជ	g	Ě	į	į		1		3	Š	Ś	į		ì			Ę	6	2	TAT	Į,	Ę	9	É	
	•	TOTALDAGE				38	3	3	GAGTATTETO	CAACTACCOO	g	8	GAAC		3	2	Ę	Š	AAGG	2	1	į		3	B	ž	វ័	ð	200	E	Į		3	ğ	Ę	ğ	ŧ	900	ð	8	1	18	3	3	į	3	;	į	1	<b>{</b> }	<b>\$ \$</b>		9	ě	É	TATA	200	500	5	900	
	-	Cuch	í					CAMECUACI	5	È	TTTCTACCC	CCACCOCCTO	CRACCACARC		3	GOACACCATO	CONCCUAGIO	TOACGCACAG	OCTOGRANGO	CHECK COMPANY			3	TO LANCOOL	narcran	GOCKANIC	CTCCAACACA	CACCTCCACA	CATTGEGEG	CHICKARTON			3	GCATTAGCCC	CACTOTICE	CTOCACACC	MOCCOCTT	NGCAAGGAG	TTTACACACA	CTOACCTOD					CCLIMANA	S COCCUCA				CLANGRAPHA		CONTRACT	CTAGAAGGG	CTTCGGGTGT	CAGGTGTGTA	TATATATATA	TICTACATOD	AACCOTTTCC	AGCTCTACCA	GCACGAAGGG	-
											-	_	_			_	-	-	_	_	_	_				-	_						٠.					-		-			_	_						- :				_			•	-	-	-	ŧ
		AGAGGGAAGG						ALGERICA CONTRACTOR	ACACCTTUCA	בהמפונה	correcerus	PANGANGO	PCAGCATCAG		3	CCTCGAACTT	ATOTOTOTA	CCCTGACCTG	CAGACCAGGT	STOCK OF THE STOCK	CONT.			ייייייייייייייייייייייייייייייייייייייי	CACCCTUAN	COMOGNOCI	TCACACCAGA	CACCCACA	regredence	PETATABGAS			3	TCGATCTGAG	מרכככומכו	CTCCCCTCAC	TTGGCCCTGC	MOCTCATCCC	GIGITATIC	GOTAGCCTC			3	רוברומרונים			MCALGOTON TO THE	TOTO COLOR		MCICCOIC.	1011110		CONTRACTOR	CTOGCTAGAO	TOTTTO	TATATGAMA	RICHTETTA	NOGCACACA	WATGGCTCA	TATOACOCA	TICCOTCCA
		AGAG	į	į		į	3		Ď	Ę	g	ş	1000	l	ì	E	Ę	g	5	000					ğ	ð	ភ្ជ	8	5	į	į			į	Ę	É	É	ğ	Ė	100		; {			3	3		3 8	3	3	į	į	g	e	ATO	TATA	ţ	980	3	Š	Ē
		č	ĺ	į	;			5	Ē	Ë	Ę	5	1		1	3	ţ	ğ	á	2	5		3 (	Ş	5	ţ	ÿ	ğ	į	Ę	Ì	į	3	Ş	ğ	E	ខ្ព	Ę	3	ģ	į	5		3		3 5	į	3 8	į	3 8	į	ξ	Í	ĕ	TAT	Ž	ş	₹	9	ğ	g
		COCCADOCC		11000000			3		MOTOGRAFIE	GCCCAGTTT	AGGGAAGTC	<b>ProdoMrc</b>	CCACCACACA			CANTOTCAGO	いると	ABCABCCTC	AGAGAGAGA	CACCOCCO					COMPLECTION	100,000,00	TTARCCACCC	CCTCATACCA	OCCUPANCE	THE PERSON		100000000000000000000000000000000000000		GAGAAATACA	1000 F 1000	AAGCCTCCTG	AGGACCTCAC	CGTTGAGTGA	CTTGCAGAAC	CAGCTGAGCT				TOCOM CALC	AGLEAGGRAL	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TW	CALCINGCI	1001001000	400000000000000000000000000000000000000	ANCACAGCIA ACCROCIOCO			ACCAAGGG	AAACOGGGC	Gregoratar	TOTATATATA	AATCATACAT	TACAACCAAA	GCTTCTGAGC	AAAACOTCCC	CTTCCTATCG
									7		. 1	_				_	-	-			_		-		_	٠.	-	-	_	_					٠.			Ξ.	_	_			-												_		7	1	Ξ.		_
	5	Ş	0000	Š	į				5	AGACAAAGAT	Ě	Š	g		Í	3	į	8	bop	ć	1				5	É	ş	ğ	8	Ė	ć	į		3	Ę	ğ	ğ	Ę	Ę	Ş	į	į	į	3	į	5		į		3 5	į	2	Í	QA TO	5	Ā	ð	ž	ğ	8	É
	WO 02/086443	TOTOCCCAG	CONCRORDE					TANAMA TOP	rerocuerce	ğ	GAAGGAGTCC	Agradaaccc	TOCCAACCC	CONTRACTOR OF STREET		INCOCALIAI	<b>ACAGGAACTA</b>	ACAGGAAGGC	CCAGTGGCTG	TO B COUNTY A A.	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN			3	ACATOCACAG	ACCTOTTONA	OCTOSTICAL	CACTGCCAGT	GGAGAGCCCG	Carper Carper Carper	THE OWNER OF THE	TARGETTA	ĺ	AGACCAGGGA	cccraccrag	GACTAGAGAG	TAGGACCTG	ATCTCCTCCA	AGGAGAGTTT	CTCCTOCCAG			3	CAGINETIC	11000000	200000000000000000000000000000000000000	A STREET	ACH POCTAT				CABADADGAG	ACTUCTACA	TTAGGGATGG	GCATACATAT	FATATATGTA	TOTCCCAGAA	CCTOTOMAC	COTTACCTCT	TTCAGCAGC	AGCTATOTCC
	20					-				- 5	_	_	٠.				_	_	_	•			٠.		0	_	_	_	_	-	_			-	_	_	•	_		_	_		٠.					-	-	•		_			_	•	-	-	-		
	8	CATCHICA	TO TO TO TO TO					101717		POSTTANAGA	DOMICCICAT	rereceroda	APTEROCHE	CONTRACTOR OF THE PARTY OF THE	3	TO TO THE PARTY OF	reagranace	CCCTGAGAG	ACCTCGAGTT	TICE CONTROLS	CACCATACT				MCAMERICA	POTTOGRADAC	retreerous.	POGGACTIC	DCCCCQQQCC	COCCOCC	STORE STORES	TANGER		SOUTH COM	שמממכננו	CCTCCAAAGG	DOCCACTGGG	DICCACCACC	CCGAGCGGGT	MANTACCTOS	000000		,	MANAGERIAL	700000000000000000000000000000000000000							STORES CONTRACTOR	TAGGACCAA	MANTOGIAC	TOTOTOTAL	mornicen	MAGCITAAT	AACCTGGGGG	AGAGATCAGG	TACCCTACT	COLLAGGAGG
		Ş	į	5	} !	į	5	2	5	ğ	ş	٤	E	ě	3 !	3	é	g	Ž	Ì	ί	į		3 3	1	Ē	ដ្	ភ្ជ	2	Ş	Į	į		3	5	g	8	g	g	3	ŧ	5 8	3	1	Ş	3 8	5 5	ś (	; ;	3 5	3 6	E	E	ş	E	E	ş	ž	Į į	Ė	Ž

Seq ID NO: 120 Protein sequence: Protein Accession #: NP\_006491.1 8

	9	120	180	340	300	360	450	480	940	909		
15 -	SOSOGNLBHV	ERI FLCOGICA	QVINYKNGRP	SCHAPKESRE	TREAEESTIN	AAPERQEGES	VPBIPGLNRT	BECOCCOPORY	GLSTSTASPH	RRSCKORITL		
<b>;</b> _	KOLPRLVCAP LLAACCCCPR VAGVPGEAEG PAPELVEVEV GSTALLKCGL SQSQCKLSKV	WFSVHKEKR TLIFRVROGO OGSEPGEYEG RLSLÆDRGAT LALTGVIPGD ERIFLCGGER	IQUNDLAIPU NSKEPEEVAT CVGRNGYPIP QVIMYKNGRP	Kebrotvhi qesqtvesso lytlosilka quvredkoaq pycelayrla sommkesre	KYMLEVEPVO MLKEGDRVRI RCLADONPPP HF818KQMP9 TREAERETTN	RKEHSCRYEC CAMMLDTMIS LLSEPOELLV NYVSDVRVSP 1	AGGGYRCVAG VPBIPGLNRT	TISMWNGTA	BLLETOVECT ASVOLGRATB ILFLELVNLT TLTPDSNTTT GLSTSTASPH	PLYKKGKLPC RRSGKQEITL	YIDLAH	
ī-	PAPELVEVEV	RESECTA	NSKEPBEVAT	<b>OLVKEDKDAQ</b>	RCLADGNIPPP	LLSEPOELLV	STDOVLERGP VLQLHDLKRB I	PWMAPKERKY WVKENWYLNL SCEASGIIPRP 1	ILPLELVNL?	KLPEPEEROV VIVAVIVCIL VLAVLGAVLY	BVKSDKLPEE MGLLQGSGGD KRAPGDQGEK YIDLAH	
12 -	VAGVPGEAEQ	COSEPORYED	VOLUMBLAIPV	LYTLOSILKA	MLKEGDRVRI	<b>QAMNLDTMIS</b>	STDOVLERGP	WVKENDOLAL	ASNOLGRATE	VIVAVIVELL	MGLLQGS6GD	
<b>=</b> _	LLAACCCCPR	TLI FRVROGO	RVYKAPEEPN 1	<b>OBSCALVESSO</b>	KVALEVEPVO	RKEHSCRYEC	LTLTCBAESS QBLEFQMLRE	PWMAPKERKV		KLPEPESROV	BVKSDKLPEE	
	MOLPRLVCAP	DMPSVHKBKR	PRSQEYRIQL !	LKBBIOTRUHI	VTVPVPYPTB :	DNGVLVLBPA	LTLTCBAESS	QLVXLA1FOP I	LSTLAVLVTP	TRANSTETER	PPSRKTELVV	
;	ç				ç	2				36	C	

Seq ID NO: 121 DNA sequence Nucleic Acid Accesson 1: NM\_018306 Coding sequence: 60-673

2							
:		п.	12.	11.	₽.	15	
33	ATAGECTACA TOGAGACTEC AAGATGTAGA CCCAAGAACA CCTCATCTEC	ATAGECTACA CAGAGCTCCC TOGAGACTCC AGGAGACTTC AGCATCCTCC TAGAGAGA CTATGAGAGA ACCAMANAA ATATGAGAGA CCCAMATCTTC TTCATCCTCC T	CTIGCTGCCC TCCCAGCCTC ACAGATTTCC AACAGTCTT TCCTCCTCAG	AGACAAGCTO AGAGCAAGA ACAAGCAAGA CTTCCTCCTC TTCCTCGGGCA	_ ~ ~ ~ ~ ~ ~	AGGACCACA GGAAAAGCA CAAGTCCAC AGAGAAACAG CCAAGTCTACA TTCTCTTCT CGGGAGCCT GACGTTTGA	37,000

20 15	WO 02/1/86443 AGATOGUETE CARGAGETE GUARANTE CTGGARDOT GUINCCTET GOS GUCTECOLAS GARGACET AND CONCOLOR OF GUINCATE GUARANTE GUCTECOLAS GARGACET CHOCAGO, OF GUINCATE CONCOLOR GUARANTE MANASA GUINCATET TECHTOTA CTGGATACT OF NOGOTICAT CONTROLL CHARACT CHARACT CONCOLOR NOGOTICAT CHARACT TO CONTROL OF GUARANTE CONCOLOR NOGOTICAT CHARACT TO CONTROL OF GUARANTE OF CONCOLOR DESCRIPTO CONTROL CHARACT TO CONCOLOR NOGOTICATO NOGOTICATO CHARACT TO CHARACT TO CHARACT CONTROL NOGOTICATO CHARACT TO CHARACT CHA	DEGRANTOS DEGRANTOS STETICAS DE STETICAS DE PROCESSOR ANTICAS DE ANTICAS DE COCCETTOS DE ANTICAS DE ANTICAS DE COCCETTOS DE ANTICAS	244995599993333333
	9sq ID MO: 122 Protein esquence: Protein Accession 8: NP_060776		
35	1 11 21 11 21 11 51 51 61 61 61 61 61 61 61 61 61 61 61 61 61	51.     SEGEVERES   STEVENYRI   GIYFGLVYRI	
	11	51  - coaccaaacc Tccaacatcc acsacaacad	
	ТОМИСТИКИ ПОВОДОВ В ОТВЕТИТЕМИ В В В В В В В В В В В В В В В В В В В	CACACACACC COTCTCTAAA TCATTACCAACT OCCCCTAACT	
	сттитост отведение отвежения отвежения гитотем и и и и и и и и и и и и и и и и и и и	GAGGATGGAG GAGTTCCCGA AATGAGGATA CTACAAGTTC	
	ATTGATICAT GTAGOGITT TCAATATGG CONTITTEC ATTACTA ATACATTA ATACATTAT TTACTATAT ATTACATAT TTACTATA TTCCAATATATATATATATAT	CTATAAGTTT ACGAGAGGTG TTATGTTTAC TTGCATGGAT	222
	TITATCTICA TITOGOGING ANAMITATI TITOGOMOT ACTITICANT TANGCINCA, TATOGCOMO CACOTOGOTO CACACTOGOTO OQATCACCOMO AGTICANAMA TITOGACCA ACANAMATRA GCTOGOGICO GTOSTOGICO ACANAMATRA GCTOGOGICO GTOSTOGICO	ATTOADAMA ATCCCAGCAC ACTCCAGCAC	22222
	AACSAGACCC T TCATGTTAT T TCATGTTAT T AAATCATTA A AAATTATTA T	AGOTTCCAAA TOTCTCCAAA TTAAATAGTA AGTAGGACAG TTATTCCTTA AATTGGCAAA	22222
	ООАСТТСАТО ЛААСТОАОТА СТЛАВАТТТО ОТАСЛОВТА ТОТСЛОВЛА АС TTGCCATTT ЛААТЛАЮТТ ОТАСЛОВАС ЛАМЛИЛЛА ЛАМЛА	ACAACTCAGA	••

Seq ID NO: 124 Protein sequence: Protein Accession #: AAH22542 75

2		DPYELABLRB	THRPHSEDGE	CALENEDICO	
7	_	KODI PAGLIV	FOAFL PVHCR	CWARBEVAAP	KKKKK
=	•	BOLHTCRLLI	ARRESOCIEC	DKTIEFFILK	VTLLITILCS
21	_	LIKVKFGEST	LBKEGEVLIY	RMIRPRPDSF	LTVATBLVCB
=		COBITLEGE VLKDOPRED, LIKVKFGEST BOLNTCRLLI KQDIPAGLYV DPYBLASLRI	NITEANNYS ENPDIZARNY LSKESEVLIY ARROSQCIDC FQAFLPVHCR YHRPHSEDGE	GIVVNNPDL LAFCDQAGER RMIRPRPDSF DKTIEFPILK CMARBEVAAP CALENEDICO	NYMKYKBYY KIVILQVPVO LTVHTBLVCB VTLLITILCB KKKKK
-	_	MC9BITLROR	RNITEAVMVB	A61VVNNPDL	MYCHAYKEVY
		8	2		•

8 2 2

Seq ID NO: 125 DNA sequence Nucleic Acid Accession #: NM\_004994.1 Coding sequence: 20..2143 82

WO 02/086443

20.

<del>6</del>

11 11 11 11 11 12 12 12 12 12 12 12 12 1	Lence 8: YM_000213 8: 8: WM_000213	11 41 41 41 41 41 41 41 41 41 41 41 41 4	COCTOCAGA GCCTACTGCA GCCTACTGCA GCCGCCGGGC GAGCCCCAGA COTCTGCGGGC	CCCGTGGACC TOTACATECT CTCAGAGAGA TGGGGCAGA ATTGGATTTG GCAAGTTGT AAGCTGAAGA AGCCCTGGCC CTGACAGAAG ATGTGGATGA	CTCMSCLAC CROSMICTIC CTRAGGEDO CTTCSATOC CACCAGGGDA ATTGGCTGG OCCOGADA OCCCACATO MICRITICAE TAYANGACTA ATTGGCCAA CONTENTAGO TRAANGAGTA CACCAGADA CANGAGGAG CTAGACCAG GYAGATAGAC ACCATAGAG CACATAGAGGAG CTAGAGCAGA GYAGATAGAGA ACCATAGAGA CACATAGAGAGAA	TCCTATAGCT ACTACGAGAA. CAGGAGACT CGTCCAACAT AACCTGGACA TCCGGGCCCT ATGTTCCAGA AGACGAGGAC CAGGTGCAGC TGCGGGCCCT	MACCAUMANA GLANCALUCA GGCATCATCT GTGATGTGTG ACCTGCACG GAGACTTCGT ACCTGCACT GCTCCACGG ACCAAGACT GCTCCACGGGGGGGGGGGGGGGGGGGGGGG	CTACOGODA BOCCOCTACO AGOTTCACT CTUCOAGTATA CUNTOCOCTACA ATOMOCCOCTACO CCATOTTCAC ATOMOCCOCA CATOMOCCO ACOCTACO CCATOTTCACA ATOMOCCO ACOCTACO CONTOCOCA ATOMOCCO ACOCTACO CONTOCOCA ATOMOCCO ATOM	CHAGGECT GOODGAND OAGACT CT CONTINUED OAGACT CT CONTINUED OACACT CT CONTINUED OACACT CT CONTINUED OACACT AT CANTINUED OACACT A	TOCACCOMO OTCACATOOT ATGGCCTCTO ACCACTTOOA OTGGTCCGCT GAAGGTCAC AGCATCAACC CCACAGAACT		GCCGGGGCA TGTGGAGTT TTATCCGGC CTGAGATGA GCAGGCACTT TGTGTGGG GCAGGTGG TGTGTTTGG CGCATCCTG CAGGAGGGG CAGGAGGG CAGG	AGGCTGGA GGGGCCGCA TGGGCCAGC TCACGAGTCA TCACGAGTCA ACCCCAATGC	TATTOGATE ATMATTAN TOCTOME ATMATTAN TOCTOME CTCCACAT ANTOTOTE CTCCACAT ANTOTOTE CTCCACAT CCCATALAN MATTERIAN CCCATALAN ANTOTOTO CCCATALAN ANTOTOTO CCCATALAN ANTOTOTO CCCATALAN	CROGRATICA BADGRAINA CUPININA CTROCCIAC CTRCCTATAD PAGGRAINA (CRCCATACA GADGRACOA CTRCCTATAD PAGGRAINA CRCTACATAG CTRCCATAG CTRCCATAGA CATAGAGAC TRACACATAGA CATAGATAGA CALCACATA CALAGATAR COCAACAD TRACACATAGA NACATRICAC CACAGAGATA CATAGACATAC CTRCACCATA
WO 02/086443	10 Muclaic Acid Accession 8: NM_000213 Coding sequence: 127-5385	15 meccacae crocoace o coccacae o	TCTCT000AC TCCCT010T0A ACACCCAGGC GCAGCTTCCA	TOTCOATGA AGCTCACCAG AGCTCACCAG AGACOGACAT CCTTCAAGAA	GAGAGCGGAT CAGCTGTGTG CCACCGAGTC GCCGCAACGA AGGACTACCC	TCTCCTCACT CCTTCAATOS GGACAGAGGT GGACAGAGGT	ACCIOCOTO ACCIONA ACCIOCOCA ACCIOCOCA ACCIOCOCA ACCIOCOCA ACCIOCOCA ACCIOCA AC	ACTOTOTOTOTO ACTOTOTOTOTO OTOTOTOTOTO OCATCOACAO	ACCCGGGCCT AGAGAAGG AGAGAGCGA AGAGCTACAC AGAAGAAGGA	GCCTGGCACT ACATGCTGCG GGAACCTCAA GCTTTGCCAC	TODGCCTOOC ACTOCOCCA ACAMOCTCCA CCATTOTOCA CAGAGAAACA	CCCTCACTOC TOBACOTACO TOBAGOCCAT CCATCATCAA GCCCCOOGGA CCCAAOTCTC	70 managrae and and and and and and and and and and	CCTTCACO CONTINUES OF CONTINUES	мастостого Астастого Ставатого с състемент с настоятила отстожент с настоятила отстожент с татестто с настоятого татестто татестто с настоятого татестто татестто татестто татестто татестто татестто татестто татестто та

9eq ID NO: 126 Protein sequence: Protein Accession N: NP\_004985.

S

Seq ID NO: 127 DNA sequence Nucleic Acid Accession #: NM\_004181 Coding sequence: 12-670

9
-
-
~
_
7
_
8
92
_
:-
-
L)
×
_

911	4300	4560	4620	4680	4740	4800	4860	4920	4980	2040	2100	\$160	5220	5280	5340	3400	3460	5520	5590	5640	
ACTOCOGAGO	TOGRADOCC	ACTGAGCTGG	CCTOCTCAAC	GOTOGICGAA	GOAAGGCTGG	GAGCCCACTO	cccacraata	CAGGCCCAAT	GCCAGCCACC	CCTCAGCGAG	GCCAGAGCGC	GOOCHOCOT	CACCCACACC	CCTOGAGGCA	GACCACCAGC	CCCTGCCCCA	CTCAGCTACT	GCTAGGTGTC	ATTTOTACC	ATGGTTTTOC	
ACACCOGIACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCCGAGG	כאכסאכדכדכ מככדסאכדמכ דממדמזמכככ	CTOGOGCCCA CATCTCTCAG ACTOAGCTCG	TOGAGTACCA GCTOCTGAAC	CAACATECEC AACCETGEE AGACETCGGT	CCAACCACTC CTACOTOTTC COCOTOCOGO CCCAGAGCCA GGAAGGCTGG	GAATCCCAGG TGCACCCGCA	отоссско	CTORDCTOOD AGCODCCACO	DUTGACCTOT GAGATOGCCC AAGGAGGAGG	TOGATOGAGA CAGCCCCCAG AGCCOGCTOA CCGTGCCCGG	GOTOCAGGCC AGGACCACTG AGGGCTTCGG	TCACCATAGA GICCCAGGAI GGAGGACCCI ICCCGCAGCI GGGCAGCCGI	GAGTACAGCA GCATCACCAC	CCGACCCTGG GGGCCCAGCA	GCCCGACACT	GCACCCACAT GGACCAACAG ITCTTCCAAA CTTGACCGCA	ocarectee agreement economics	CCCGCATGCA CAGAGCAGGG	GCCCAAACCT	CITTGITCTG CACITAATAA ATGGITTTTGC	
GAACACTCAC	CACCIACTOTO		GCCGCTGCAG GGCTACAGTG	AACCCTGCCC	CGCGTGCGGG		AGCACTCCCA		GAGATGGCCC	AGCCCGCTGA	AGGACCACTG	GGAGGACCCT	GAGTACAGCA	CCGACCCTGG	TOTOACCEAG GAGTITOTOA	TTCTTCCAAA	<b>OACTOCTOTO</b>		recreator	CTTTGTTCTG	
GACCOGCTCA	20122000	OTTCTCTOCC			CTACOTOTTC	CATCACCATT	CITICACTITO	CTCCCTGCAG	GOTGACCTOT	CAGCCCCCAG	GOTOCAGGCC	GTCCCAGGAT	OCTOCAAGC	ACCCUTCCT AGTGGATGGG	TGTGACCCAG	GCACCAACAG		ACCCCTGGGG GCCCAGCCCA	<b>acwagatoca</b>	GAGCAGCACA AGGACCCAGC	
COGACT ACAACTCACT	מאכדאכזככא כפכדכאככזכ	CCCCCCTOOT	GOTOCCAGCG	TOCATCOOCY		GTGAGGGTGT	CADOCTCCGC	TOAGCCCAGA	TCGGCTACCT	TOGATOGAGA	ACAGITICA		TCCAGCACC	AGCCCTTCCT	TCACCCGGCA	OCACCCACAT	STOCCACTAG	ACCCCTGGGG	CATGAAGGGG	GAGCACCACA	
ACACCOCIACT	SACTACTICCA	CACACGCCCA	CAGGAGCCGC	OCCURINAC	OACCTOCTOC	GOCCGAGAGC	TOTOCOCTOC	TTCACTOCCC	GGGGATATCG	GCATTCCUOG	ACOTOCCCT	GAGGCCATCA	<b>OCCODECTOR</b>	AGCCCACCO	GGCGGCTCCC	CONACCCTTA	CCCCCCCAT	CCATCCTTGC	TOCTGOGAGG	AAAGAGCTGG	
			,	^				•	2				,	2					2		

Seq ID No: 130 Protein sequence: Protein Accession #: NP\_000204

		;	1	7	:	40		
ç	_	_	_			_		
₹	MAGPRESPWA	RELEMALISY	BLBOTLANRC	KKAPVKSCTB	CVRVDIDGAY	CTDENTRDRR	9	
	CUTCABLLAA	GCOREBIUM	ESSPOITEST	<b>QIDTTLRRSQ</b>	MSPOCLRVRL	RPGERHFEL	120	
	EVFEPLESPY	DLYILMOPSN	SMEDDLDNLK	HONDQUILARVIL	SQLTEDYTIG	FORFVDKVBV	180	
	POTOWRPEKL	<b>AGOSNAMOSX</b>	PSPKNVISLT	ROVDEFRUKL	OCER I SCIPLLD	APEGGPDAIL	340	
;	QTAVCTRD10	WRPDSTHLLV	PSTESAFHYB	ADGANVLAGI	MSRNDBRCHL	<b>BTTOTYTOYR</b>	300	
લ	TODYPSVPTL	VRLLAKUNII	PIPAVTNYBY	SYYEKLHTYF	<b>PVBSLOVLQS</b>	DSENIVELLE	36	
	EAPWRIRSNL	DIRALDEPRO	LRTEVTSKMP	OKTRIOSPHI	RAGEVELYOV	QLRALEHVDG	. 029	
	THVCQLPEDO	KONTHUKDBP	SPGLKMDAGE	I COVCTORIO	KEVRBARCSP	MGDFVCGQCV	9	
	CSBOWSOOTC	NC9TGBL9D1	OPCLARGEDK	PCSGRGBCQC	GHCVCYGEGR	YEOOPCEYDN	340	
•	POCPRISOPL	CNDRGRCBMG	QCVCRPONTG	PSCDCPLENA	TCIDSNGGIC	MORGHOSCOR	909	
5	CHCHOOBLYT	DTICEINYBA	THPOLCEDLR	SCVOCQANOT	GEKKGRICEE	CAPKVXXXXDB	9	
	LKRABBVVVR	CSPRDRDDDC	TYBYTHEAD	APOPRIBITULA	HYCKOCPPGS	PHYLIPLLL	20	
	LEPLEALLEL	LOWRYCACCK	ACLALLPCON	RCHWVOPKED	HYMLRENLMA	BOHLOTPMLR	280	
	SCALKORDVV	RMKVTNAMOR	POPATHAABI	KPTELVPYGL	BLRLARICTE	NLLKPDTRBC	8	
:	AQLROBVEEN	LMEVYROISG	VHKLOOTKPR	COPYACKYOD	HTIVDTVLMA	PRBAKPALLK	906	
5	LTEXOVEORA	PHDLKVAPGY	YTLTADODAR	GHVEPOEGVE	LVDVRVPLPI	RPEDDDEKOL	960	
	LVBAIDVPAG	TATLGRRLVN	ITIIKEQARD	WHFEEPERS	VBRGDQVARI	PVIRRVLDGG	1020	
	REGVEYRTOD	<b>OTAQGNRDY1</b>	PVEGBLLFQP	<b>OBANKELQVK</b>	LLELQBYDSL	LACROVRRFH	1080	
	VOLENPRINGA	HLGQPHGTTI	IIRDPDELDR	BPTEOMLSSO	PPPHGDLAAP	ONPNAKAAGS	1140	
	RKIHPNMLPP	SCKPMCYRVK	YMIQCDSBSB	ARLLDSKVPS	VELTALYPYC	DYEMKVCAYO	1200	
2	AQGEOPYEST	VSCRTHQEVP	BEPCRLAINV	VSSTVTQLSN	ASPAETWGEL	TAYEVCYGLV	1260	
	NDDWRP I GPM	KOKYLVDNPKO	RMLLIENLAS	SOPPRITTURA	RNGAGNOPER	ENTINIATOP	1320	
	KRPMSIPIIP	DIPIVDAQSO	EDYDSFLAY8	DDVLR8PGG9	<b>GRPSVSDDTS</b>	HLVNCRMDPA	1380	
	PPOSTNBLHR	MITTRAMAYO	THESPHYPHR	VLSTBSTLTR	DYNGLTREEN	SHOTTLPROT	740	
;	STLTBV6SHD	BRLTAGVPDT	PTRLVPSALG	PTSLRVSWOE	PRCERPLOGY	SVBYQLLNGG	1500	
ያ	ELHRIMI PNP	AQTEVVVEDL	LPMHSYVFRV	RAQSQEGINGR	ERECVITIES	<b>GVHPQSPLCP</b>	1560	
	LPOSAPTLST	PBAPGPLVFT	ALBPDSLQLS	WERPRRPNOD	IVOYLVICEM	ACCOCRATAR	1620	
	RVDCDSPESR	LTVPGLSENV	PYKPKVQART	TECHTOPERED	INTERSODO	PPPQLGSRAG	1680	
	LYCHPLOSEY	<b>BBITTTHBA</b>	TEPTLANDER	LGACHLEAGG	BLTRHVTGEP	VERTLITEGI	1740	
9	Lethindoopp	5						
3								

LATHMOOPP UT

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession E: BC06472
Coding sequence: 132.,223.

	Courses and	corng sequence: 1344431	1677				
65	4-	<b>11</b> -	12.	#-	<b>5</b> -	51	
	cercorocco	CGGACCCCAG	CCTCTGCCAG	orresores	CCATCCTCGT	ccorccrcc	9
	OCC00CCCCT	30000000000	CAGGGATCCT	CCAGCTCCTT	100000000	ccrccorred	120
4	CTCCOGACAC	CATGGACAAG	TITTOMOGC	ACCCAGCCTG	<b>OCCIACTOTO</b>	CTCGTGCCGC	3
2	TOAGCCTOGC	<b>GCAGATCGAT</b>	TTGAATATAA	CCTGCCGCTT	TOCAGGLGTA	TTCCACOTOG	3,0
	AGAMANATOO	TCGCTACAGC	ATCTCTCOGA	COGNOCCOC	TOACCTCTGC	MODITITICA	8
	ATAGGACCTT	<b>GCCCACAATO</b>	OCCCADATED	AdMAGCTCT	GAGCATCCCA	TTTOAGACCT	360
	<b>GCAGOTATCO</b>	OTTCATAGAA	<b>GOOCATOTO</b>	TOATTCCCC	GATCCACCC	AACTCCATCT	420
	STGCAGCAAA	CARCACAGOG	<b>OTOTACATOC</b>	TCACATCCAA	CACCTCCCAG	TATGACACAT	480
ণ	ATTOCTTOM	TOCHTCAGC	CCACCTGAAG	<b>ANDATTOTAC</b>	ATCAGTCACA	GACCTGCCCA	540
	ATOCCTTICA	TODACCMIT	ACCATAACTA	TTOTTAACCO	TGATGGCACC	COCTATOTCC	900
	ADANAGGAGA	ATACAGNACO	AATCCTGAAG	ACATCTACCC	CAGCAACCT	ACTGATGATG	9
	ACOTTOAGCAD	COGCTCCTCC	ACTONANCOA	OCAGCACTIC	ACCADOTTAC	ATCHTTACA	720
5	CCTTTTCTAC	TOTACACCC	ATCCCAGACG	ANGACAGTCC	CTDOATCACC GACAGCACAG	GACAGCACAG	780
3	ACMANATOCC	TOCTACCAGT	ACCITCATION	ATACCATCTC	AGCAGGCTGG GAGCCAAATG	GAGCCAAATG	940
	ANDAMANTON	AGATGAAGA	GACAGACACC	TOGETHE	TOGATCAGGC	ATTOATOATO	006
	ATGAAGATT	TATCTCCAGC	ACCATTTCAA	CCACACCACA	<b>GOCTITIONC CACACAMAC</b>	CACACAMAC	960
	AGAACCAGGA	CTOGRACCCAG	TOGAACCCAA	<b>GCCATTCAAA</b>	TCCGGAAGTG	CTACTTCAGA	1020
5	CACCACAG	GATGACTGAT	GTAGACAGAA	ATOCCACCAC		FOCTTATIGNA GOMACTOGA	1080
သူ	ACCCAGAAGC	ACACCCTCCC	CTCATTCACC	ATGAGCATCA		TOAGGAAGAA GAGACCCCAC	1160
	ATTCTACAGO	CACAATCCAG	GCACTCCTA	<b>STAGTACARC</b>	GOARGAACA GCTACCCAGA	GCTACCCAGA	1200
	ACCARTCACTO	GTTTGGCAAC	AGATOGCATG	ACCCATATOO	CCARACACCC AGAGAAGACT	AGAGAAGACT	1260

a TOTTCEANT TATAGCACC
A GATACCOCO TOCTCCAGA
C ACCOLOGO GOLGCAGOO
G COCOCOGO G COCOCOCOCO
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCCAGO GOCGOAGOC
G CTGTCAGO Beg ID NO: 115 DNA sequence Nucleic Acid Accession \$: NM 000077.2 Coding sequence: 277-742 Seq ID NO: 113 DNA sequence Nucleic Acid Accession \$: NM\_002882 Coding sequence: 150-755 Seq ID NO: 132 Protein sequence: Protein Accession II: AMP4372 Seq ID NO: 134 Protein sequence: Protein Accession #: NP\_002873 S 

cocaverso apparerry, derentocae Arronerius for rotrocale Arronerius disponent reteriories and custificate accusate anticonerie treoricuse and confronte procedural arronerius accostratos ere disponente custicates excessione expensation de comproment accusates excessiones excessiones and compression procedure excessiones accusates anticonerius provinciaria procedure excessiones excessiones arronerius ring provinciaria procedure excessiones expensationes expensationes.

9	
-	
7	
~	
=	
$\rightarrow$	
~	
9	
S	
=	
⋝	
-	
î,	
·	
₽.	

PCT/US02/12476								٠								
000000000000000000000000000000000000000	960 1020 1080 1140		120		9	2 2 6 6 6 6	200000	720 780 840	٠.			60 120 180	5 4 4 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	1020 1020 1140	1350 1360 1460 1500
ODGAGGGTT OCCAGGTACT CCGCGGAAGG GCGAAACTTA CCCACCCGC	ATTCTTATAA TTCTGGAGTO GCAGCCTCCO GGGTTACTCO AAATAAAATA		S1 } VMOMGSARVA GRLPVDLAEB		sı       corcatocco	ACCCGCCAC TCGTGGTGCT CCGTGGACCT	TCCCCATO ACCAAGOTC TCATTTAGAA CCCACTACCO	CCTANGOGCA CTTCATGACA TCACACTGCT TTCACTC		S1   Arldvrdang	•	51 TAATAGCACC TCCCTCCAGA GAAAGAGGA GCDGAAGAGGG	GCAGCATOGA CCGCOGCCCO ACGCACCGAA CAGGGGGAATGG CTTCGATTCT	ACAGACETC CCACGOOGT TAGATGCAAG GCGGAGCCCA GAGGGCTTCC	COGTACCTOR COGTACCTOC GCOGLAGGTC GAACTTAGAT ACCCCGCTTT	CTTATAMAA TGGAGTGAGC GCCTCCGGAA TTACTCGGCTT
GACGETGCCC G CTGGAACOTGC G CGCGAAGATG G GACGAAGATG G GACGAGATG G	TITITIATAE A TOTTOGAGTE O TOCCAGOCTE AAGCTCAGOG GCTCAAATAA		41 		t s	AACTGCGCCC A ACTGCGCCC A CTGCACACCC C GCCCGTCTGC	CCCTCAGACA T ATCATCAGTC A TTGGTAGTTT T TAAGCCTTCC C			41   	•	1 TOCTODARD TARACTORY TARACTORY OF ACCORNOLA GO CTCGGCGCC CTCGGCCC CTCGGCGCC CTCGGCGCC CTCGGCGCC CTCGGCGCC CTCGGCGCC CTCGGCCC CTCGGCCC CTCGCCC  CTCGCCC CTCGCCC CTCGCCC CTCGCCC CTCGCCC CTCGCCC CTCGCCC CTCGCCCC CTCGCCC CTCGCCC CTCCCCC CTCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	acadeogada o crodecaco o acadeogeca a ocadeogada o reagradeo		CONTRICACY CONTRICACY CONTRIBUTION CONTRIBUT	TTATATAT  TOCAGOOOG  CTCAGOOOG  CANTANAA
CCCOTGCAC SOCIOCICAT STROCCAT MACCATGCC MANGAGCTCT MCANCTGCC	TTTATATCA TTTTCACTO SGCATTTCT GAACTAGGG		31 	96.1		TCTCTGGCAG 0 CGCGGAGCCC A CGCGGGCCTCC C CGATCCCTGG 0	COCOGNAGOT C COCOCOCOCT 1 CCACCCOCT 1 AACOTAGATA 1			31    -     VHDAAREGFL D   HARIDAAEGP &	1.16	ATTCACTANG TO TECCECAGE A TECCECAGE A TECCECAGE A ACCRECAGE C A ACCRECAGE C	CATGGACTGG OGCTGACTGG CGAGGCGGGG TAGAAGGTCT GGAATTGGAA		TOOCCATCO ACCATGCCO GAGGCTCTAA AACATGCCCC AACATGCCCC AAAATTTCC AAAAATTTCC AAAAATTTCC AAAAATTTCC AAAAATTTCC AAAAATTTCC AAAAATTTCC	
TCTCACCCG FGCACCGGGA FGCACGGGGA FCAGAGGGA FAVAGAGCCA FCTACAGGGC FATAGAGGCC	TAAATGTCC CCCTTCTGC ICATTCATGT INGCATTTTGG	in sequence: NP_000068.1	ARGRYBEVRA I	ence 8: Mr_038196.	נ 12    -  -  -	CATTCTGTTC TOCTCCACGG ACGCTGCCCC TCGACGTGCC	AGATAGATGC AGAGACCTCG CCGCCCAAC CCTGCCTTTT		476103.1	21 	ence 8: NN_0581 4	adottocce i		CTTGGGAAAC GAAGATCTGA A CGAATGGGGG	ANGAGGENTA ANGAGGENGTA ANGAGGENGTA ANGAGGENGTA TAGAGGENTA	
002/08/443 occ ascercaces cra eccoraces cra eccoraces acr accoraces asc accoraces asc accoraces asc accoraces asc accoraces	CCCCACTACC AMGAMANCA CCCTAMGGGC ACTTCATGAC GTCACACGC ATTCACTC ATTCACTC ATTCACTC	10: 136 Protein Accession 8: NI	11 	NO: 137 DMA mequence : Acid Accession 8: NM_ mequence: 104-421	t	CCCOTOCACO CCCOTOCACO CCCOTOCACO	AGCATGCCC AGAGCTCTG ACAACTGCCC TTAAAAATGT	DESCRIPTION OF AGAINGT AGAINGT AGAIN	138 Protein sequence:	11 LLLLHOAEPN GHRDVARYLR A	39 DNA sequ   Accession nce: 272-68	11.   	CAGCOOCOO OOGAGCAGCA GACGAGCTGC GAGGAGCTGC CGGAGGCCGA TTGACGACCAA TTGACGACCAA		CCTCGATTGA GOOGGCCCC CCCCGATTGA CCAAGGTCCT	CACTACCOTA MAMACACCO TAMOCOCACA TCATGACAAO ACACTGCTAG
WO 02/0 CACTOCACACO CCTOCACACO GGGCCOTCTO GCCCCCACACA ANTICOTACAT	ATATOCCTIC AAATGTAAAA A AGCACTCACO CAAGCTGTOO A CTTCTCTTCA O	Seq ID MO: 1 Protein Acce	1 	Seq ID NO: 1 Nucleic Acid Coding seque	1    -  -  -	CCCAAGTGGGG G CCCAAGTGGGG G TCTCACCCGA C GCACCGGGCC G	CAGAGGCAGT A ANGANCCAG A CTACAGGGCC A ANTAGAGCTT T	CONTINUE O CATTONIO O AGCANATOGE A	Seq ID NO: 138 Pro Protein Accession	1 	Seg ID NO: 139 DNA sequence Nucleic Acid Accession B: NN_058197 Coding sequence: 272-684		GCCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		GCCOTCTGC GCCOTCTGC GCCTCAGACAT CCTCAGACAT CATCAGTCAC	TOCKTECCC C TOTALANA A A ACTOACOCC T COTOACOCC T COTOACOCC T COTOACOCC A CTCTTGAGTC A
S	01	15	20	25	30	35	40	45	20	55	9	\$ 59	92	75	80	. 88

•	-	11	21	11		15	
10	HEPAAGSSME RRSAAGAGDG KEBB		ADMLATAAAR Elebosabil	GRVEEVRALL GRYEEVRALL RKKGRLPGEP	Badalpnaph Bedvchhrpp		- 3
15	Seq ID NO: Nucleic Ac: Coding megn	NO: 141 DNA sequence Acid Accession #: N sequence: 163-684	quence n #: NM_058195 684	195.1			
2	-	=-	<b>a</b> -	<b>5</b> -	<b>\$</b> _	. 51	
20	CCTCCCTACG			ccocorococo	AGGGCTCAGA	OCCUTTOCOA OCTOGOGOGO	- 22
3	OCCOCCCA OCCOCCCA					GOTOCOARO	2 % %
25	CACATCCCCC		GCGCGCGTGC		COCCOOCOC	TOTOGRAPH	¥ ¥ ;
3	CATGATGATG				CTCCACOGC GCTGCCCCCC	COGAGCCCAA	- 3 6
Ś	OGACACGCTO CCGTCTGCCC	OTOGRACETOC OTOGRACETOC	ACCOMMENS	GOCCATOSC	GACGTGCGCG GATGTCGCAC	ATGCCTGGG OTTACCTGG	5 12
2	CTCAGACATC	CCCGATTGAA	ACAGGCAGTAA AGAACCCAGAG	AGGCTCTOM	ATAGATGCGG AAACCTCGGG	AAACTTAGAT	- 2 2
36	TOCCTTCCCC		TAGAGCTTTT		TOCCTITIAN	CTTATAAAA	ă Ş
ç	ACTCACGCCC GCTGTCGACT	AMANGACCA TANGCOCACA TCATGACAAG	CTTCTGCCTT TTCATGTGGG CATTTTGTGA	CATTICTTOC ACTAGGGAAG	GAGCCTCGCA CTCAGGGGGG	DCCTCCOGAA TTACTGGCTT	222
40	CTCTTGAGTC	ACACTGCTAG	CAAATOOCAG	AACCAAAGCT	CAATAAAA	Tamantartt	
?	Seq ID NO: 142 Pro Protein Accession	3 =	NP_478102.1				
45	-	ដ	ដ	ı,	=	a	
	GRGRCYGPB RVFVVHIPR	LOLROGEWRC LTGEWAAPGA	BPLVPKOGAA PAAVALVLHL	AAELGPGGG Lregriggop	NAVRRPLVTL LPRRPGHDDG	RIRRACOPPR ORPSOGNAMA	4 4
20	PREGAGLERE	2 3	CPOGLPGHAG	APGRGAAG	RARCLOPBAR	8	
	Beq ID NO: 14 Nucleic Acid / Coding sequen	No: 143 DNA ser Acid Accession sequence: 412.	il DNA sequence Accession 6: NM_018131 Accession 1: NM_018131	4			
25		;	;	;	:	;	
	GANATTOCAC	11  - ACTTANAGAC	21  - ATCAGTGGAT	31  - GAAATCACAA	41  - 97999AAAGG	51  -  -  -	•
9	<b>GATAAAGAGA</b> AATGCTTATC		TTTGGAGAAA				2 2
	AGGAGGGAGC	QTACTACCOC ACCTOTTOAA	AGCCTTATCT	CAGCTOGAAG	AGACAAGAAA	ACAACAGTTO	× × ×
. 65	CAGACTORAG		CTTCAACTCA	TCMTAAATA CAGTGGCTCG	ATATTCATOA	AATGGAAATA	# <b>?</b> #
	GTCTATGTAA	AAGGACTTTT	ACCAMANTO		AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TCMGUGG	200
92	CHARGEATA	CTCAGCTGAG	TTTTGAACTO	AGTGAATTTC	GAAGAAAATA	TOMOGRACC	2 7 8
	CATCTGGAAG		TAMACAGAG	MONTACAAA		AGAGAATGAT	3 %
7,	GAGACACAAA				AAAAACTCGA		. 3
Ž.	GTTGGAATCC				GAGCCATTAG		
;	CAATGOAAGC	CTGGTGGAAT	OTCCCAAOTO AATACTOTTC	CANTATACA	TATCCAGCCA	CTGAGGATO	
<b>2</b>	TTAMAGATT	CATACTOTA	TTTCTGTTA		ATTTOAATT	ATATATTCA	33
	CTTTTAGGCT	SCTOTOCATT	TCTCTTOBOLA TCTCTTOBOLA	OTONTACCTC	CCTGACATOO		
88	MANTACTTO	GTGAGGAAAA	GATAGCTCAG	CTTATTOCTA	ATOCOTTAAT	GCACCAGCAA	2
3	ACTOTOTTCC	CATTITIAL	CCAGCACT	AGAMACCTA		TTTGATGTCC	17:
	ATTOTTANGA	COTCOTORIA	CATACTATT	THEFT	TTOTATAGEG	CTTATTAGAA	2

WO 02/086413
MORTGOOD THETETETEM CETATIOGS GETROCKT GAMCTIME COGCOTOR
TOCCOLACT STREAMS ATTAINED GETROCKT GAMCTIME CONTROCKED
COCICANTOT STREAMS OF TAXACTOR MINISTRA CONTROCKED
THEOGRAPH STREAMS THANKING THANKING CONTROL CHANGES
THEOGRAPH STREAMS THANKING THANKING CONTROL THANKING

Seq ID ND: 144 Protein sequence Protein Accession #: NP\_060501

ន

Seq ID NO: 145 DNA sequence Nucleic Acid Accession #: NM\_001168 Coding sequence: 50..478

	***	
6443	MAMMA	
<b>VO 02/0864</b>	WARABA M	
_	3	

quence	054895.1
teta	÷
D: 148 Protein	Accession
Beg ID NO	Protein !

Seq ID ND: 149 DNA sequence Muclaic Acid Accession 8: NM\_003812 Coding sequence: 224-2722

		<b>=</b> -	<b>:</b> -	<b>1</b> -	<b>\$</b> _	<b>3</b> -	
6	recrement	0000000000	avaracerae	GAGGCTAGGC	GAGCCGGGAA	AGGGGGGCCC	9
2	<b>OCCCABCCCC</b>	GAGCCCCGCG	CCCCOTOCCC	CGAGCCCCCA	OCCCOCTACC	COCCOCCOCCA	120
	CCATGCGCGC	CONOCCOOCO	TOACCOOCTC	200000000	COCCCCCCCO	CTAGCCCGGC	100
	00000000	GCCACACGGA	000000000000	DOADCTATOA	<b>OCCATOMAG</b>	COCCODOCAG	<b>5</b>
	CAGCTCGCGG	CAGCCCCCC	TOGCOOGCTO	CAGCCTTGCC	DOCUCTACCT	GCGGCCCCCA	300
č	ACGCGGGCCC	accoactcoa	TOCCTOCCAO	2200000000	COCACOCCOC	CCTGCGGCCT	960
3	<b>acmeterne</b>	CITICICCIOC	TOCCTCCGCT	COCCOCCTCO	Tecesacies	900000000	<b>4</b> 20
	accrocraco	CCCAGCCCTC	COCATTOGAA	TGAAACTGCA	GAMAMAATT	TOGGAGTECT	480
	OCCADATONA	GACAATACAT	TOCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	940
	AATGCAGAAA	DANATCACAC	TOCCTTCANO	ACTCATATAT	TACATCAACC	AAGACTOOGA	909
ć	AGCCCTTAT	CACOTTCTTO	ACACAAAGGC	AAGACACCAG	CAMMACATA	ATANGGCTGT	99
3	CCATCTOGCC	CAGGCAAGC	TOCAGATTOA	AGCCTTCOGC	TOCAMETICA	TTCTTCACCT	720
	CATACTORAC	AATOGTTTOT	<b>ADICATICIDA</b>	TTATOTOGAG	ATTCACTAGG	AAAATGGGAA	780
	ACCACAGTAC	TCTAAGGGTG	GAGAGCACTO	TTACTACCAT	GGAAGCATCA	<b>ANDCOOTCAL</b>	840
	AGACTCCAAG	proocector	CARCCTOCAL	TODACTICAL	OCCATOTITO	AAGATGATAC	900
,	CITCOTOTAL	ATGATAGAGC	CACTAGAGCT	COTTCATOAT	GAGAMAGCA	CAGGTCGACC	960
ç	ACATATAATC	CHANNACCT	TOGCAGGACA	<b>OTATTCTANO</b>	CAAATGAAGA	ATCTCACTAT	1020
	COMMONGST	avecyotooc	SCHARGE	TGAATTACAG	TGOTTGANA	GANDONADAD	1080
	AGCAGTGAAT	CCATCACGTG	GTATATTEDA	AGANATGANA	TAITTOGMC	TTATOATTOT	1140
	TAATGATCAC	AAAACOTATA	AGAAGCATCO	12000	GCACATACCA	ACAACTTTGC	1200
,	AAAGTCCGTO	<b>GTCAACCTTG</b>	TOGATTCTAT	TTACANGAG	CAGCTCAACA	CCAGGGTTGT	1260
5	CCTGGTGGCT	<b>GTAGAGACCT</b>	OGACTGAGAA	COATCACATT	GACATCACCA	CCACCCTGT	1320
	GCAGATGCTC	CATGAGTTCT	CUMATACCO	GCAGCGCATT	ANGENGEATG	CTCATOCTOT	1380
	GCACCTCATC	TOCCOCOTOA	CHITCHIA	TAAGAGAAAGC	ACTICTOACTT	ACTITIOGAGG	7440
	torcrotter	CCCACAAAA	CACTICOTOR	GAATGAGTAT	OCTOTACON	TGGCAGTGGC	1500
•	ACAAGTATTA	TOSCAGAGO	TOOCTCANA	CCTTOGAATC	CAATGOGAAC	CTTCTAGCAG	1560
4	AAAGCCAAAA	TOTORACTOCA	CAGANTOCTO	gggraderae	ATCATGGAGG	AACAGGGGT	1620
	STOCKSTICS TOTAL T	COMMITTE	CONSTRUCTO	CATTITIOGAG	TATABABACT	TETTACABAB	1680
	ADGAGGTDGA	OCC100CTTT	TCAACAGGCC	AACAMACTA	TTTGAGCCCA	COCAATOTOO	1740
	MATGGATAC	OTOGAAGCTO	COGNOCIACTO	TCATTOTOGT	TTTCATGTGG	AATGCTATGG	1800
	The state of the state of	-		-	Section of the second	-	

<del>\$</del>

A OGGIOGATE PROJECTOR PRO MOGRANA TROCADADO A A OMOGRANA TROCADADO A TOTOCADA TROCADADO A TOTOCADA TROCATOR PO TOTOCADA TOTOCADA TO A TOTOCATOR TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF TOTOCATOR OF OF TOTOCATOR OF MITATOGEN MARANTET COCTETION OF THACANDER TO THE THEOGRAPH OF THE THEOGRAP

11 41 51 | | | | | | | CACTPERNAE AGFINCPTEN REDIAGCFFC NQFESTITUS FINLDRENAN MIANETHNE

1 12 21 HOAPTLEPAN OPPLICHES TPROMPPLED OF PRESENCY SECURIFY REPEBY OF KREPESTAKK VRRAIBOLAA ND

Seq ID NO: 146 Protein sequence Protein Accession #: NP\_001159

Beg ID NO: 147 DNA sequence Nucleic Acid Accession 8: NY 014176.1 Coding sequence: 117-720

Seq ID No. 150 Protein sequence Protein Accession 8: NP\_001803

decoclace creatacce dragatical departement of trataloga drawcate and deformed transmission of

9
-
-
Ñ
_
~
0
Ø
-
_
_
_
C
Σ
ρ.

	PCGPEIGIC 720	DPVRNLHPP 780	
	CTHLTRAPA ICQLOCETIP TEPYHCORVI DCSCARVVLD DOTOVCYVED GTPCSPERMC	LORKCLOIGA LAMSSCPLDS KOKVCSCHOV CBNEATCICD FTWAGTDCSI RDDVRNLHPP	KEREPKOPSA THLIIGSIAG AILVAAIVLG GIGNGFROVK KRRPEPTOOG PI
	DCSCARWLD	CHWEATCICD	OTGNOP/ONVK
	TEPTHOGRAI	KOKVCSCHGV	AILVAAIVIG
080443	ICOLOGETIP	LIMBSCPLDS	THLITOBIAG
MO 02/08644	LCTHLTLADA	LDRKCLOTOA	KOEGPKOPSA

Seq 1D NO: 151 DNA sequence Mucleic Acid Accession #: NM\_033915 Coding sequence: 250-1326

Seq ID NO: 152 Protein sequence Protein Accession #: NP\_076404

MOPNITIANG P GLAVMIPHI R FYANKTSIV P NGQPTEDNIH D 16QSSKKKH N FLBACKVCLO P <del>2</del> 

D80008.1 Sed ID NO: 153 DNA sequence Nucleic Acid Accession #: D Coding sequence: 149-719 S

ACTIONICAL
MATABORA
CETTIONICAL
MATABORA
CETTIONICAL
MATABORA
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN
MATABORA
CONTROLIN COMPANDED OF CONTRACTOR OF CON WO 02/086443

COCAMATT TOTAL MOTTORA CINCTRACT COL
COCAMATT TOTAL MOTTORA ACTORDAC COL
COCAMATT TOTAL MOTTORA ACTORDAC ACCORDACA COL
TOTAL MANAGEMENT TOTAL MOTTORA ACTORDAC TOTAL
TOTAL MANAGEMENT TOTAL MOTTORA ACTORDATION TOTAL
TOTAL TOTAL MOTTORA ANAGEMENT TOTAL TOTAL
TOTAL TOTAL TOTAL ANAGEMENT TOTAL TOTAL TOTAL
TOTAL TOTAL ANAGEMENT TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
TOTAL TOTA 

Seq ID NO: 154 Protein sequence: Protein Accession #: BAA11503.1

Seq ID No: 155 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 149-709

တ္တ 

WO 02/086443
PPECKNELL PERAPADO LANFEDIA QUEDALLY ENGEWIRA ESCREDLIP TIERRIGHL BRRETTALL UNBLAIRA BYRTON-PR ALAPHWAES VELLOYOSF BYROTSOLL MOSEILES

Seq ID NO: 159 DNA sequence Nuclaic Acid Accession \$: Eos sequence Coding sequence: 149-229

\$

	WO 02/086443  torogram creocrats  Acceptage granding  AMENGER ACCEPTED  ACCASA ACCEPTED  TOGGRAM  TOGG	(086443 carocerora orcavanced acretatere acceptora	TCACAGTTA AGTGAGCTG AAAAGAAAT OCACCTTGA TAATATTGA	CACOOCAGG AGATCACAC TAGGATCAT TTOAGATTGC OTCTTCTGGC	TOTOGRAPH ACTOTACTOC TIGTCAATTT ATTOAATTTA CTATAAACAA	OGNICACTIO ADCCIGOONG CTACAACAC TATAAAACTO GOTCIGICTT	2880 3000 3000 3060	PCT/US02	ñ
	CCTAGGTATT CAGGTCTACC TTCTAGCAC CCTTGCTAAA	ATOTCAGCAT TTOTTGCTAG CTOTGAGTTC GAGTTTTACT	TCATAGETT TCATAGETT MATTAGEMA CATGOTOTT CTTC	TATATATA TACATTAL TACATTAL	CITTIONAGE TOOTATTITA OTTOAACTTO ACATCAACAG	AMITTCAM TATCCTTCAG TCATGTGTTC	3300 3300 3300		
	Beq ID NO: Protein Acc	10: 156 Protein Accession #: Ro	n sequence: Ros sequence	-00					
	1   PCEKAMEL!   TIKPRHCSLL   LATYMRSLQG   KSLMR!	1 11 21 NPCEKAMELI RELIEMARGO LAPREGILA TIKRRHEGLI RHRECTVAYL YDELAIRAL MATHREGGO DEGIGITQDM KPPKELVIEM	21 	11 QVLEBHKALY RMEYGBVLPN GCSGA1BAQP	41 	51 	60 120 180		
	Beg ID NO: Nucleic Act Coding sequ	157 DNA seq d Accession sence: 148-6	8eq ID NO: 157 DRA sequence Nucloic Acid Accession b: Eos sequence Coding sequence: 148-621	quence					
	<b></b>	<b>=</b> _	12_	<b>z</b> _	<b>.</b>	15.			
	TTCGGCGCCA	AAGCGCGGAG AGGCGCCGAG	ACCCAGATA	GCCAAGAGCC	TOGGGCTOTA	OCACTACAAC: OTGOTTOGCA	120		
-		ACTOCOCACCA	MODECACATE	TTCTGCGAAA	ACCACCATOCA	ACTGATCGGC	180 240		
	GTTCTGGAGG TCAGGTGGAC	AGATGAAAGC	TTTOTATOA GATACCAACT	CAMACCAGT	CTGATGTGAA	TOMOCAMO	360		
		OCACTOTAGC OTAGCOTCTT	ATACCTOTAT OCCAAATGCA	TACCATTIC	TTCOGATCAG ACATGGCTGC	AGCACTCAGA	<b>4</b> 50		
	COGTOTICTAA	ANDACTATOS	ACCTODATE	CTTCATCATC	<b>AGCTOATCAGT</b>	CCTATTAAAA ACAAGGAGTC	540 600		
		TOCTOTCATO	ACCATGOGGC		COCTETITION	TCAACTCATO	660		
		<b>OTTTANGATA</b>	ACTAAGAATA	CTTOCCTANO	AAGTATAATT	TGCTAACTAT	780		
	TTOTTTOTA		CACTATOTTC	CCCAAGCTGG	TCTCAAACTC	CTGGCCTCAA	0 0		
	GCCCCTACT		TCTCAAAGTG ATAAGCTGTA	TETETANTEA	AGGCGTGAGC CAGCATTCCT	ACAGITIGITA	960 1020		
	ACTION	TTTAATGAA	AGTAMACATO	GTTACATTTO	AATCTCTTAA	ATAMGCAGTC	1080		
						ANOTGANGAT	1200		
	GCTATTTGGG	ANDOMADGAC	ACACATOGAT	TTTGCACATT	TCCACCATOR	TOGCTOGTOT	1320		
	GCCTTGTGGC	TATEGOSTGA	TCACCAGTAT ACAGTTTTCC	CACCACTITIO	CANGOCICACA	AAAGTCACAT	1380		
	GAAGAGTTGA		ATOUTATOTT	TTAMACAGCT	GACATTITAA	ATTITIONION	1500		
	CATCCCAAGA		TTTTCCTTT	TACTTCTAGA		TTTTAAGCTT	1620		
	TATACTITION	ATGGAGTCTT			CTGCAGTGGC	GTTTGTTTCT	1680		
	CTCACTGCM	TCTCTATCCC AGGCACAGGC	COCCACOCCT		TOTATTTTA	TCCCAAGTAG	1860		
	AGTTTTACCA	TOTTOOCCAG	GCTGGTTTCA	AACTCCTGAC		CCACCTTGGC	1920		
	ATGNATTITE	TATATOGTGC	AAGOTOTCAA	TCCACCTTCA		CANTATAGA	2040		
	ANTIOTITE		TCAATGTATA			CTOTTTOT	2160		
	TTTCTATA		AGATAGTATT			TIOTTIOIT	2280		
	CATACACT	GCCTCCTCCT		TGGGATTACA	OCCUTOMOCC	TOTOCTOC	2400		
	ATOTOMATT		CAGGGTGTGG			AGACTITO	2460		
	GAGGCCTAGA		ACTTGAGGTC	AGGAGTTCCA		GOCCTATOOC	2580		
		CACGGCAGGC	ТОАВОТОВОА			OTCAAGACTG	2700		
		TAGGATCAAT				ACCCTGTTG	2820		
	ATATATTOA	TTOAGATTGC	ATTOANTTA CTATAAACAA	COTCTOTCTT		MATOTETTA	2880 2940		
	TTCATAGITE	TCTTAATAAT	CTTTTOTAGE	AMITTOM	CAGGICTACC	ATGITGCIAG	3060		
	TAMTAGAMA TCATGOTOTT CCTTC	TTTGTAATT	GTTGAACTTG	TATCCTTCAG TCATGTGTTC	TATGASTAA	CTGTGAGTTC	3120		
	Sed ID NO	158 Protein	- segmence						
	Protein Accession 8, Eos	ession 8: E	tos sequence						

seq ID No: 160 Protein sequence: Protein Accession #: Eos sequence Seq ID NO: 161 DRA sequence Nucleic Acid Accession #: U10694 Coding sequence: 1313-2280 10 13 20 22 8 35 8 <del>.</del> S 55 8 છ 2 75 8 82

seq ID NO: 162 Protein sequence Protein Accession (I: AAA68877.1

247

2

73

	7
	ч
7	
	į
11001	
٤	
ι	
	Ξ,

WO 02/086443

PCT/US02/12476 60 130 130					
	US02/12476				
	PCT	•	09	20	9
		<b>#</b> -	STTS SEDSKEEEVS A	PAGE BEMPOBALKE KVASEVHPLE	NOVI POTOVERVDP AGRETILIVIA
41 			8	PAGE	1000

WO 02/086413

Beg ID NO: 163 DNA sequence Nucleic Acid Accession 8: AP292100 Coding sequence: 30-809 တ္တ 

S

8eq ID NO: 164 Protain sequence Protain Accassion #: AAG06606

80	Protein Ac	Protein Accession #r AAG00606	AG00606				
		=	12.	11.	<b>;</b>	31	
	_		_	_	_		
	MAKERSSORD	nklkssond kvrofmifto bbektavscl sondmildva tompfompel yiresvrosl	BBERTAVSCL	SONDMICLOVA	TOWPPONPEL	YIRESVKOSL	
ż	DRKKLEGLYN	PRINTEQUYN RYNDPODENK IGIDGIQQPC DDIALDPASI SVIJIAWKPR AATQCEPSK	101DQ1Q0PC	DDLALDPASI	BULLIAWKFR	AATOCEPSKO	
S	<b>EPPECATELO</b>	EPIDGMTELG COSTEQUEAG IPEMEDELES PORPEDITOF TENFACHDOG KGLDLEGALA	I PROFESSLIKE	PORPXOPYOF	TENTALONDO	KCLDLEMAIA	
	YMNLVLNGRP	PRILVENGRP RPLDLANKFL LENHKRBIPK DTWILLIDPS THIADDMSHY DESCAMPVLI	LENHKRBIPK	DIMMITTORS	THIADDMSNY	DEECAMPULI	
	DDFVEFARPO	DDFVEFARPO IACTESTIV					

	Seq ID No.	Mo: 165 DNA sequence : Acid Accession &: AF256215	Tuence 1 6: AP25621				
S	Pos Birmon						
	.   checuareca	11   catscroor	21   	31    - 	4.1   coodacoaco	51   TCCCTGCGC	8
10	CCTACGGGC CCTGCTCCAG CAGCGGCGG	TOCOOTOOCO AGCOOCOCO OCTOCOOMOC	GCCGCCGCGG TOGGCCGGGG CGACCAAGTG	CACCCCGCAG CAGGGCGGGC GCTCCTGCGA	GGCCCGCCAG CCGGGGCCCC TGCCGGCGGA	TCCCCGCTTC TCCATGCTGC AGAGGAGGTT	222
2	GCCCTGAGTC CCCCTGAGTC TTTCCACGAA	OTAMOTOTT CAOGGAAAG AACGCAAAG	GAGAGAGGA ACCAACAGCT AAGTGATTCA	AACCAGGCA ATGGGGTCTT GACCCATCCC	TCACCTCACA TCACCTCACA AAGTOGAAGA	CATCACC CATCACACACA TOCATCACACAC	2 2 2
2	AAATGAATA	ACCTGATTGA ACCAGATTGA ACAMACTTAC	AGAACTOTCT	OCAATGATCC ATGGCTOTTC	CTCAGTGCA	CCCCATOGCO	2263
70	CTCAGACATT	TANTOCTTAN	GACTGCAGAA	DOCTTCT1AT TCCAAATAC	TOTOGOTTO	ATOTOANGA TCACOCTAGT	780
	CAACITICAT	CTTTTGATAT	TOACTICITA	CATCCAAAG	ATOTTOCCA TAGATOCCA	ACTOSTITO	900
25	ACTOMAA				ATTOCACTOO	ATGCTTACCC TTACTTGAGA	
	AATTTACCT	GCCTTOTOGC ATOTOAAACC		TTACAGCCAT ATAACCCGGT	ATATTOTTCC TTGCAGTGAA		1200
30	ACTICITORS	ATCAMAGGC ATGAMTATTT	AACAGCGATT TCATCAAGAT GAAAATACTT	TAGGATATE	TOCCTCAGGA ATTTGACTGA ACAATTCAG	CANGCACAAA	120
	GGCTCTTTTG	TAACTTTAAA	AAGCCAATGG	TITAGETTICA	CAATCCTTO	GACAAAAGAA TGGAGAAAGCA	1500
35	TCATTTTTAC GTACCTGGAA	CTTOTAGCTC TOTCTACTOD	ACAGEACT		CTAGACAGTC		1620
	ACAGGITTAA	TGAAAGATAC	TCATACTOTA		DEATOTCAAA OTATOTCAAA		
40	GTTGCTGTCC	ACAOCCATOA	AATOGGGGAA GCCACTCCTC	ACTOATOOTO	CACAGTTOGA	TTTOOATGC	1920
}	GOCCTGGGAG		CTTCAGTOAC	ATCCAGTGGA	CCCTCTAGCC	TOACTATE	2000
	THECATOTICE		GATCHGOGGA	ATACCTATA	TTCTACCACT		222
45	TATTATAGAC		ACTACTACTTA		ACTAOTTOCC TGGCTTTGTT	ATATTTTOC	228
	GATTTATAT	AGTAGGTTTG	GTAATGTAAT TATAATTTGG	ATATTGATGT	ATGCCTTGC	AATTTCCTTA	2 5
20	ACTGAGGATA	ATAOTCATAA	TCACATTGAA	TACTOTATT			2580
	GATTICTIOC	TTAMAGTCA	DANAGECALA	AGAGTTTCAG	CTTTCCTTAC	AGANAAGGAA	276
55	CCAGACOTOG	TOCTCACOCC	TOTANTOCCA	OTACTTTOOO	AGGETGAGAC	GOCAGATCA	2820
3	TOACHANA	MATTACCCA	GOCACTCACT	CTTCAGGTAA	CTANCCARCT	CCCACCATAA	2360
Ş	ACTOCTTOGG GCCGAGATCG	AGGCTGAGGC	CTCCAGTCTO	CTTOAACCTO	COAGGCAGAG	TCTCANANA	
8	TOACATTOOA	AACATACTTA	ATANTCACTO GOGATAGATT	AMGATETETA TOTECTAMO	GAMANATA	OCCCOGGCA	25.5
į	TTTAATOTT	TANDIATA	AACCAGTT	CTTTATACAC	ATTTOOONA	ACATTGOTCT	196
65	GCAATTACAG	TTATTGCTG	H < 1	MCCATTT	AAATGACAAG CTAGTTATAA	TACATOTTTA	1540
í	ATTATTAMA	ATACTOCATO		COCOCATCAT	ACTITATAC	ACTITICIOCIA	1720
₹	ATGAMAGTCA AATCCAGTTT TCGCCAAAAC	GCTGTTCTAT	ATGGTGCTAC ATGGTGCTAC	ATCTTTCCAG CARGCTATTT	AGACTTCAAT AAAATTTCCC	OTGGGCTTCA TCAGAGCCCC AGGTGATAGA	3780
7	TTAGAACTIC	TOTCAGACAT	<b>GTTAATGACA</b> TGTGCAGGGG	AACATACCAA CTCCTTOGGCA	CAGACAATAA	CCANGCAA	1020
2	TTGAGGACCT	GAGAGACATC	AGOTTTAGAA	TOAGCCAAG	AMATICETACA AMATICETACA	AGATGGGAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAA	1140
ć	CATTOCAGG		AGGGCCTGC	CTACCIATAT	CACTITITAG		500
ခွ	CATCATAOCT		AAAAGCAGAT	OCCOCCACAC ACTOCTOCCT	TTGCCCTCOT	CASTITITIC	<b>1</b> 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
	ACTICITACIONA		CTTTATTAGT	ATAGACCAGT	GGGCAGATAG	AGATTGAAT	1200
82	OTTICCTICA		OTTTCTC	ACTAMATTO	ATTTTOCTO	TAGAAGTGA	
	TCOTGAGAAA	GAATATATET	ACMATTECA	COMMOTATE		тастстава	0

Seq ID NO: 168 Protein sequence: Protein Accession 8: NP\_055115

2

Seq ID NO: 169 DNA sequence Nucleic Acid Accession 8: NM\_006875 Coding sequence: 186-1190

15

_	
Ī	
Ñ	
-	
7	
0	
အ	
_	
↸	
_	
Г.	
_	
ã.	

						_:
4 9 8 0 4 9 8 0	\$040 \$100 \$150	5340 5400 5400 5520	5640 5760 5760 5820	5940 6060 6060 6120	6360 6360 6420 6480	6540 6600 6720 6780
TCTTCTAGCC TCAGTATATC TTACATTCTT	ATCTCACTTT TGCACTGGAC CCAGAATCAG GACGCACAGA	TTAMAAAAA OGAGGCCGAA GAAACCCCGT OTGGTCCCAG	AMAMAMA DOTTATTATT TTTGAAGAAC CATGTTACCA	TATTOTOMA ATTTAAAGA GTCTTTGAGG TCCCAGACCA TCAGGTGGGT	CCACTAGGTO CCACTAGGTO OCTCCATGGG TGGTGTGAGT	MAACCTGCC ACTTCTCATA TTCACTTGTB GTGAAATTAT TCCAAAAGT
ATTATTTA ATTATATA ATGREATATA	TTGATAGCAC TAGTGGCTAC GATTAGAATC TGAGGAGGCT				TATANGO TATANGO TATANGO TATANGO TATANGO TATANGO TAGO TAGO TAGO TAGO TAGO TAGO TAGO TA	ACCTOGAMG GGTGTATGTC TCTTTTCCAG AATGAMAGA ATAMCTTCC
CCACATUTAT ACTALITATA AAAATTATTA	CACATOTOGC CACATOTOGC AAGTCCTGTG CTTTTAAAAA					ATAMAMCTO OAGAGTOTAT AATTITAGC TOTGOTAAAT TITTAATTIA
ATAATCTGAG TACAAGTAGA TAATTAATAT	ANTCHOOTAT OCTCAOTAGC CCTAACACC ATCAACCTC	ACTACATTAC OTOGCTCATO GOAGATCGAO AAAATTAGCC	AGCCTGGGCG AAGAAAGTC CCATAAGGAT ATCTGTAAGA	OTTATATEOT CAGACAGAAA ACGACAGAAA CACAGGTACA CACAGGTACA	GUNDACTCAT TAGAAGCCAT TGCTTTCATT ATTTTTGTGC CCAAGGGAAG	TOTAGNOCCA GAACTCACTT TCTTTTATAC TTTAAATTTT TAGTTTTTTTTTT
WO 02/086413 COCTOTO CANTAGAAT TIMAGA AGTAAAAGA AATATCA TITGAACATG	CATTGCAAT CATTGCAAT TAGGTTCCAC AAACATAGAG	TTCCCACTCC OCCOOCCCA CACCAAGCCAAAGC AATACAAAGC	ACTGCACCCC AAGAAAGAA AAAGTTTATA TGATCCTTGA	AGTGAAATGA CAGGAAAGTA TTACAGTGTC AAATCTGGGG	TATOATTAGC OTTTITGTAA OGCATTTATG	GCTTTCCAGG CATGCTTTCT TTTAGATTTG TATTGGTATT TACTCATTTG
WO 02/ CAGGGCTOTC ACATTAMBA	TTGGTAATAC GTACTAGCCA AGCACAGTTC AGCTGGAAGT	CCAGGCACTC TOTAGAGTAG OTOGGCGGAT CTCTACTGAA	AGATCGCGCC AAAAAAAAA GAAGTAGACC AATTATTTAT	CTTGGAATCA CAMGACAAA AAGTGTTAT GATCTCCGTA TGTTTAGTAG	GOCCIATION GCCTTTTCT GCCTATGAGA TGTTTTATGA	GGCTTAGAGA CAGCACGGAA TATTCTTGAG CTCGTCGTA ATTTATATAT GCTCCCTTAA
	S	01	15	20	25	30 . 33

## Seq ID NO. 166 Protein sequence: Protein Accession #: AAG34652

### Seq ID NO: 167 DNA sequence . Nucleic Acid Accession 8: NM\_014400 . Coding sequence: 86-1126 . 55

8	180	240	900	360	430	480	240	9	999	720	180	940	900	960	1020	1080	1140	1200	1260	1320	1380	1440	1500	1360	1620	1680
S1 .    ACCCAGGGG	AGGCCTGGA	TOAAGACAOT	AGACCATCCA	AGAATGACCO	CTCAGGATCG	ATGAGAGTGC	AGGCGTGCCA	ACAAGGGCTG	CTOTCCOOO	TCACGCTCAG	CCTACTTCTC	racereac	CCAMCCCAT	CCCGGGATGA	CHOGOCHOTA	CACAGCTOG	CTCCACCTOO	ACTICCION	GTATCCCCAG	ATTCTGGCNG	TCTCCCCTTG	DOTORONGNO	ocorocoro	TCTTTGGGGA	GOONCCOTTGC	THATTACT
15 _ 15	AGGC	TOMOT	AGACC	AGAAT	5	ATGAG	AGGCG	ACA3G	E	ş	ĝ	10000		8	9	ğ	ğ	Ę	GTATC	ATT	Ē		ğ	Ę	9	
41  -  -  -	GOAGGAGGGC	CCDACAGA	0000000000	CTCCCCCGCCA	CASCALISCO	CCGGCAGGTA	CTGAGCCGGG	GATCATOTCT	<b>OTOTOCHTOC</b>	GOCCCAGGGT	COCAACAAGA	CCCACGACTO	ACATOCACOA	CACCAGGGCCT	COCHOCHATT	TOTOTOTOCTC	CTGTGAGCTT	TCTTCTCATC	ACATTCCCCA	CONTOTATAT	CATCCTAGE	TCACCOCCAA	GGACTTTOGA	ACTOCCCCCA	CTCGAGGGCA	TCANTANGA
31   CCCGAGCTCG	OCTOCTICOC	COGATOCTCC	COAGGCCOTO	CONTRODOR	CATCCAGCTO	GOCOCTCOAC	crororogo	CACCCCAGC	TAATOTOACT	TOGROTANCA	CTCTGACCTC	CCCTCCAGAG	AGTOAGACCC	GGGAGTAGAA	CCACCAGGAC	TAATAAAGGC	TOOTOTOCTA	TOGGTACCCC	TOTTTTOCA	AATAAAATAC	GTATCCTTCT	AAGTCAGCTO	TAGCCAGCCT	тосстоссся	CTOTORAGETC	CATAMATOCC
21       GOTANGNOGO	TOCTOCTOCT	AAGCAGATCA	ACOTOTOCAC	TOCSOGITTO	TTCTCGCGTT	TCACCTCGCG	ACTOCTACAG	TCACCTOCTA	TGACGGCAGC	<b>OCACTCOOCIA</b>	CCCCCTOTAL	TCCGGCTGCC	ccreacece	CTCCGAGACA	GOGCOOCTOG	AGCAGCCCCA	contractide	TCTCTGGCCC	аоссидение	GOCTTTOOOA	GACAGCTCCT	AGAGTGAGAG	CACTITICICC	CTCTAAGCAC	CCTTACTAGA	OTTTCT00CA
11    - 	GCAGGCTGGC	TOCOTOCAGA	ccooccordo	TOSCTOSCAS	CTTCACGGGC	ANGCTCAACC	AACGGGGTGG	ccaccaatca	AACOTCACCT	DATOMATICE	TOCCADOGOT	CCACCCCTTG	ACCACTTCTA	ACCAGTCAGA	TTGACTOGAG	00000000000	CITCHOTTOD	CTCACCTACT	<b>GACTOOGCTO</b>	CCTOOTTTGC	OCTITITIONS	ATOTTAGGAC	מכתומכתאנת	TOUCHOCOCCA	CATATGTCTT	TOTOTOTICA
GOTTACTCAT	GATCTCOACT	STRETACAGE	CANOTOCOCO	COCACAATTC	COCCIDENT	CTOCARCOCC	ATACCOGCCC	<b>OCCTACATICS</b>	CTTCGACGGC	CTGTGTGCCAG	10001001	CCCTCOAATC	CACATCHOTC	<b>GCCAGGGCCA</b>	CCACCCCACC	TCCTGCANA	ATTOCCADCC	ANATHROCCT	CCCACCACTO	CTTCTGCTGC	COGTOTTCTA	TCCTCTTGTG	AGGATGCTAA	OGTOGGACAA	ATCGGTTCCC	CTTATOTOTO
9			ţ	3				ć	?				ć	C				ć	Ş				2	S		

	70	1   GAATTCOOCA	11 	21   OCCANTETEA	31   Acoettococe	41   Otcroccoc	\$1   	5
	25	CCCCAGTTTC CCCCCAGGC CCTCCATGTT CGCCAGGAGG GTAAGGGGG	CACACCCTAC CACACCCTAC CAACAACCT CAACAATOSO CTTTSOCAC CATTTSOCAC CAACAATTCCCCG	ACCCTGGGGG GGGCTTAGG GAAGGGTTG GAAGGGTTG GAAGGGTTG GAAGGGTTG AATCGTGGGA	CCCCAACC OOTTCACTO CTCCCOOCC AGGCCAATA BACCCOCCT TOOGCTGTC	TOUCTOCCCA OCTCAATCTG CCCCGGGACC TCGACTCGGC CACAGATCGA CCCCTTGTCA	octocactoc cichaecea cichaecea cichaecea cichaecea cichaecea cichaecea	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
	8	TOATCCGCCT CTTTGCCCGC CAAGCCGCTG TTGTCCATCG	acttaactaa ccaaaatctc cttctttaac taacatcaa	TTTGAGACAC TTTGAGTATA CAAGTAGTGG GATGAGAACA	AGGIAGGCTT TCACAGAGAA CAGCCATCCA TCCTGATAGA	CATOCTOOTC GOOCCCACTO GCACTOCCAT CCTACOCCOT	CTCCAAGCGGC GOTGAAGGCC TCCCGTGGAAG	2002
	35	MCTCATTGA GGACMGGGT CCACTGTCTG AGAGGGACCA GCTGTGCCCT	TTTTOOTTCT GTACAGCCCC GTCACTGGGC GGAGATTCTG AATCCGCCGG	GOTGCCTGC CCAGAGTGGA ATCCTCCTCT GAAGCTGAGC TGCCTGGCCC	TTCATGATGA ATGACATGGT ACACTTCCC CCAAACCTTCC	ACCCTACACT CCAGTACCAT GTGTGGGGAC AGCCCATGTC TCCCGACCC	GACTTTGATO OCACTCCCO ATTCCCTTTG TCCCCAGACT TCACTGGAAG	1020
	. 04	AGATCCTOCT AAAGGAGGCC TOGCCCCAA GTTGACTTOG	GGACCCCTTG CTGCCCCTTT TGGTCAGAAG TTTTACAGGT AGGGGTTAGA	ATGCAAACAC GGCCTGGTCC AGCCATCCCA CATTACCAGT	CAGCCANGOA TTOCTACCCT TGGCCATGTC CATTAANGTC	TOTTACCCT ANGCCTOGCC ACAGGATAG CAGTATTACT CAGTTCCCTT	CAACCCTCC TUGCCTGGCC ATGGACATTT AAGGTAAGGG	1200
	45	CTCATTTTOC TTATTTTOAT TCATATOCTT AOTAMAGGGA	TAMBANDTT ANDRANDTT CANTIDICAC TAACTTOOGC CCCTTTCCCC	AACCTOTOGT TATTTGGTG CCCACATTOG AAGGGTGCTT TAGCCTAGGG	AAGTTGTTCC CACCTCCTAC TCCTTCCAAT	CATTITICACC TACCACCACA ACCCCACTAG GGTCAAGCTG	CCCGGGACTC CCAACTTAGT CTTTTATTT	1500
	20	TCMGCCMGG TTTTTTTTT CTGGTGAMA CACCACCMGA GCTGCTGTT CTGMGCCGGG	ATTITITATE TITTITITO GNACCTIAN CANTAGGNIG TOTTITCCTO ATTOTCCANT	TTGGGGGGGG GGTGAGGGG TCCATAATT GGATGGATGG GGGCGCTCCC TACTAAAATG	TANTOCCETO CCCTACTITO GOGAAGGAAT TITITIGGG TCCANTITIG	TTATACCCANO OGAMANTOON GATOGOCTAO CAGNITITIO	MAGCHTCTT TGCTCTTATT CACCACCOOA GOOMATAAG CAACCTCCTC	1920
	\$5	CCACTATTA ATAAAGTAL CCACTATTA ATAAAGTAL Seq ID NO: 170 Protes	CCACTATTS ATABANGTAN 1 CCACTATTS ATABANGTAN 1 Seq ID NO: 170 Protein Protein Accession (): NI	A TAGATCAGA A TAGATCAGATCAGA A TAGATCAGA A TAGATCAGATCAGA A TAGATCAGATCAGATCAGA A TAGATCAGATCAGATCAGA A TAGATCAGATCAGATCAGATCAGATCAGATCAGATCAG	AMAMAMA	AAAAAAA	TIGTIGOAAAC.	207
	8 8	1     MLTKPLQGPP   KVIPRNRVLG   PAGDLET   DPGSGLLH   DQBILGAGLH   RPCPPGLVLA	11   APPGTFTPPP WSPLGDSVTC EKGPLGDSVTC EKGPLGDSPT PPARVSPDCC TLSLANSPOLA	11   OGKOREAFEA   OGKOREAFEA   PLEVALLMKV   RCF POGVVA   RCF POGVVA   ALI RECLAPIA   PNDOKSHPNA	31 	41 dgratvrach Rildmrator Krdikorit Vrsikolilyd Lildmratra	51     GPMLVLERPL   IDLRRGCAKL   MVCDIPPER   EDVIPQPLQR	25 25 25 20 20 20 20 20 20 20 20 20 20 20 20 20
	2	Seq ID NO: Nucleic Aci Coding sequ	Seq ID NO: 171 DRA sequence Nucleic Acid Accession %: NM_001646 Coding sequence: 69.,2875	uence #: NM_0036. 875	<b>.</b>			
	75	1 decerceda decercede dateAdedace	11 	TOTAL TOTAL	31  -  -	41 	51  - TCTCCCGCGG CCGAGGCCCG	120
	œ ·	CONDECEDAR COCCTOGOCC OTCAGOOACA	AAGGCGCGC AAAGCCATCA CCGTGCAGCG TATGGGGAGC		CANDICACIO CCTCCAGCAC GCAGATCCOG CONGACCAAC	TTCCCOODOC CTOOCCCCC AGTACAGTGG GTGTCCGGGG	TOCOOCTCTT CTCCOCCCAC ACTGGAGCGA ACTTCTGCTA	2000
•	88	COTTOGGGAG AGCCTGCAG CTGTAAGCC GCACCACTGG GCACCACTGG CCAGCAGAAG	CAGTACTOTO ATTOTOGTOC TCCTTCCOTO GTACACACAC TTCACCTTCC	TAGCCAGGAT ACACGCCCTG AATCAGGCTC GACGCCAGGA ACAGCAAGGA	OCTGAAGTCA CATCGAAGTG CAGGAATGTC CGGCAAGTGT GATTGTGGGC	OTOTCTOGNA CTOGNACANA CCCCAACCAA CCCCAACCAA ATCACCTOTC	CCTTOTACS CCTTOTACS CCTTOTACS CCTTOTACS CCTTOTACS	1 2 5 5 5 5

92229

THE CHECKORICH MANICETING CATACCACC
OF CHANNELS AND CHECKACC
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHANNELS
OF CHERICICE TETECTINI TICOGGCTT CT
TOCOGGCT TOCOGGGT
TOCOGGCT
TOCOGGGT
TOC HPVGLTTAIR VOTBLPALA VAGGILAANY OF LAFALERINE BRADGALEVILE TRAGGERYET 19 PTSCELPHOR GORGENITE TRAGGERYET 19 VGCNOGLIAK TOSHEFLAS VATHARNER BA VGCNOGLIAK TOSHEFLAS VATHARNER BA VTRAGTA GORGENITE TERVITATE PE LITRATRACTA ROMASHENS LINGGEL LINGGEL LITRATRACTA ROMASHENS LINGGEL LINGGEL LITRATRACTA ROMASHENS LINGGEL LINGGEL LITRATRACTA ROMASHENS LINGGEL LINGGEL LITRATRACTA ROMASHENS LINGGEL LINGGEL LINGGEL LITRATRACTA ROMASHENS LINGGEL LIN Seq ID NO: 175 DMA mequance Nucleic Acid Accession #: NM\_000691 Coding sequence: 43..1404 3eq ID NO: 174 Protein sequence Protein Accession 8: AAP36984 ecuatorece curracess al accertation descented accertances of rescuedade accertances of rescuedade accertances of rescuedade accertances of rescuedade accertances of rescuedade accertances of accertances accessivates of rescuedade accessi <del>\$</del> S 

DOXCHICKD PROPERTIES GENURALLY RECUBERED SERVIETTY REHINNERRO 1
POTITIOAN POTITIOES TRAINGERED SERVIETTY REHINNERRO 1
POTITIOAN POTITIOAN STRAINGER PROGRESS CHOUSERS 
8eq 10 NO: 173 Protein sequenc Protein Accession N: NP\_003637

MEPRDOSPEA R GLOHLAPPP T MLKSVSRRKC A DOKCRHCGKG P

Sed ID NO: 173 DNA sequence Nucleic Acid Accession 8: AF232772 Coding sequence: 1-1662

င္ပ

ATGCCGOTG OTGCTGGOTG CACTACCTGT

TECCOGOGO CONTENCACIONE CONTEN

TGCCATOST G
AGACATCOS T
TGCCCTTOSG C
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACTTCTC T
AGACCATAA
AGACCAATAAA G CONTECCED TRATECHARA GOLDATETE GOS AGCTROLOGO ACRICANOST GISTRADALO CON TECTCOLOGO ACRICANOST GISTRADALO TE CUCAGLOGO ATRICANOST COLOSTOCA TA ACAGCOSO ATRICANOS COLOSTOCA TA TETTCOCEDO TROMECER GENERATRAT EN TETTCOCEDO TROMECER GENERATRAT EN CECOROGOS TROMECAS COLOSTOCA CECOROGOS PRODUCES CONTESTOCA TO CECCLAGO TROMECAS CONTESTOCA TO COCCLAGO CENCACATE CANTESTOCA TO CONTESTOCA ACTUACO TE

S

seg ID NO: 176 Protein seguence Protein Accession #: NP\_000682

Seq ID NO: 177 DNA sequence Nucleic Acid Accession 8: NM\_001057.1 Coding sequence: 108-4701

THE THEORY OF COTTOCOME THE THEORY OF COTTOCOME OF COTTOCOME OF COTTOCOME THE THEORY OF THE THEORY OF COTTOCOME THEORY OF COTTOCOME THEORY OF COTTOCOME THE THEORY OF COTTOCOME တ္ထ

The Mathematical tradational advantances on the mathematical tradational or attractional advantances on the mathematical advantances on the mathematical advantances on the mathematical advantances of anti-depth o WO 02/086443

FROMANTA DESCRIPTION AND ACCUSATE AN ACCUSATE AN ACCUSATE AN ACCUSATE ಜ 

Seq ID NO: 178 Protein sequence Protein Accession #: NP\_001038.

HEYBELGEWIN TREATFURD LEXTREDILL HALDRIGGED DESCRIPTION TO SERVISION SERVI တ္တ 

Seq ID NO: 179 DNA sequence Nucleic Acid Accession #: Bos sequence Coding sequence: 148-7095

ACUACUA ACAGECCEA CGCTTGCATT ACAGAGAAA TTGGGGAAAG AGATCTTACA 11 11 21 21 COLOLATA O COCIONANTO COLOCATA O COCIONANTO COCIONANTO COCIONANTO COCIONATO COCIONATO COCIONATO COCIONATO COCIONATA O COCIONATO TOTATANA TITI CANATATANA COCIONATA TITICANA COCIONATO TOTATANA TITICANATO COCIONATO TOTATANA TITICANATO COCIONATO TOTATANA TITICANATO TOTATANA COCIONATO TOTATANA TITICANATO COCIONATO TOTATANA TITICANATO COCIONATO COCIONATO TOTATANA TITICANATO COCIONATO TOTATANA TITICANATO COCIONATO TITICANATO COCIONATO TITICANATO COCIONATO TITICANATO COCIONATO TITICANATO COCIONATO TITICANATO COCIONATO TITICANATO COCIONATO COCIONATO TITICANATO COCIONATO COCIONATO TITICANATO COCIONATO COCIO 

PCT/US0															
						-			•						
4	2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1020 1020 1140	1320 1320 140 140	1560 1620 1740	1860 1920 2040	2220 2220 2280 2340	2580 2580 2580	2820 2820 2820		1360 1420 1540 1540	2560 2720 2720 2840 2900	4020 4140 4200 4320 4380 440	4 4 6 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4920 4920 55040 5100 5220 5280	5340 54400 55460 5530 5540
	TOACTOGGA ATTECACTT AGCATCAAA AGAMATTTO OCAGICTOCT			TCGCATAGGG ATTCTCTGGA TMATTAGCC TCACACTGTG	TCCACATATG TGAGGAGGAG CTCCAGTCCC ATTTTCCTCC		AAGTAGTGAT AAGTAGTGAT ATCCATCCTG TAGTGAATTG	ATTAGAGECE GACGETGGAA TGAACCACEC TGCCTTGTCT	ACCIGIGATA TATACCATA TGCCTCTCT TGACACAGA ATATACAACA	CACAGITICC CICIGITICC FAAGGITITI ACAIACIGIC AGAGCCAGCA	ATTTATOMO TTCTGATOTT GOTTGAAACC TTCTGCTTCA TACTTCTCAT		TAGAGATCA TCAGATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA	ATTACTOCT TATACTOCT TATACTOCT TOCACACTT TATCTTCCA	CCAGGAAGTG AGACAACAAG GCTAGCACAG TGATGGCTAC TGATGGCTAC TGAAGATTTC CCTCGTGGAG
	MGATACTT MGGACANA OTTTTGAGA OTTTTGAGA	ACTGGATTOT AAGTTCTTAC TTCGAGGGA AGATTCATGA ATACCAGCCT	AGETTOCAGE CAGATGOCTA TTCTTCAGAT TTGTCGACAT AAGAAATAAT	CACACTACAA GAGGAAGTGA AACCAGTCAC	TTCTTABATC TAACABATA ATTCTTCAGG AAGGGTATAT AATCTGCTAG	ATCTGAGA ATCTGAGA TTACAGATCT CTCATGCTT CTCATGCTTT			OCCCTACCA ACCTACTCA TICTITIACC CTGAATTIAC	CTTCTGAMG TACCACACA ATACCACCAC TTCAACCTAC GTGCAACTC	CTCAGCTCTT CCTTTCAGG ATCCAATATT TTGTATCAAA ATGTGTCGGC	CTTTGTACAG CCCCAAAGG CACTAATAA CTGGTAAGGT ATTCTGTTCC GTTCTGTAC GTGCCAAATC GTGCCAAATC	GCTCATCCTA GTCTTATGA ATAGAGTCAC CACCATCAGC AGACTGAGA GTGATGAGA GTGATGAAGA	GTGACTCAGA ACTCAGAGT TTGGTCTAGC CAGCCTGAC GCTTCCAGAC CTCCAAACATGT	ANGAGITITA CCACCACC CCACCACC CCACTATOT ATCCACAC TGATACCAA
	AMACCAGO CATAGTITOA COATITICAA TIGITITAAGO AGTGTITAGO	GACACAGTTO GTTTTTTGG CAAACAGT GGAAAGGAAG CCAGAGAATT	ATGATTGAGA GAATTTTTGA ATGAGTTATG GACCAACTGA ATTGGAACTGA	TCCCCACA TCCCCACAA TCCACTTCCC	TCTAMACTO ACAGTTTCTA GGAGCTGAAG AACATATCCC CTTATACCAG	GCACAGCCCG CCTGTTGATO OGTCCTCAG GAGGTAACAC	ACCTACAGNA AACACTACCC AGTGTCCATG TTTTCCTCTG		OTTICITACA TRATTIAGOS TCATTACTOC GATACTGANT OTTICIOTAO	ATGCOTCT TCCCTTGCT AACTITICAG CCTGTGCTA	CTACAACCTT OTACAACCTT OTACCAGTO TTACATCTCA CCAOTTTTTO	GOOGCCATT COOCCCATT AGTICTATA AGTICTATA COCCATA AGTICTATA	TOTATOTON CACADANCA GAGAAGATA CCTGGTAAAT ANTGACATTC GTTCTGACA	CTGGCAGCA ACTAGCGAGA GAGTCTCGTA GTGATCGTGT TGGAGGAAT ATATCCACAC AGGCACTTTC	AUGACACTUA AUTOATOAT TATACAATO GOCCACTUA GTATTOTCA
2000	MTGGTCAGAG TGATCCGGAC TGATCCGGAC TTATCCGAT TGGAGTCGAA	CCCTGCACA CAGTTGGCT AACTACTTA TCATACACT CAGGCTGAC	TTATGATACC AACCAGCAT GCTACCCAAT AAAATACAGC CCCTGAATTA	ACCCCAGATT GACTAACCGA ATCTTTAAT GACTTCTCAG	AVATGATGGC ATCCTTAAAT GCTTGATACT GCTCCTGAG CATCTCTGAG	AGACATACA CACTGAGATA GATGTCACAG CTTCCCAGGTC	TCAGATCCTC TGAGATCCTC TGTATTTCCC TTTGCTTCCA		CATCHTOACT TCAGGGTTCC CCCAACTGCA AGCCTCTTCT TTCTTCACCT	F 4 0 F F	TOWARTOTTA TOWARDIATEO TOTTOCOGOT TICTACOALO TACATOTOTA		CATTCATANG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA		TOMAGNATH AGGTATTACA ANGGTATTACA ACTOMETOR ACTOMETOR TOMETOR TAMTETOGAM
086443	DATE AND A STATE A	TCACATCTCC TCATCCTGATA ACCITITATIC CACAMATOT	CTCGAGTGGT GAGAGGACCA TCAATAATTT GCTTATATGG TTGATCTTTT	MUNCATTON GOARANGCAA ATGRAGCAA TTCCCAATAC ATATTTCCTT	CAGCCTCTTT GGACTGCAGA CCAGTTTCAA CTATCCCATT AGACAATAAC		OTGAGACACE TOCTTGACAA ATGCTACGCC ATGCTGCACC	· U & & U :	OCTOCCAACA OTOTAACTTA COTTAATAAC AATOOTCTOO CCCTTAACAT	AAATTCCTTC ATGATAATGT CCAAGGGCAT TTAGTCAAGT CTGGTGACCC	CTCTTANTAC TTANACTOT ATANACTOT ATANATAG TOCTGCACTO	MATTANA CONCENTITA CONTITANA THOCTICIO CONTINOS	ATOGCTFATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA	ANAMATOR ANTECCCAMA AGAGGCATA AGAGGCATA TOTOGGTAT ACAGTACATC ATOTOGGTAT ACAGTACATC	
WO 02/086443	MATGOATA MATGOATA GAMMAGGA GAMMAGGA GATTCAMG	AATGGCTCAT ACAGTTACA TCTGGTTATG TTCTCTAGAC		AACCAATCA ACGAAATACA AAGGTGATG ACGAAAAAG	GAAGGTACTT AACTTGTCGG AGTTTATTGA GCAACTTCTG GAAAACCCAG	OTOTACTICA AGCTTICAC TCCTTICAC CATTATICA	ACCCTTTOT TCGGCCTTGC TCTTCCTATG		OATAATOAGO OATTCTGTGG CCTAAGTCTT GCTGATGGGG GGGCTGACAG	ACTGAACTGC CCCAACATGT ATTTCTAGCA GATCATGAGA TCTCAAGCAT	ACCTCAGCTT ACCTCAGCTT GACACCTTGC CCCAAAGTTG AGTGAAAACA	TTTOCTACA CATTCCAAA ATTCCAACA GGGCATTCTTC TTGCTGTTC TTAGTGGTTC	AGAGGTAGTO CAGGAAAAG CCAATCTCAT TCAGACAGTC TCCCAAAAGC CCTCTCAGC	GACACTIMATO GGATTCCCAC TCAGAGGCAO GAATCCCACA CTAGTCGTC TACTTCACATO	CATGCMGTA CACAGANTC CACAGANTC CTTGCTGANA MCAGACCAA TGGAGAATGA
	v.	10	15	20	25	30	33	40	45	20	55	65	20	75	82

	AMAGGAAGGA	CANALICIOA	TCAGTACTOG	CCTGCCGATG	GUNGTUNGON	GACOGGAAC	
	TITCIONICA	_	TOTOCALOTO	CTTOCCTAIT	ATACTOTOAG	CANTITACE	2
	CTANGANCA	_	AMAGGCTCC	CAGAAAGGAA	CACCCAGTOO	ACUTOTOMIC	
	ACACAGTATIC	ACTACACACA	OTOGOCTOAC	ATOGGAOTAC	CAGAGTACTC	CCTCCCAGTG	Ē
^	CTGACCTTTG	TEMORANDOC	AGCCTATOCC	MOCCCATO	CAGTGGGGCC	TOTTOTOTO	ŝ
	CACTOCAGTO	CTCCAOTTOC	AAGAACAGGC	ACATATATIO	TOCTAGACAG	TATETTOCAG	ě
	CAGATTCAAC	ACCUARGOLAC	TOTCARCATA	THEOGETICS	TAMARCACAT	COSTICACIA	ğ
	AGAMATTATT	TOGTACAAC	TOAGGAGGAA	TATOTOTICA	TTCATGATAC	ACTOSTTOAS	3
	GCCATACTTA	GTAMBAAAC	TOAGOTOCTO	CACACTCATA	TTCATOCCTA	TOTTANTOCA	3
2	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	MCAATTCCA	acrectionae	Š
	CAGTCAAATA	TACAGGAGAG	TOACTATTCT	GCAGCCCTAA	ADCAATOCAA	CAGGGAAAAG	š
	AATCGAACTT	CTTCTATCAT	CCCTOTOGAA	AGATCAAGGG	TTOOCATTTC	ATCCCTGAGT	ē
	GGAGAAGGCA	CACACTACAT	CATGCTCC	TATATCATOO	<b>GCTATTACCA</b>	GAGCIATGAA	3
•	TTCATCATTA	CCCAGCACCC	TCTCCTTCAT	ACCATCANDO	ATTICIOGNO	GATGATATOG	Ī
	GACCATAATG	CCCAACTOOT	COTTATANT	CCTOATGGCC	AAAACATOOC	AGAAGATGAA	Š
	TITIBILITACI	DOCCAMINA	AGATGAGCCT	ATMATTOTO	AGAGCTTTAA	<b>SOTONOTOT</b>	š
	ATGCCTGAAG	MCACADATO	TCTATCTA1	GAGGAAAAAC	TTATAATTCA	DOACTITATE	ž
	TTAGAAGCTA	CACAGGATGA	TTATOTACTT	GAAGTGAGGC	ACTITICAGES	TCCTAMATEG	Ë
;	CCANATICCAG	ATAGCCCCAT	TAGTAAAACT	TITOMOTITA	TANGTOTTAT	AAAAGAAGAA	5
2	GCTGCCAATA	GOGATOGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACCOCCADOA	Š
	ACTITICION	CTCTGACAAC	CCTTATGCAC	CALCTAGAAA	AAGAAAATTC	COTOGATOTT	Š
	TACCAGGTAG	CCAAGATGAT	CATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGGAG	Š
•	TATCAGITIC	TOTACAMOT	GATCCTCAGC	CTTOTORAGCA	CAAGGCAGGA	AGAGAATCCA	2
,	TCCACCTCTC	TOGACACTAA	TOGTOCAGCA	TTGCCTGATG	GAMATATAGE	TOAGAGCTTA	Š
22	GACTETTAD	•	AAAGGGGTGG	GOGGACTCAC	ATCTGAGGAT	TOTTTOCT	ż
	TACATAMAT	TAGGCAGGAA	AATCAGTCTA	OTTCHOTTAT	CTOTTOATT	CCCATCACC	ř
	GACAGTAACT	TTCATGACAT	AGGATTCTGC	COCCUMENT	ATATCATTAA	CAATOTOTOC	ž
	CTTTTTGCM	GACTTOTAAT	TTACTTATTA	TOTATION	AMATGATTO	AATTTTACAG	Ë
ć	TATTICIAND	-	TOGENTETE	TTCTOTATTO	ATTITANCAD	AAAATTTCAA	2
2	TTTATAGAGG	TTAGGAATTC	CAACTACAG	AMATOTITO	TITITAGIOI	CONTINI	Ž
	GCTOTATTTO	TAGGMETAT	CAGGITTIGGS	ACANATATA	CTITIMING	AGTAGCCTGT	ř
	AAATAAAACA	CTCTTCCATA	TOATATICAL	CATTITACA	CTOCAGTATT	CACCTAAAGT	7.9
	AGAAATAATC	•	TOTABATACT	OCCUMOND	CTCCATOOAC	CAMPITATA	26
;	TITATATIT	TAGATTTTTA	ATTACTA	CTGAOTCAAG	TENTOTE	CTOTOTAATT	ĕ
ર	GTTTAGTTTA	_	TCATTAGCTO	<b>OTCTTACTO</b>	ACCAGITITE	TGACATTOTA	5
	TROPOTTACC	•	ACTITIONAL	ACCATGTAAT	TTTMCTTT	<b>OTCONNATA</b>	2
	GAMTACCTT	CATTITIONA	GAAGTTTTA	TCAGAATAAC	ACCITACCIA	ACATTOTTCA	2
	AATOGETET	ATCCARGGAA	TTGCAAAAT	AAATATAAT	ATTECCATTA	AAAAAAAAA	2
Ψ	AAAAAAAA	AAAAAAAAA	MAA				
2	. 61 40	And Daniel					

AAAAAAAA AAAAAAAAA AAAA Seq Ib No. 180 Protein sequence: Protein Accession #: Sos sequence

Y		#-	12.	11.	₹-	- 51	
2			-	-	-	-	•
	MRILKAFLAC		MANGYTROOK	KLVEBIGNBY	TOALROXAMO	KKYPTCHBPK	•
	CSPINIDEDL		KPUCHUKIBL	ENT PHATER	TABLETINDE	KVPCCVBEAV	::
	PKABKITFHM	GKCAMBBDGB	EKBLEGOKFP	LEMOINCEDA	DRIBBREAV	KAKUKUKALS	- 3
ç	ILPEVUTKEN	LOYKA! DGV	KSVSKPGKQA	ALDVILLIA	PARTORITY	INCELLAPPIC	
2	TOTODAINE	Codenianos	AVECEVETRO	CHARLESON AND A	THIRTHROOM	APSKOVESST OOLDGEDOTE	3 2
	SERVICE CONTRACTOR	TOTAL MALLE	NASVIO TUB	TOTALINET	TOWN TOTAL	DIVERTOLPER	; ;
	LIGIERIKE	EEBOXD1 EBO	ATVNPGRDSA	TWOIRKKEPO	IBTTTHYNAI	GTKYNEAKTN	7
	REPTRUSSPE	_	NBTSOPVTKL	ATEXDIBLTS	<b>OTVIRLPPHT</b>	VEGTEASLAT	š
22	GSKTVLRSPH	_	NTVBITBYEE	BBLLTBFKLD	TOAEDSSOSS	PATGAIPPIS	ĕ
	ENI SQUYIPS	GENPETI TYD	VLIPBSARNA	BEDBBTBCEB	BELICOPENTO	NVMPP88TDI	3
	TAQPDVGSGR	RSFLOTINYTE	IRVDEBEKTT	KBFSAGPVMS	<b>QGPSVTDLEM</b>	PHYSTPAYPP	7
	TEVTPHAPTP	BSROODLVBT	<b>OTTOSYVVIV</b>	PVYNGBTPLQ	PBYBBBVFPL	VTPLLLONGI	7
;	LATTPAASSS	DSALHATPVP	PBVDVSPES1	LEBYDGAPLL	PPSSAGPSSB	LPRHLHTV60	ž
3	ILPOVTBATE	<b>SDKVPLRABL</b>	PVACCOLLLE	PSLAQYBDVL	BITTHAABETL	RPGSRBOVLY	ž
	KTLMFSQVED	PSSDAMMAR	<b>SEGPRPBYAL</b>	SDNEOSQHIP	TVSYSBAIPV	HDSVQVTYQO	š
	glascopen19	19Y8BLITPT	ASLIGPTHAL	SUDDEMBOAS	TOUTHANDS	DOLTALMISS	2
	PVSVARPTYT	TRVFGDDNKA	LSKSSIIYGN	KTRLQIPSFN	EMVYPSEBTV	MPNINTENTAR	2
;	LANASLOSTSV	8185TKGMPP	GSLANTITRV	POHELSQVPE	THETAGVERNIN	VEGABODTEL	ž
65	KPVLSANGEP	ASSDPASSEM	LSPSTQLLFY	STSABFBTBV	LLQPSPQASD	VDTLLKTVLP	ž
	AVPSDPILVE	•	MLHLIVENBA	BBENKHBIB	BIABAGAAAA	HPRIBABLOOL	ž
	TISYASERYE	PVLLK6ESSH	QVVPBLYSND	BLFOTANLEI	NOAHPPRORH	VPATPVLBID	Ξ
	EPLATLINKL	IHEDEILTET	KBBVTOKVPA	GIPTVASDTP	VETDHSVPIG	HGHVALTAVS	Ξ
í	PHRDGSVTBT	KLLFPSKATS	BLEHSAKEDA	GEVOCATEDED	TODOGGOODD	DRGSDGLBIH	ž
2	KCMSCSBYRB	SQEKVYRIDSD	THENSLADON	NPISYBLEN	BEEDNRVTSV	BEDSQTONDR	ž
	BPGKSPSANG	_	ENDIGTOBAL	LPLSPESKAM	AVLTEDEEBG	<b>BGGOTEDBLM</b>	ž
	ENSTATOFSP		ILAAQD8BIT	PGFPQ8PTS9	VTBENBEVPR	VSEARASNEG	3
	HESR IGLADO	_	LVIVBALTFI	CLWLVGILI	YMRKCPOTAR	PYLEDSTBPR	3
ž	VISTPPTPIP	_	I KHPPKHYAD	LHASSCPTER	PETLKEFYOR	VOSCTVOLOI	Š
C	TADESNIPDN	_	AYDHSRVKLA	<b>QLABIDGKLT</b>	DYINAMIVOG	WRPKAYIAA	=
	QGPLKSTAED	PWRMINEHNV	<b>EVIVALTMEN</b>	BKGRRKCDQY	WPADGSERYG	NPLVTOKBVO	ž
	VLAYYTVRNP	TLRINTKIKKO	SOKORPSORV	VICYHYTONP	DMCVPBYBLP	VLTPVRXAAY	2
	AKRHAVGPVV	VHCSAGVORT	GTY IVLDSML	COLONEOTVN	I POPLICHIRS	<b>ORITYLVQTES</b>	3
6	QYV# INDTLY	_	LDSHIHAYWH	ALLIPOPACK	TICHEKOPOLL	AGSO/INSOS	Š
2	BALKOCNRE	KARTEBIIP	BRBRVGIBSL	<b>BGEGTDY INA</b>	GYIMOYYOSH	RPI LTQHPLL	ដ
	HTIKDEWRMI	MDREADLAVM	I PDGQRMAED	SPVYNPNKDB	PINCEBPICVE	LMAESHKCLS	2
	ACCI I TXXXX		LEVRHPOCPK	WPMPDSPIBK	TPELIBUIKE	ELANREDGENI	2
	VADEHOGYTA	_	HOLEKENSVO	VYQVAIDMINL	MAPGVFADIE	OYOFLYKVIL	ž
8	BLVBTRQBEN	PSTBLDSNGA	ALPDONIAES	LEGIV			
à	. m	101 711	97000				

Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Bos sequence

2616010011170	0/471/7000/17
	•

PCT/US02/12476

WO 02/086443 Coding sequence: 148-4518

. 90		20025	10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			1800 1920 1980	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2400 2460 2520 2580	2640 2760 2760 2760 2880 2960	1060 1060 3120 3160	3100 3160 3180 3540	3660 3720 3780 3840	1960 4020 4140 4200	4260 4320 4560 4560	4860 4860 4860 4860 4860
S1 AACAACAAA AAGAACCAAA	ACATTGCATT ACAGAGAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA			TTTGTACCAG TCANGACTTG AGTAGCCATA GCCTACTGAT	CAGTGCTACA TCSCATAGGG ATTCTCTGGA TAAATTAGCC	TCCACATATO TGAGGGGGAG CTCCAGTCCC ATTTCCTCC		AACCCAACCO ACCTATAGOOO GACTTTTATC			CTCCCTGCCA OCCTOTTGTC CAGTATGTTCA CACCGGTTCA	CCAGCTCCTG CCACCTCCTG CCACCCCTG TTCATCCCTG CCAGAGCAAT	GCCAGAGAT TAAGGTCACT TCAGGACTTT GTGTCCTAAA	AGTGACGGGA TTCCOTGGAT TGACATTGAG GGAAGAGAAT AGCTGAGAGC CATTGTTTTC	THEORYTCH THEORYTTH CHEOMATTH THEORYTCH THEORY
41 	ACCALANAA ACCALANAAA ATCALANAAA ATTTCATCA GOCATANAC		ACTOSATTOT ANOTTETTAC TTCSASAGCA AGATTECTOS	AGTTTGCAGT CAGATGCCTA TTCTTCAGAT TTGTCGACAT	CTGGTAGAGA CACACTACAA GAGGAAGTGA AACCAGTCAC	TTCTTAGATC TAACAGAATA ATTCTTCAGG AAGGGTATAT	ATCCTTCTAT ATCTGGGTC AATCTGAGAA TTACAGATCT	ACTEDIONAL GTATTODIET TOTCAGEET AATGETTECA		TGAAATCCAC TCATGATAAC ATGGGAGTGA ATTATACTGT GAAGACCCAG	ATGCAGAGTA ATGCAGAGGA TTGTGCTAGA TCTTAANACA TCATTCATGA	AGARACATT TANAGCANTO GGGTTGGCAT TGGGCTATTA	GCCAMACAT GTGAGAGCTT AACTTATAAT GGCACTTTCA TTATAAGTGT	AGCATGGAGA AAAAGAAA GAGTCTTTGC GCACAAGGCA ATGGAAATAT CACATCTGAG	TTATATEAT ACTAMATOA TTGATTTAA TTGATTTAG TTATTTAG CACTGCAGT
31     TCTATACACT   CTCTOCACTC	GCTANTGGAT GCTANTGGAT GCTANTGGAT TCTCCTATCA TTTCAGGGTT	CATACTACA CATACTACA CGATTTCA TTGTTTGAGG	GACACAGTTG OTTTTTGTG CAAACAGT GGAAACAATT	ATGATTATOA ATGAGTTATO GACCAACTGA	ATTOTOMATO TCTACCACAA TCCCCACCAA TCCACTTCCC	ACACITICA ACACITICA GGAGCIGAAG AACATATCCC	TCACTAAAOO GCACAGCCCO CGTGTTGATO GGTCCCTCAG		GTTATATECA ATAAAGCACT TTTGAGACAC ACAGCAGACA GCCTATGATE GATTATATACA	CAAGGCCCAC GAAGTTATTG TGGCTTGCCG GTGCTTGCCT TCCCAGAAAG	GCCAAGGGAG GCCAAGCGCC GUCACATATA ATATTTGGCT CAATATGTCT	ACAAAGCTAA TCTGCAGCCC GAAAGATCAA TCCTATATCA	ATTCCTGATG CCTATAAATT AATGAGGAA CTTGAAGTGA		TOCOCCUA TATOTITO TITTICIOTA CAGAMATOT GCTAGAMATA GCTAGAMATA
21 CTCACTTCGA CTCCCCCTCC	CCTOGATTOO GTCCTATACA CCCAANCAA GANACTTAAA	ANTOGRAFITE TOGATCAGA TITATCCAIT TOGAGTCGAA	TCCTGCACA CCAGTTOGCT GGACTACTTA CTCATACACT	TTATGATACC AACCAATACCAAT AAAATACAGC	AGAAGGGGCT ACCCCAGATT GACTAACCGA ATCTTTAAAT	AAATGATGGC ATCCTTAAAT GCTTGATACT CATCTCTGAG ATATGATGTC	TTCAGAAGAA AGACATAACA CACTGAGATA GATGTCACAG	CTCCACGGTC TAATAGTAGC AGTTATACCC TATTCTCATC	ATCCCTAGA AGCAATTCCA TACTGAAGAA CTTAGGTATT AAATATCGTT CAAACTGACT	TATTGCTGCC ACATAATGTG TGATCAGTAC GAGTGTGCAA AAAAAAGGGC	GCAGTGGCCT GGCAGCCTAT TGGAAGAACA AACTGTCAAC	AGCAGCAAA	GOTGOTTATO TAAAGATGAG ATGICTATCT TGATTATGTA CATTAGTAAA	ACCCTATATT AACCCTTATG GATCAATCTG AGTGATCCTC TAATGGTGCA CAGAAAGGGG	CATAGGATTC ANTIACTTA TTGTGGTATT TTCCAACTA TATCAGGTTT ATATGATATT
11 CACGCACGAT ATTICCTTCO	CUCOMACCO OTOTTOCCO ACATOTATA CATOTATA TGATCTTA	GAGTTTCACA TOTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA	TCATGCTGAAAG		ANGACATTGA GGAAAAGGA ATGAGCCAA TTCCCAATAC	CAGCCTCTTT CAGCTGCAGA CCAGTTTCAA CTATCCCATT	CTTCATCAGG CTAGCTCTAC AGACTAATTA CAGGCCCAGT CCTTTGCCTA	AGGATTTGGT CAGAGGCCAG AGAAGAAGGC TTCTTGTGGG	AGGACAGTAC ATGATGGGG GTAGTGGGTT GTACTGTTGA ATGGATACAT	CAAAAGCTTA TGATATGGGA GGAGAAAATG TGACTGAGAA ACACAAAAAT		TTCCTOGACC ATATACAGCA CTTCTTCTAT GCACAGACTA	ATCCCAACT ACTCCCAAC AAGAACACAA CTACACAGGA CAGATAGCCC		ACTICATOR ACTICATOR ANGATORA ANGATORA ANGATORA TOTAGGAA ACATOCTEC
1 CACACATACO CAAAAAAAC	CAGCTCCTCT CTTOTTGAAG AAATATCCAA CAAGTAAATG	ANATOCIATA GAGATICAAA GGAAAAGGA GATTICAAG	AATOGCTCAT ACAGTTAGCA TCTOGTTATG TTCTCTAGAC	TOGGANGAC CAOTTGGATO GGTGCTATTC TOCACTAATO	DANGAGGAA AACCAATCA ACGAAATACA AAGGGTGATG ACAGAAAAAG	AACTTOTCOG ACTTATTOA GCAACTTCTOG	GANGATTCAA GROTOGTTCC AGCTTTCTCC TCCTTTCTG	TECADACAAC OTATACAATO TTGGAATCCO TOTCTAGTOG			OTCACACAGT OTOCTOACCT OTCCACTACA CACCAGATTC CAAAAAATT	ACCASTCA ACCASTCA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACTOSACA ACCASTCA ACC		GANGCTGCCA GGAACTTTCT OTTTACCAGG CAGTATCAGT CCATCACCT TTAGAGTCTT	COTOLOGIA COTOLOGIA CASTATATO CASTATATO CASTATATO TAGGIGIAT
٠	10	15	20	25	30	35	40	45	20	55	09	65	۶ ۶	۶ %	88

8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		8889	3 4 4 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	09289	1020 1020 1100 1100	1200 1200 1320 1380		90	20000	2000	9999	2000	8 0 0 0 0		1980 2100 2160 2220	200
GACCAMITT SO OTTCTAGATE SI TITUTAGAM SI CANCATTOT SI CANCATTOT SI		S1 KKYPTCHSPR RVGGCVSENV KGKGKLRALS YNGSLTSPPC				ENNERGEILP INDRAGONV IN FILEATGODY AGTECALTIL NPSTELOGNG I		S1 						TAAATTAGCC 16 TCACACTOTO 17 TCCACATATO 10 TCACACATATO 10 TCACACATCCC 19		
ATO GACC COTA TOTA TOTA TOTA TOTA TOTA TAC CANA		S1 DMMG KKYP MDY RVGG RAV KGKG RYI RVGS	NOV KPSR VLY COLD MPT DNPE MRI GTKY	MEG NYWP LEM PHYG LAE GLES	HPD NKSK TAB DPWR VRM PTLR GPV VVHC	CNR ERONR MRM INDH IQD FILE GVT AGTP QEE NPST		TAY AACA	CCT CCCT ACA ACAG AAA TTGO TTGA AGAT AAC ATCA	TAN TONC TIT TONC MAN ATTIT SON AGON	GAN GCAG GTA TTAC TTT TTT TAC ANTO	CCT TCT CCT TCT TCAN CTA TCAN	CAT GCCT	ACC TCAC NTC TCCAC NTA TGAO NTA TGAO	TAT ATTT TAG AAAT TAT GGAG ATC AGGC	TET GRAN TET TACC TAC AACC NGC TGAG
MOTTICA MOTTICA TEACCAUT MATTIACE MACCETAC		41 	I LQNAPREDOY  TALEKFAVLY  CEDQLIVDAPT  LETTHYNRI  QTVTELPPHT	TGARDSGSS E ESLADPENED OOPSYTDLEM SHESRICIAE	ITADSBNHPD AGGPLKSTAB OVLAYTTVRN YAKHAVGPV	YBAALKOCNR LHTIKDFWEN BNEEKLIIOD IIVHDEHOOVT LGLV8TRQEE		41 	ACTACABACA ATCAMAMA ATCAMAMA ATATTOATOA GOGATAMAAC	ATCTCACTAA AGATAACTTT AAGGACAAA OTTTTGAGGA	GTTTTGGGAA CTGACAAGTA ACTGGATTGT AAGTTCTTAC TTCGAGAGCA	ATACCAGCT AGTTGCAGT CAGATGGCTA TTCTTCAGAT		AACEGGECAC AACTGCCACC TTCTTAGATC TAGAGGATA ATTCTTCAGG	AAGGGTATAT AATCTGCTAG ATCTTCTAT ATGTTGGATC	
ACTGCCCTAG CTACTGAGTC CTGGTCTTAC TTCAGCATGT TTATGAGAAT ATTAAATATA		31 KLVEEIOWSY EMTFIBITOK LEMOIYCEDA ALDPFILIAL	QGGYYHLMDY TWERPRYYYD ICTNGLYGKY TWQIRKKEPQ ATEKDIGLTS	ESLLTSFKLD SEDSTBEGGE KSPSAGPVMS PVYNARASMS	RVOSCTVDLO GYBRPKAYIA GNPLVTOKGV PVLTFVRKAA BORNYLVOTE	Legenioged Nefittchpl Tlmrefrcl Beankdopm Eqyoplykyi	eodneuce	31  -  -  - 	GENATOCTAN GCTAATGGAT GGAGCACTGA TCTCCTATCA	GTGGMATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAA TTGTTTGAGG	AGTGTTAGTC CCAACTCAA GACACAGTTG GTTTTTGTG CAAACAATT	CCAGAGAATT ATGATTTGAGA GAATTTTTGA ATGAGTTATG		ACTOTOACTO TCTAAAACTO ACAOTTICTA ACAOTTICTA GGAGCTGAAG	AACATATCCC CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG	фотестско фастаске масстеота фастеота
TATTOTAAT TTATATTTA ACTUATTA TTAACTTOT AMOUNDIT GAATTOCAA	In sequence: Eos sequence	21 	AVPCEVLTHO DPENYTBLLV NHBYVLGIVA AIVNPGRDSA NBYSQPVYKL	NIVEITERER VLIPESARNA IRVDESERTT VAVVYSQTTQ	EPETLKEPYQ TOY IKANYOD YMPADGSEEY POMGVPEYSL NI POPLKHIR	KTKLBKQPQL ABYIMCKYQB EPINCESPKV KTPELISVIK LMRPGVPADI	uence #: Eos sec	21  - CTCACTTCGA	CCTOQUATO OTCCTATACA CCCAMACA	TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCAGAC	TOGAGTCOAA GAACCTTCTG TCCCTGCACA CCAGTTGCCT GGACTACTTA	TEAGGETORE TTATGATACE AACCAAGCAT GETACCAAT	AAVATACAGC CCCTGAATTA AGAAGGCGCT ACCCCAGATT GACTAACCGA	ALCTITAMAT GACTTCTCAG AAATGATGGC ATCCTTAAAT GCTTGATACT	CATCTCTBAG ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA	GATOTCACAG CTCCACOOTC TAGTAGCCAT
086443 ATCTOTTACT TTANTOACTT TTANTOACTT ACCTANTOACT CTTCATTTO TTTATCCAND	. 3 =	11 	DTV818E8QL C8SEPENVQA LGAILANLLP BEEGKDIEEG GKGDVPNTSL	MALGGTAESL SENPETITYD ESFLOTWYTE SSROODLWST	DIAMBEGETE AGLARIDOKL VEKORRKCDO VVTQYHYTQW LOOIOHEGTV		BBLV. DNA sec Accession	11    - 	CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA	TTCATAACAC GAGTTTCAGA TGTCATCTGA TGTACTGCTT AGTTAAGAGC	CONTINTION TCATACTOTT TOACATCTCC TCTCTOAAAO	CAGAMATOT CTCGAGTCOT GAGAGGACCA TCATAATTT	GCTTATATOG TTGATCTTTT AAGACATTGA GGAAAAGGA ATGAAGCCAA	ATATTECETT CAGCETETT GOACTGCAA CCAGTTTCAA	CTATCCCATT AGACATAAC CTTCATCAGG CTAGCTCTAC AGACTCATA	CANDECCANT CCTTTGCCTA AGGATTTGGT AGGCCAOTAA
WO 02/086443 ATHAMA ATTOTACT ALLITANA ATTOTACAT TANABAST TANABAST TANABAST TANABAST TANABAST TANABAST ATTOTACT	Seq ID NO: 182 Pro Protein Accession		TOTODMIVPK TOKEBIHBAV HEPLTDOYOD LIGTBELIKE REPTROSEPS	GSKTVLRSPB ENISQCYIFS TAQPDVGSGR TEVTPHAPTP					CAGCTCCTCT CATOTTGAAG AAATATCCAA CAAGTAAATG	ANCACATTCA GTCACCGGAG ANATGCAATA GAGATGCAAA GGAAAAGGGA	DATTTCAAAG TTAGATCCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG	AGTECAGAC TOGGAAAGAC CAGTTGGATG GGTGCTATTC	TOCACTANTO AATCCTGAAC GAAGAGGGAA AACCAAATCA ACCAAATCA	ACCOLOUTE CONTROL OF C	GCAACTTCTG GAAAACCCAG GAAGATTCAA GTGGGTTTC AGCTTTCTCC	***
<b>v</b> n .	10	15	20	25	30	35	40	42	20	55	09	65	92	25	80	82

<del>수</del>

COCCURAGO GONCATAN CONCECTOR ATTACACAN ATTACACAN ACCORDANA
COCCURAGO GONCATAN CONCECTOR ATTACACAN ATTACACAN ACCORDANA
CONCURATION CONCECTOR ATTACACAN ATTACACAN ATTACACAN
CONCURATION CONTRIBUTION CONCURATION ATTACACAN ATTACACAN
CONCURATION CONTRIBUTION CONCURATION ATTACACAN ATTACACAN
CONCURATION CONTRIBUTION CONTRIBUTION ATTACACAN ATTACACAN
CONTRIBUTION CONTRIBUTION CONTRIBUTION ATTACACAN
CONTRIBUTION CONTRIBUTION CONTRIBUTION CONTRIBUTION
CONTRIBUTION
CONTRIBUTION S <del>2</del> 

Seq ID NO: 185 DNA sequence Nucleic Acid Accession N: 509 sequence Coding sequence: 501-4514

Seq ID No. 184 Protein sequence: Protein Accession B: EDS sequence

S

PCT/U																												
5220 5280	<b>:</b>	2.5	2000	2000	2008	<b>6 9</b> 8 <b>9</b>	1020 1080 1140 1260 1320			\$ R 6	<b>\$</b> 8	9 2 1	200	720	2 2 8	900	28	823	200	222	1800	1980	2100	280	2 60 0 2 4 60 0 2 4 60 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2800	260	
																								444	~ ~ ~			1
TOGRAMATAG		S1   AVKGKGRLRA	OYKPBROVEB LYQQLDGEDQ PIDNPBLDLF	HIOTKINEAK HTVEGTSASL BSPATSAIPP EHVWPPSST	EMPHYBTPAY EGLEBEKKAV 1PP1SDOVGA	DUNCHRURYIN EDPWRMIWEH NPTLRNTKIK VVVHCBAGVG	LVEATLBKET REKNRTSSII MIMDHNAQLV DFILEATQDD TAGTPCALTT ENPSTSLDSK		15 <u>—</u>	AGGAGGGGGA	ACAGAGAAAA TTGGGGAAAA	AGATCTTACA	TCACTOCOCA ATTICCACT	AGCAGTCAAA	TTTTAAGAT	ACAGTACAG	TETTOTACA	AGTAGCCATA	CAAGGAGGAG	TCGCATAGGG ATTCTCTGGA	TCACACTOTO	CTOCAGTOC ATTTCCTC	GCAGGGAAAT AGGCAGAGAG	GACAACCAAG	AACCCAACC AACCCAACCG TGAGGGGTTG	TOCACACTT	TOCAGAATTA CCAGGAAGTG AGACAACAG	
CCTTACCAM		41 	DYLCHNFREG YDTHIEKPAV KYSDQLIVDM	TEQUATELPP LDTGAEDSEG		GITADSBNHP AAQGPLKSTA VQVLAYYTVR AYAKRHAVGP	EBOYVFIIDT DYBAALKOCH LLATIKDPAR LEWRETLIO MIVHDERGOV ILSLVSTRQB			TOAGAAGCAG	ACTACAGACA	ATATTGATGA	AGATAACTTT	TTGGGACAGA	CTGACAAGTA		NTACCAGCCT	TCTTCAGAT	AAGAAATAAT	SACACTACAA SAGGAAGTGA	AACTGCCACC	ATTCTTCAGG	ATCTTCTAT		ACTORCIAC	CAGCCTTOCAGAC	CHAMBOATOT	
CATGTAATT BAGALTAACA	WINIMA	PPLEMOTYCF	MODSGYNALM I LUTWERPRUV VAICTHGLYG	SATROIRKKE KLATEKDISL BEESLISPK I	TTKSFBAGPV TOPVINEAGN AHPYLEDSTS	QBVQSCTVDL DGYNRPKAYI YGNFLVTQK8 LPVLTFVRKA	RBORNYLVOT LLEGGNICOS SHEFITTQHP VTLAAEEHKC KEEAANBOGP IEGYQPLYKV	epuenbee	. z_	CTCTATACACT	CTAATOGAT GGAGCACTGA	TTCAGGGTT	ANACCAGCA CATANA	TTOTTTOAG	CCANACTORA	CAAACATT	CCAGAGAATT	ATCACTITICA	ATTOGAACTO ATTOTOTATE	TCCCMCN	ACTIOTOACTO TCTAMACTO	ааластама ментатесе	TCACTANAGO		AACGTGGTAT A	TOGACCANT	ANGCACTTC GAGACACTGA GCAGACACTGA	
THOTHCA	AA sequence: 3 sequence:	21   GBEHSLEOOK	OLAVPCEVLT GADPENYTGL LPNMSYVLQI	Boalvapord Slastsopvt Slatvsitey Ydvlipesar	TEIRVDESEK BTVNVVY60T LIYWRKCFQT	EEFETLABPY LTDYINANYV OYWPADGSER MPDMGVPEYS	VNIPGPLKHI GKTKLBKOPO HABYINGYYQ DBPINCESPK BKTPBLIBVI HLMRPGVFAD	NA sequence sesion #: EOS seq 146-4633	<b>z</b> _	CTCACCTTCCA CTCCCCCTCC	CCT0GATTGG GTCCTATACA	CCCAAAACAA	ATOOTOTT	TTATCCATT	CARCETERS	CCAGTT@CT GGACTACTTA	TCAGGCTGAC	ACCAGGAT	CCCTGAATTA	ACCCONDATE	AAATOATGC AAATOATGC	CATCTCTGAG	TTCHGAAGAA		CTCCACGGTC 1	TOTOATCAC	AATTCCATA	
086443 MOTCATTAN ATTITUDAMO	ANAMANA ANAMANA AN ANAMANA ANAMANA AN Beq ID Wo: 186 Protein esquence: Protein Accession #: 508 sequence:	11   HWGXCNMSED	PKDTV818E8 AVCBSEPENV QDLGAILNNL	KERECKOIB PSCKCOVPNT PHONLSCIAE	GRESFLOTHY TPSSROQDLV PICLVVLVGI	ADLHASSOFT LAQLABKDGK LVEKGRRKCD RVVTQYHYTQ	MLOOLOHEGT VMALLIPOPA GLEGOZOTOYI EDEPVYMPIK PKWPIPDSPI VDVYQVALMI	D 0 -	<b>=</b>	ATTICCTION	DIDITIOCO	CATGTAATAG	DADITICADA	TCTACTGCTT	TCATACTOTT	TCATGCTGAT	CAGAAAATOT	TCATAATT	TEATCTTT	OCHANAGOA ATGAAGCCAA TTCCCAATAC	CAGCCTCTT	CTATCCCAT	CTTCATCAGG	AGACTAATTA	AGGETTEGETA	TTOTGGGTAT	ATOTOGOAGC OTGOGTTAC	
WO 02/086443 TOTOTACCT MOTCATTM C	AAAAAAAA Beq ID Wo: Protein Acc	1     WPKASKITP	PCTDTVDM IV SYTOKEE IHB TKHEFLTDDY	TNRSPTROSE NDCSKTVLRS	DITAGEDOS PPTEVTPHAP IPLVIVBALT	I PIKHPPRIN I VAYDRBKVK NVEVI VMITN KGBOKORPEG	RTOTT IVIDS EVLOSHIHAY PVJRSRVOTS VMI PDOORNA YVLEVRHYGG LAHQLEKENS	Beg ID NO: 187 Nucleic Acid Ac Coding Sequence		CACACATACO	CAGCTCCTCT	AAATATCCAA	OTCAGOGAG AATOCATA	GAGATGCAAA	TTAGATCCAT			CACTTOGATO	MATCCTGMAC	ACCUATCA	GAAGGTACTT	ACTITATION	GANGATTCAA	AGCT TTCTCC TCCTTTTCTO	TCCAGACAC	CTAGTGGTC	ATTICAGATO	
	8	2	15		ຂ	\$2	<u>e</u>	35	<b>Q</b>		45		S		. <b>.</b> .		S		55		2		22		8		<b>32</b>	

2	CACTOCAGTO	CTGGAGTTGG	AGCCTATOCC	ACATATATTO	TOCTAGACAG	TATOTTOCAO	200
	AGAATTATT	TOGTACAAC	TOTOMOGRA	TATOSCITICA	TAMACACAT	ACTOSTTOMO	250
	GCCATACTTA	CTGGACCAGC	TORGOTOCTO			DOTTANTOCA	3600
13	CTGTCACCCA	остодисто	CAGAGGCACA	ATCTCGGCTC		TOCTOTOCT	3720
	TCAAATATAC	AGCAGAGTGA		OCCUTANGC		CONNICAN	3840
	CGAACTICIT	CTATCATCC		TCAAGGGTTG	OCATTICATO ATTACTACADA	CCTGAGTGGA	3960
20	ATCATTACCC	AGCACCCTCT	CCTTCATACC	ATCANGGATT	TCTGGAGGAT	GATATGGGAC	4020
	CATAATOCCC	CAASTAAAGA	TATGATTCCT	AATTOTCACA	ACATOOCAGA	CACTOTTATO	40B0
	GCTGAAGAAC		ATCTAATGAG	DAMAACTTA	TAATTCAGGA	CTTTATCTTA	4200
25	AATCCAGATA	ACCCCATTAG	TAMACTETA	GAACTTATAA	TTCMOTOTICS	ADAMAMACT	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
i	GCCAATAGGG	ATGGGCCTAT	GATTOTTCAT	DATOAGCATO	DAGGAGTGAC	OGCAGGIACT	4380
	TTCTOTOCTC	TOTALACET	TATGCACCAA	CTAGALANG	MAATICEST	TOAGCAGTAT	4440
6	CASTITUTE		CCTCAGCCTT		GOCKOOKAGA		4560
₹	ACCTCTCTGG	ACAGTAATOG	TOCACCATTO	CCTGATGGAA	TOACCATTOL	DADCTTAGAG	<b>6</b> 50 60 60 60 60 60 60 60 60 60 60 60 60 60
	CTAMATTAG	GCAGGAAAT	5		TTOATTTCCC		4740
	AGTAACTTTC	ATGACATAGG	ATTCTGCGC	CONTITIATA	TCATTACA	TOTOTOCCTT	4860
35	TYCHAGAT		TATTETEC	TOTATTOATT	TTAACAGAAA	ATTICATIT	4920
	ATAGAGGETA	CAATTATCOA	ACTACAGAAA	AATATAACTT	TRATACAGE	AGCCTGTAAA	2040
	TAMACACTC		TATTCACAT	TTACAACTO	CAGTATTCAC	CTANAGTAGA	5100
40	ATAICTOL	-	AAATACTGCC	CTAGEOTOTO	CATOGACCAA	ATTIATATE	5160
}	TAGETTAATO	-	TTAGCTGGTC	TACTCTACC	AGTTTTCTCA	CATTOTATE	25
	TOTTACCTAA	OTCATTAACT	TTOTTTCAGC	ATCTAATTT	AACTITION	GAAAATAGAA	9340
,	GETTTTATE	-	CAAAATAAA	TATAAATATT	GCCATTANA	AAAAAAAA	2460
6	AAAAAAAAAA	MAMAMAMA	<				
	Seq ID No. 188 Pro Protein Accession	188 Protein se cession \$: 508	n sequence:	ا ا			
20	н.	3.	<b>a</b> .	11.	<b>3</b> .	31	
	_				_	-	\$
	OSPINIDEDL	TOWNVNLKCC	KPOONDKTBL	ENTP INVIOR	TVBINLTNDY	RVSGGVBENV	2 2
33	PKASKITPHW	_	EHBLEGGKFF		DRFSSFSEAV	KONCHURALS	180
3	TOTADAIVER	DIVERSEDIA	AVECEVLINO	OSCIVATION	LONNVREDOY	KPBRQVPBBY	2 8
	TOKERIHRAV	_	DPERYTRLLV		THIBKPAULY	<b>OOLDGEDOTK</b>	360
	HEPLTDOYOD	LGAILMNELP	METVICIVA	ICTNGLYGKY TWO TOWERDS	SDOLIVOMPT	DNPBLDLPPB	420
9	RSPTRGSEPE		NSTSOPVTKL		OTVIELPPHT	VECTBABLAD	340
	DSKTVLREPH	-	NTVBITEYES	ESTETSFILLD	TOARDSEGSS	PATGAIPPIS	009
	ENI SOCY 1PB	BENPETITYD	VLIPESARNA	KAPADATAN	BSLKDPEMED OGDSVTDLRM	PHYSTPAYPP	220
;	TEVTPHAPTP		VNVVKBQTTO		HEBRICLAEG	LESEKKAVIP	780
G	LVIVBALTFI	-			VISTORTO	PISDDVGAIP	9
	AVDREBUNG		DYTHANYOR	WESTABLES	OCPLKSTARD	PWRMIWEROW	9 6
	EVIVALITALV		WPADGBETG	NFLVTORBVQ	VLAYYTVRNP	TLRNTKIKKO	1020
70	GONGRESCRY		DMGVPBYSLP	VLTFVRKAAY	AKRHAVGPVV	VHCBAGVGRT	1080
2	LOSHIHAYVN	ALLI POPAGK	TKLEKOPOGL	TLBPRLECRO	TIBAHONLPL	POLTOPPTBA	9
	BRVAGTILLS			NRTBBIIPVB		GEOTOY INAB	1260
	THOUSENE	MAREHICIAN	REKLI TODFI	LEATODDYVL	EVRHPOCPEN		1380
75	PELIGVIKES			TOUTHOR			1440
	RPGVFADIEQ	YOPLYKVILE	LVOTROEBNP	STELDSNUA	LPDGNIABBL	RBLV	
	Sed ID NO.	189 DNA sec	enence anence				
8	Nucleic Ac Coding seq	Acid Accession #1 M sequence: 304.,831	n 8: MM 002820	02			
	-	=	2	1	<b>\$</b> .	16	
85	COUTTOOCA	AAGAAGCTGA	CTTCACAGGG	 GGAAACTTTC	TTCTTTAGG	AGGCGGTTAG	8
	COCTOTACCA	CACTACTTAT	CATTGATGCA	<b>OCCADATTAA</b> TATATAAAAC	CATTITATES	CTATGGGAGA TCGCTATTAT	2 2

9
7
5
<b>US07/</b>
5
٢
٠.

PCTA										•												
																•						
					9.0												00					
		7 7 8 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6			156		120			9 2 6	2 8 2	44		2 2	10 20 20	116	122			21 12 60 24 0 20 30 0 20	•	120
тоастотата	ACCOUNTY ACCATICITIC GGAGGTGTCC GTCTCATGT	GCAACCOCTC GGAAAAGAAA GCTAGAAAGGG ACAGGCTTCT TTCTGCCTTG	TAGCATTOA CACACACCC COTCACCCAA GCTAGTGACC	AGCCATTCAC OTANGMCT CTGGTTTCTA	Chaggreata Tagggtaatg		51     IODLRRR <i>PFL</i> VBTYKSQPLK ELOSR		<u>ة —</u>	CATGTCCCGC ACGCGATGAG GGTCAACGGT	ATCBCTBCTC	CCCAGGCGTG	COCCTOCOCC	CCCCGACGCT	CTCCAAGAGG CTCCCTACTC	GAGCCAGGAT TCCCTGGGTA GAGTTTGAGC	GCAGAGCATT		<b>a</b> .	ELARRES PT EELEAQUSCF TWLEAPARAP GTLAGHTLITA VQLCALDDUD		51   OTCCTOGAGE CTCCOCTCAG
TTGCTCTTTC	TOTTCCTGCT GCCTCAAAAG ATTTACGGCG GAGCTACCTC TCCGATTTGG	COTACANDA GCNAGAACCA CTGGGAAGTGO ATTCACGOTA GGAGCCTCCC	ATCACTACCA CCTTCCCCAC CTTTCCCCAC	GOGRADATAT AACGATTCTO TTATTTAAT	TATTAACTTA ATAATTTTC		41 		₽_	CCCAGGCGGC ACTGCCCGGG TOTCCCTGCT	GCATCCCCAC OTGGCGCCTC	TAMBCTGCTT	COCMOCCTT GCCACGGCCT	CCCTGACAGC	ACCACCTOCA TCCTGGAACC	CAAGAAAGGG TCTGTTGACT ATGGCATCTA	GOGGCAGTOO		<b>\$</b> .	H VNGAATBBAA AGDVDLPQVR LPLERGVGGC VBGALARVLB TLRAQLAQDG		41    -  - 
TTTCCCTT	AGCGTCGCGG CTCAGCCGCC TCCATCCAG GCTGAAATCA	AAOGTOGAGA CCCOGGAAAC TCTGGAGTGA CTGGAGCTCO	AMAGNATAC OCCATTCCT TTCATATTCA	TCATGLOAT TCATGLOATA ATCTCAAT	AATOTTAAG OCAAGATGAA AAAAA		11   Sarlkravse Hpvrpgsdde Ovtgsglegd		<b>1</b> -	GACTTTOGIT GACTTTOGIT GTGACCAGCG	CCCACCCCCC	GAGGCCCAG	GCCTTCTCCC	ACCOGCOCOCA ACCOGCOCOCOC	TOCOCCETCO CTOGAACCET	CCCTTAGTAC TOCAGCAGGA ATGCCTCCAA	OTGGCAGCGG CTTCACCACT		<b>1</b>	AGAVTSVSLL GROUPREAVA LQAYGVRFTR TCGRHHSANR LHELRVLTAP	005688.1	31     arrangeaca   charctotan
THOTTICH	TCAGCAGTOS GOTGGAGGOT CAAGGGAAG AATCCACACA CAACACAAAG	GUANACTAIC GUANGOCAIG CTGOTTAGAC CACACOTOS GOTGCTCTCA	TOTCTGCCTTT TOTCTGCCTT AGGCGCTAGA ACCAATAAT	CTTACOTTCT CAGAACACCA TATTTAATTA TGCCTTAATT	CACATTICALA CACATTICALA	in sequence:	21   PSCGRSVEGIL NBKPSPNTYN RRTRSAWLD8	guence 5 4: XM_059328 1023	<b>z</b> _	CTOGGAGCGC CACCGCGGAAC GGCCGGGGCT	OGAGCTOOCC CCCCOTOOOT	GGAGGAGCTC	CACTTOOCTO	AGGTACCCTA	GGTGCAGCTT CGTGCAGCTT TGAGCCCACT	AGCACTAATC AGCTGGGACC TCAGGTCCTC	ATGCAAACAC GTGTCTTTC	n sequence: XP_059328	<b>:</b>	RDEGIVEAPL I BLIGPEGPL C POVCOVPAEA RWTDAFVGLS I PDAFSCSWER I SLL	Tuence n 8: NM_005(	21   COOCACCTTO CTCAAACTAA
086443 GESCELETAA AGCACAGTTO	GORDACTORY GORDACOCTC TCCTCCATOA TGATCGCAGA AGCCCTCTCC	OGANGANA CTCSCTCTGC CTGACCCTC GCCTCAGCGG	CTCAGAATA CTCAGAATAT CACCATAGAG TTACCACTCT	ACAMCACTO TANTAMATO	CAMATANT ATOTATCTT AATAMACTT	Seq ID NO: 190 Protein Protein Accession (): Ni	11 21 21 VALLEYAN PSCCREVEGIL BIRATBEVSP HSKEEPHTYN GYRKEGERKK RRITSAMLDS	ND: 191 DNA sequence : Acid Accession 1: XV o sequence: 521023	=-	OCCCACTCCC OCCTGOTOOT AGGCCTTTCT	AGAGCGCGGC CCGAGGGCGG	CCCCAGGG	TOOOTOOCTO ACCCCCCCCC	GOTCCTOON GCTACCCCAG	CCCAGGATOG AGGTCCCCTO	COCACCCAG CCCAGCCCAG ACTCTGGGC	OCTOCAGGCA CCATGTTGCA AAAATAACGT	192 Protein cession #: XI	<b>1</b>	TADDFGYCPE PYCPARRGAS ADGHGHYNYY AVGPPBRHGI VPPTGGCGEG EPTLGPPLES	O: 193 DNA sequence Acid Accession #: NN (equence: 1264439	11   
WO 02/086443 TTCAGAGGAA GESCETT OTTTGGAGAA AGCACAC	ACCATOCAGE GRACATCAGE CTTCACCATC	GAGGGCAGAT AAGGGCCTG AAACGGCCAAA GACCACCTGT CTGGCCCGTA	CAGAGALTAA CAGAGALTAA TOTCCTCCAG CATCAATCCT	TICTICADIO GATATTATCT ACTITITATT	CCAGCTCATA GOTTTTCTC CCGTAGGAAA	Seq ID NO: Protein Acc	1     MORRLUGGWB   HHLIAEIHTA   TPGKKKKGKP	Seq ID NO: 191   Nucleic Acid Ac Coding sequence		CCTCSCATOC CCTCSCATOC	OCCUACTOT OCCUACTOT	OTGGATTTGC CTGGGCAGGG	GAGCGCGGTG	OCCCTOGOOC GCOCACCCCO	GCCCAGCTTG	TOACCCCTA TTAGTCCTOO GOACACTOCC	AGCCTTCTTG TGGTGCCCCT CTATATTAAT	Seq ID NO: Protein Acc	<b>.</b>	HELLGRAPTH ACAVERDARA ELLGRAPTH ACAVERDARA ELAMPROYES SXAPGERVPC	Beq ID NO: Mucleic Aci Coding sequ	1    CCGGGCAGGT  AGGGGCGCAG
	S	0	S	0	S			_	5	ς.		٠,		S		>	S		0	٧	0	8

	WO 02/ AGAGGATGAA GTGTGAGGGA	02/086443 ua gratatorac sea granaccago	ATAGGAAAAG ACTTCTGGGA	AGTATATCAT CGCACAGAGA	CCCCAOTCCT	DOGIATIONA	~ ~
S	GGAGAACTCG TCTCTTGA GAAGTACCA ACCAGTGGA	ACCOTTOGA TOCCTCCATO TCATOGCTTO CAATOCTOGG CCACAAGAA	TOCCMANTO CATTCTCAOC AGTGCTCTOA CTTTTTCCT GGGGAGCTCT	CCTTGGAAAC TCAGAATCCT AGCCATCCG GTATGACTTT	AGCAGCCCGA GOATGAGGAG GACTACTTCC TTCGTGGCTT	GCCGAGGCC CATCCCAAGG AAACACCAGC TCTTCTCTGG	
10	AOTTCOTTC TCATCCTOTC TCATCCTOTC TCATGGTGAA			COCHODOS COCACCIGO ACCCACAGA AATCGTGCO	OTOCCAGA OATCTTCTOC TOCCTTCAGT OTCTAGCTO OTCTTOOTCO		9.9 F F B
15	TTAGGACATT TTAGGACATA TTTGCTCCAA GAGGACCCGT GCTTCCTGGG	CCTTAAGTTA CCTTAAGTTA CCATGGGCAG TOTTGCCATC	ACCOGNOTICE ANDACATINA AGANIOTINO TINGGCANDA TITAGGCANDA	ACTTGGGGGG AAGAGNATC AGGCAGCAGC TTTATAATGT TTTACCCAGC	OGCCATCCTA CCTGGGTGAG CGTTGGCAGC AATTATTCTG	ACCATOGEAT CTCATCAACA CTGCTGGCTG GGACCAACAG GCATCACGGG	****
20	TCACAGCATA ATGAGTTCT AGAGTATCA AGGGTATCAC CTGTTCATAT		AMTECOTOS AMTTTATO GAGGAGGAG GAGGCCATT TTCGATCTGA		TOLACOTOTC CTGGTCAAA GGAAAAAGCC TGCCAGGGTG GGCTTTCACA		22222
25	AAGCCTCAGT TAAAGAACAA GGGACTCCTC ACAAGAGGGC ACAAGAGGGC				ANTOGANGAG GALCCCCAAA GCTGCAGGIC CAGTGAGGIA		22222
30	CCGAAGAGGA ACAGCATCGA GTGGAAAAAC TTGCAATCAG TGCAATCAG	ADANGGCAAG TCTGAAGATC CTCTCTCATT TGGAACCTTC	CACATCCACC CAAGACOOTA TCAGCCATTT GCTTATOTOG GGGAAGGAAT	TOGGCCACT AACTGGTTGG TAGGCCAGAT CCCAGCAGAC ATGATGAAGA	GCGCTTACAG AATCTGCGGC GACGCTTCTA CTGGATCCTC		22222
35	ACAGCTGCTG GAGAGCGAGG TGTATAGTGA TGGGCAACCA	CCTOAGGCCT AGCCACCTG CAGGAGCATC CATCTTCAAT		HAKOK	CAGCGACCTO GATCAGCCTTA CAGTGCCTTA CAAGTCCAAG		22222
40	CCATTITIA AACCAGTGG AGGAAAAGC	GGAAAGAGGC TAACCTGTTG TTCACAGAAG AGTAAAGCCA	ACCCATGAGG CTGGGAGAGA AAGTCACAAG GAGGAAGGGC TATGGTGTCT		TTTAATGOT TGAGATCAAT TAAAACAGGA GCTGGAAAGAG TGCTGGOGGC		22222
45	CCTCGGTTAT CCTCGGTGAG CCTCTCCAT CCTCTCCAT						22223
50	TOTALGAMOTT TOTALGAMOT TOTALGAMOT TOTALGAMOTT TOTALGAMOTT	TTTTAACAGG TGACGTGCGG CTGTGTGGGA CATCCTCTT GGACAATATC				TCCAMBACA ACOTTATCC OTOCCATOO ATTCOCCAGC TCCAGCATAC	224444
\$\$	AGCTGCTOGA CTGTGCCOGCT TTATGCACOO TAACGGGGGCT COGTGGAAGAG	528855	GCTCCTTTT AGCATGGCC CCAGCCTATG ACGGCCTATG ACGGTCAGAC		ONCAGANGCT ONCAGANGCT ONCAGANGCT GALCHCTTAT		*****
9 8	AGAACAAGC AGATGAGGTA CTAAAGAGAA CCCTCTTCCG GTGATATTGG	58458			AGTATCCTTC GAAGTCCTCG GAAGTCCTCG GATTGATGGA CATTCCTCAA	GAGAACGCAG ACGATCAAAC CTGGGGATGG GTGAGAATCA GAGCCGGTGC	72222
8 8	TTTGGGATGC TTGAATCTGA GCATAGCTAG CCATAGACTAG CCATAGACAC TAGACATGCT TAGAGACAC TAGAGACAC TAGAGACAC TAGAGACAC	CACTOTCADA CCTGGAGAGO AGTGATGAGO AGGCCTGCTC AGAGACAGAC GACCATTGCC GACCATTGCC	ACACACATOR ACACACATOR ANTOGOGATA COCCACTOTA TTATTGATTC CATCACATOC		CCAGTACACT TOCTCAGCTA GGGGGAACGG TTTAGATGAA CCGAGAAGCA AGGCTCCGAT		551444
75	TECTOCOATT TCCTCCCTOATC CCCCTCATCA TTCCCATATT ATTCCCATATT OGGNACCOTT	CTATGCCATO TOACGAAGTC COTCCTCCTA OGCTTGTGTA OGCTTGTGTA ATTATATATA	TETTOCTOCTT CCGAMCCTT TITCACTTTT AMATTIAGE TATCAGAGGC		OUTCOCTOTIC CATTERATED ATATETATAT ATTOCACTOT OCTITATAGO		12222
80	TATTANAATA TTGCTGTAGT CTCTAGCTGG ATAGTGGGCC GAGACGGGCG	AGCACTIOTOC AGAGATCTGG TGGTTTCACG CTCCGACAGC GGCGGCTGGA			MONOTAGA CCANGGANG AGCCACTCA OTTCTCAGG		# # # B B B B
82	TITCACTOCC TITCCTGCCT TITCCTGCCT	TCCATCCAGA TCTTCTTTTT TCAGGTTCCT	ATGGGGATCA GCTGTTGTTT ATGGCTGGCC	CAGAGACATT CTAAACAAGA ACTGCACAGA	CCTCCGAGC ATCAGTCTAT GCTCTCCAGC	CCACAGAGA TCCAAGACA	2 2 2 2

WO 02/086443
мостоятия осмосост озвостосом мотостова илискиого тамоскасто 2400
осмости от птитили илитилиого мосомите семенете импесонт 2400
осмость от птитили илитилиого мостоми омилаков одмостим 3320
ометоста мамантаса одитилем мизамитес тамоттост

Seq ID No: 196 Protein sequence: Protein Accession #: NP\_006461

WO 02/086443

Ē																		
88888888888888888888888888888888888888		9	120 180 180 180	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	9 6 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8							660 720 780 940	900 960 1020 1080		1440 1500 1560 1620	1740 1860 1920 1930		
TCATTTGCCT CATCTTTANG AMAGNACCT TTTOTGCTOT TCAGCOTTCC CTTTTOTGCTOT CAMAGNAMA AMAGNAMA		51   KTAARAEGIA	TPSWLEBLAR VNIPCRTRLI VREHSLACO AAVOBLLACO TDERVQROSE	VIASVVTPSV FLMBEVHNIK RQLQRTEHQA VQICGEVQBG EERYNSVLMS	PLSALDAHVG HOLMODYATI VQLEEKGQGG TTVTRGNETG	FPNFLVAVOP OEFLHRYGEL LAISYAVOLT GEVTFENGEN IKIDGVRISD CIAQLPLKLE	NKVAVKO		S1 TGCATCCAG AGTTANATC	OCTCTCAGCC CCTCTCAGCC GNAGAGGACG	TCTGCAGAGC GATGACACCA GAAGAGCACT CCAGTGAAGG	TECTGECCTO ATAGTETCCC GACTTGGAGC AAGTCTGTTG		GOCTGAAGG ATCCAGTTGC GACATCAGAA CCCAGCACCA GCACACAGT		TTTGCCTGCA GCCATCCGA ACTGCTCCCT	TTCYCTATGT TTCYCTATGT CCCAGGCTGG AGCATTCTC CAGCTAATGT	CAACTCCTG
TOCAGOTTT TCANAGOTC TCANAGOTC TCANAGOTC TTTGANCOC GCANACOCC AGTTGANTO		11 	ONAGLPSCH PDAASLRRV VLGLLLTB! NDGQRHPBA YPRRKCVAA	TVOVAPIVV VAVDRPKSI ASRORCKERV DLEIQEGKL MILPGKEYD	SDRBIYILDD 17ERGTHEEL KAVKPEEGGL SYMIKQGSGN LRASSRLHDB	PPCVGHIACV LATIHAYNG HQQIPPAYAG KADBPDWPQB FRLVELSGGC DALERTHWKB	REYAMPAAS		41 COCATCTOOC GOGAGGAAAC	CTCCCA0ATO GCCCCCAGCC CCCCAGGGC	GOACAGCOAC CTTCTGCCTT GAATTACTOT GCTGACCGAG	OTCTGCTTTC TOGCCACACC CACCCAGTTA GGCTAACCAA		TOTATACOTA TOTACACTTA AGAGGAGTAT CAACCTGAG				AGCAGATC
CTTTTTOADO CCTCAGANT CCTCAGANT CCTAGANGT TOTOTOTOC TTAGANTOT TTAGA		31	INTERCHENT REMOTERNEY TECNICATELINIC KALCELINIC PANCHARLI	ILERACYPOG PPSVKSLSEA KLTPICKKICK HLALQRTLAS QAWILKATLA	ORIBLARALY DEVIPMKEGC OPKTGEVKKE GSTAFSTWML IRGVVFVKOT	EMPTONVILV TATOLNIVLM SLEAPARING SOKESLOMAL PROTTEDOIM	VLLBNDSS	. 07	31   THOTOGECAT TECTETOGGA	CCACTGCTCA GGAGCAGAGC CCACTGCTCA GGTCAGCCAG	CCGAGGAACA TCCTOTOTOTA CCTOCATGGT		CTGAAATGCA TCTTCTTAGA TGGAGTACAG	CCTTCCCTAG CGGAATCCAC TTCCAAGGA ATTGGACTTC	TCACCACAC GGCGGCAGGT TCTTCGGGGC AGCGCAACAG		OCTAGOTOCO TTTTOCTCCA GACGOCACT AGCTCCGCCT CAGGTCCCTG	CATOTTOOCC
CCACTOCTO CCACTOCTO CCACTOCTO CTCACACTO CTCACA		21	YHHOLGALKP BSDVNCRLE VRHLLEYTOA KILKLKNIKE LGBAVFILPY	VOXIREBERR NSMTFALKVT SSHEBIQUSP EEECKHIHLG ISGTFAVVAQ	RCANLEGGGR THOLOYLYDC GGSGKKSGDK VINALPHLIN SHAVHLILKA	EVDVRLPPOA RLDNITQSPF RLDNITQSPF ERINHYIMI EXIGINGRTG BGTVRSNLDP	ARALLEHCKI	Seq ID No: 195 DNA sequence Nucleic Acid Accession 4: NM_006470 Coding sequence: 2281922	21    -   TCTAGCTGCC   TGGCCGAGCT	TAGGCGTGGT AGACAGCCTA CTGCCCAGGG CCAGATTCTG		CCTGCCCAC GACTGTTGCC AAGGAGGCTG	AAAGCGCTGG AATGTGATGC AAGGCCCACC AAGGCCCACC					OCCUPACION
ACCCTORA CTCCACAGT TAATCAGTO TAATCAGTO CCCAGGTO CACCTAGACA	AAAAAAA 194 Protein ession #: N	11	ILDEBHPKCK EDVMSLBKHE LAGPEGPAFM RQAILTWAFK	YAWYKAPBOB AQAPTVVTVP BAGUATLAND LOSDERPBPE QMTLLEGGSIA	PREDLIEIGE HLKSKTVLFV PVEINBKKET QAAGGPLAFL MOVYASIYAL	ILINAPEKOMO VSRVLIRELK PTCAMRNIAV SETEARPTSV KKVSPTIRDK SIIPOSPVLF	SVGERQLICI VLGSDR IMVL	195 DNA sec Id Accession	11    -     CAGTANTGAG	TGCAATCATC GACAGAAGAA TCCAGGGGCCA GTCACCCAGC	GGAGAAGCTT TGCTGGTGAG GGCAGTGAAG	CATCTGCCAG CCATCTGCCAG CCCCAGGGAC	GTCAGAGGTC GGCCCAGGC CACGGTATC GCTGGAGAGG	TANGAACACT GGGCATCGC TANGAAAAG TGCCGTTGTT	CCCAGCAGG CCCCAGCAGG GTACTATTT CATCGACCGG		ACCARCTT	TAGTAGAGAT
OTTOOTHECK ATTOCCACK CTCACCOCK CACTCTTOC CACTCTTOC ATOCCTOOTA ATOCCTOOTA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		LDASPHSOLR VAHRKOELSH LBIVCLMITQ ALNYRTOVRL PVVAILGHIY	VLTYIKPIKM HMTARPHIKI VLARONGHLL KTELISAILG	CCLRPOLAIL INITIASAIRK PRALLIGETP VPMSVYGVYI VRDSMINNEH		BEVWENDDNP WLTIAHRLHT	Seq ID NO: Nucleic Aci Coding sequ	1    -  -  - 	TTGCAGCAGG TGGGCCAAGG ATCTAATGGC CAGACTCTGG	TOOGCTCCTC AGGOGATCC GAAGAGTGAA	ACCACAACTO ATCAGCAGTO TOGATGCAGC	CTOTOAGGAA TOAGCCAGGA	ACTGCAAGTT ATAACTCTC TOGAGAACTA CTCAAGTGTC	ACCTGCACAG ACCTGCACAG CCTGCAAAGG	CCCCACTOR TCCTTCCACA ATTTCACA	OCTORATION CTTTCCACTOR ACACCACTOC ACACCACTOC	TITIOTATIT
٧ı	0	v,	8	λ:	0	8	<b>\$</b>	45	20		25	09	65	92	75	80	85	

10	-	· #_	- R-	#-	₹_	<b>s</b> –	
15	MAELDLAAPG DSAEGGDPAG EPVICHENKLKIA LOLERKLKLA EQAALEGANG	PLPRATAQPP ECKEVICOPC CPARISPLSA EKAISKLOAN IKALEYRSA	APLEPDSGSP LDDTRRVKAV PCCPDQCIC QKGVLVSVSB EMEKSKQELB	RECLTCHVNY ODCCOEHSON VKAVAENOPO RAKA I SNIVO	EZEDVOSSEK CZZHLÓPHOV TIVSLDAARR HLLAAVRKNO PLEEYCKPKN	LGRETERDB HIROSHLIT DREAELGCTO ANYMLFLEEK TEDITFERY	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
70	RPSTREGGLO QOSLYLARYY SOMETPLKAC NAIRIVDLOB	KAVITESTVI YAYDITEDED PEVELFOAGT PPRRLGOVID BPEKRAVELO	TANKYLALOE YVGLTCKGID PPGGILBPYG VTAP	ENKKVINTTP RKGEER/BCI VBYDTMTLVH	MEHPYPOLPS SCHIPFWBLQ KPACKPSEPV	RPLHWRQVLS WNGKBFTANY YAAFWLGKKE	2552
25	Beg ID NO: Rucletc Act Coding Begr	Bog ID NO: 197 DNA sequence Ruclaic Acid Accession N: NN_004316 Coding sequence: 433-1149	sequence 1on #: NY_0043 3-1149	91			
:	1    -  -  -		21   	31   TAGTAGGAGA	41             	S1    - ACGCGGCAGA	8
ဓ	acacettcaa acaceadaaa aanaanaaa		TOCTOCTOCT COCCAACCOCC ACCCGGCGTG	ACGCGAGGCT CAGGGAGGAG	CCCGAAGCCA AAAAAGCATT	ACCCCCAAGAG ACCCCCCAAGG TTCACCTTTT	120
35	OTCCCCTCO OTCCCCTCO CCGCCCTCO	CATATTACCT COGGCCCGC GCATGGAAAQ	ACCTCGCGTC CTCTGCCAAG	TCTCTGTTCC CCGGATCGCT ATGGAGAGCG	Tackcccuad CTAATTCCGC GCGGCGCCGC		2 4 2 0 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
40	GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCGCAGCCGC AGCAGCAGCA GTCACAAGTC GCTGCAAACG	COCHOCOCCA OCHOCOCCANO COCOCCCANO COCOCCCANO GOCOCOCCANO	CAGCTGAGG CAGCTGAGGC CAAGTCAAGC TTCAGGGGCT	COCCOCACCA COCCOCCCA COCCOCCCA CACCOCCC TTCCCTACAC		2 2 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
45	AACCTGGGCT AGTAAGGTGG GACGAGCATG CCCAACTACT GACGAGGGCT	TTGCCACCCT AGACACTGCG ACGCGGTGAG CCAACGACCTT CTTACGACCCC	CTCGGCGGTC CGCCGCCTTC GAACTCCATG	GAGTACATOC CAGGCAGGCG GCCGGCTCGC GCCGGCTCGC	GCGCCCCCAA GCGCCCCCCAA TCCTGTCGCC CCGTCTCATC	CAACAACTOCTO CACCATCTCC CTACTCOTCG CTACTCOTCG	900 1020 1080
20	TOGTTCTGAG ATCGCACAAC AAAGAAAAA CCAACCCAT AGCGCTCAGA	GGGCTCGGCC CTGCATCTTT AAAAGAAGAA CGCCAACTAA ACAGTATCTT	TOTTCAGGCC AGTGCTTTCT GAAGAAGAAA GCGAGGCATG TGCACTCCAA	CTGGTGGGAA TGTCAGTGGC AGAGAAGAAG CCTGAGAGAC TCATTCAGG			1200 1260 1360 140
55	ACCTGAGTCA GAGCAGCACA GCTCGGGTCC GAGTTGGTGT	ATGOCANAA COCGITATAG CITCACCICC CITTC	TAACTCCCAT TAACTCCCAT CCGCCCTTTC	OTGCAAAAGC CACCTCTAAC TTAGAGTGCA	ACCICACACC OTTCTTACCC	TOGCAGAAGG GAAAGTTCTT CTCTAGAAAC	1560 1560 1620
09	8sq ID NO: 198 Prot Protein Accession N	198 Protein scession #: NP	sequences			•	
65	1     MEBSAKMESG QQQQAPQLRP AVARRNERER AVSAAFQAGV	2842	21   QOPFLPPAAC HKBAPKQVKR ATLREHVPNG NDLMSNAGSP	11 PPATAAAAA QRBSSPELAR AANKKMSKVB VGSYSSDEGG	41 Aaaaaagba Ckurlapgop Tlabavbyir Ydylbbbegir	51   000000000 0YSLPQQPA ALQQLLDEND LLDFTNWF	120
92	Seq ID NO: Nucleic Act Coding sequ	Seq ID No. 199 DNA sequence Nucleic Acid Accession #: NM_00701S Coding sequence: 1-1065	Tuence 1 #: 121 _ 0070 35	18			
75	1   ATGACCCCC TGCACCCCC AAGGTGGGAG	11 	21 	11   GCCCTGGTGG GTGAAGCCCT GCTGTGCTGC	41   dACCTGATGA CCAGCCCGC TGCTCTTGG	S1 COTOGIANTIC GCGCTOCTC GGCCATCGG	120
80	GCCTTCTACT ATCAATGGGA TTTAAAATGG ACAGGAATTC ATTCCTGAGG		GAGCGACAGT TGGGTCAATG TGAAGAAGCA AGGAGAGAAG GACCAAACAG	CACATTTACA GAAATAGACG ATTGCAGTTA TGCTACATTA AGCATCTCCT	ATGRECATTA CTGGGAACAA ATGATTTCCA AAGCGCAAGT CCAAACTGGA		2555
85	ATGCAGTGA GACAACAGC CTTAAACCAA GTTCCAACTA CTGAATAATG		MATTCTCTT TANGOTOTTA AGNATICAG ACCACACTOT CAGTOTTCA	ATCTGGGTGG GAACTCTGGG AGGGAAAGAA GGACCACGGA GAACCACGGA	CTOTABATCA OTGACCTTCC GAGAGOTOGT GCAGCCGAGG AAGCCTTCAA	OCCIOTAMO TAITTICEDO AAGAMANT COCTOGAGA TCCTGATAAT	8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

L	•	
ř	٤	
	3	
	3	
	2	
	₹	
	5	
	_	

5			•							
840 900 900 900 1010 1110 1110 1110 1110	60 1120 120 340 300		1000 1000 1000 1000 1000 1000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	960 1020 1140 1260 1260 1320	1440 11560 11620 1620 1740 1800	1920 1980 2040 2100	60 120	120 180 180 300	
TCACCAAGGA TGAACCCCTG CAGAGTCATC TCACATCAT AGGCAGTTG TTGAAAGGTT TTGAAAGGGT ATTGATTGC GAAAATTTAC	S1 AVLLPGAIG IAVHDGRII IAVHDGRII IAVHDGRII IFFANTIGEE THOGKIGEE		TTCATCCCGG CATGGETTTC OGGCGCCTC GAAGGCCTGC AGGGGGCTGC AGGGGGCAGG	ANTECANTOR TERCAGAGOC GANCACTETC AGANCTOTOR GNOWCCETA GOGATTGETO TTCTGANGTG	ATCTCTCTC ATCTTCTCT ATCTTCTCT ATCTCCGGA ATCTCCGGA TAGANCTCT GAAANGTCT	TTGTATANGG TTGAGTGCCA COUMAGGAA GATTGATTTG GAATTTCAM TTAGCTACAT TCTACANAT GGAGAATTAG	ACTTATTTAG TATTCTACAC GTACTTAAAC AATATTAGGA	B1 	51 CCTCCCCCA TCTTGTCCT GCAGCCCAC TCGTGCAGGA GCTCCAGCCT	
TRAACTOOA AGNAATCTO TITOSOCCTO TOTOSANTCA CAGGENTTO TOCAANTOCA TITTATITOCAANTOCA	41     Prodaveled   Prodagared   WPVTTRRPHS   CCLECREY	<b>\$</b> _	AGAGAGGGGG AGCCGGCCAC ACCCGGCCAC ATGTGCAGAT CTGCCCAUA TGAGCAGATC CCTTTGGCAG	GLANGTOCTA GLANGTORCA CAGLATCACA TCCAGCTTCC AATTTOTTAT GCCTTGGAGT CCCAACTATT	TCTAGRATT CCCATGACT OTCTGTTTAA TTAAAGCTCT CCTTCCCCTG AAGTTCATGTCT AAGTTCATGTCT AAATCATGTCTTCTT AAATCATGTCTTCTT	ACCCATTOT CCCCTTOT CCCTTTOT CCCTTAAAO CAAAAAATT TOTOTTACTA	ACATGETETC TCACAGAAA AATGEMATG CAATATETAA	41     LEKEDARLILL   GGAVKENPVP	41 ATCCARGCA GCTCTCACA COCCTCBACA COCCTCBACA COCCTCBACA A GAGAGAGAGG	
ACATTOGACC ACCCACTGCC CAAGGGTGCC TAGGGCATOG TAGGGATOG CTTTAGTATA ACTTAGTATA	31 VKPSBPARLA BIDAGNALER BIDAGNALER BIDAGNALER TEDPRLEHEG LGNV	31.	CGCCCACAGC ACTAGNCGCCAG ACCAGCCCAG GTGCAGGACT TCCAGCTCCG GCAGGCTCCG GCAGGCTTGC GGTTCCAAG	CACATOTOCA CACATOTOCA TACCACANGC AGTITOCA AGTITOCA TAGGARAT TAAGAAACTO	ATATEMANG TITUTATTE TTATEMENT TOTTEMENT CACAGAGAN TIGHECTTT ACCTATECT	QUICTNITT  QUATATAGAT  ANTIGCCCT  OTTCTCATT  GATTAGTOT  CATTCTTOT  TRAGAATCAG	TOTOGOTT TITTGOTT TITTGOTGT OATAGAATA	11   13   ALESENDAT 7T HRLAGLESRS	11 	
ZAAAGCATG ZGGAGCTAC TATANTTAT ZGCCCTAAG TATTCTAAA TATCCCAGA TATCCCAGA	- PX00XH		GCCGGGAAG GCCCTGAAC GGCTCCAGT TGCCCTGAG GGCACACTG ACACAGGC TCATCGCTG	TOATCACTC ACTCAGNAA ACTCAGNAA ACTCAGNAA ACTCAGNAA TOACACTAG TAACCACAA TITCATTAATT	CONTRACTOR  CONTRACTOR  CONTRACTOR  CANTANTAN  CONTRACTOR  CONTRAC	TCAPACETOT TCACCATTT AIATTICTOS AIATTICTOS AIACTTT CAACATTOTT TTATACATT	OTTCAFTCA TTTACAGTG CTATTTATT ATTGCTAGTA	HP_000719.1 21 21 DA GSLQAAPERS 3X RACHTATCH	aquence on 4: NM_00174 31 c GCCCCTGC C C ANACTTCT C ATGCACACC O AGGCACAC O AGGCACACAC	
086443 wccacawas rasarting cccarcacc wccarcacc wartanaa ancaranaa rrttanics rasartinics	200 Proteil eeston #: 1 11 ALWORDDVZP ALWOVATWG ELGODLOTPW EDSQAPRPDM GOGRSACKVI	Seq 1D NO: 201 DNA sequence Nucleic Acid Acession 1: NM_0 Coding sequence: 112495	COCCTTCCT CCCCTTCCT CCCCTTCCT CCTCCTCCT CCTCCT	CCTGAGCAA TAAGAGATTC AAGCCAAGGA GCAGCCTGC TCTGTTGTTT ACAATACATT	TACCATIC TACCATIC TACCATIC TATCATICA ATTACTICA ATTACTICA	AGGTTGAAAT AGGTTGAAAT TTGTGTGGGT TTGTGGGGT TTGTGGGTTAAT TTGTGGGTTCAAC TTGTGGGTCTAAC ATTGTGGATCTAAC ATTGTGATCTAAC ATTGTGGATCTAAC ATTGTGATCAAC ATTGTGATCTAAC ATTGTGATCTAACAC ATTGTGATCTAACAC ATTGTGATCTAACA	ANTITUTE ANT	Protein Accession 6: Nr_000715. Protein Accession 6: Nr_000715. HIT	NO. 203 DAN sequence *Acid Accession # INS. sequence: 71486 11. 21 TO ACCESCOC GEORGE OF ACCESCOC GEORGE OF ACCESCOC ANAMAT OF ACCESCOC ATTOM SEC ACCESTOON ACAMAT DAN XTRANGOCCA GEORGE OF ACTION ACAMAT	
WO (12/ ATCHOLDO A ATCHOLDO A ATCHOLDO A ATCHOLDO A ATCHOLDO A ATTHOLOGIC ATTHOLOGIC ATTHOLOGIC ATTHOLOGIC	Beq ID NO: Protein Acc  I HTENSDKVPI AFYFWKGSDS TYGIRPAGGSK LANETRSPWQ GGYYPWFNY	Seq ID HO: Nucleic Ac Coding seq	GTATAGAG GTCUACEGGC COGAGGTCT CAGGGGGGG GAGGTGAGG AACATGGGA GTGAAGAGCA	OACCTTCANO CATATCCTA AAGAAGING TYGAAGAAGA GNANTINTT GOAACTAAT	ACTOTACCAC GTATOTACCA ACATETIVAT TACATATOCACA TOCCATATOT TOCCAMITOT	TATACTTTTA TOAGAGGTGT TTTGTTAAAA CTGATCATT ACCATTCTTT ACCAGATAAT CTAAAATATT	CATATTAATA GTTTTCTCTG ATATCTTGTT ATATTTGTTT AAAAAAAAAA	Protein Accel 1 1 MGPRKFSPFL KASELKOSOE RRRDLQA	Beq ID NO: Nucleic Acid Coding seque  1 CTCTGGCTG GAGAGGTGC GTTGCAGGCA AGACCCGGCC CTNTGTGCAG	
\$ 01	15	25 25 30	35	45	20	\$\$	65	65 25	85	

)	TACTIONAL CANONATION UNICENTE TRANSCENT INFOCUONATIONAL SEGONATION OF TRANSCENCE ANALYSIS ANALYSIS OF SEGONATION OF ANALYSIS OF SEGONATION OF
2	
	Sed 10 NO: 204 Protein dequence: Protein Accession #: NP_001712
15	1 11 21 31 41 51
20	מינינות מינינות ביינית
	eeg ID 80, 120 RM sequence Nucleic Acid Accession #: NM_005161 Coding sequence: 1-949
25	n n n n n n n n n n n n n n n n n n n
30	TOWCHATGE ANGESTAMA ANGECETAN GRECOGNADA TROGEGGET CETRETAETA ANGERGACA ANCECETEET MOTTACCTO GROUNDING CTGTGCOOA CTCACCANT AGCCTCOAC TECTGACAL COATOACTA CACTETTEO
	ATMORDETC CACCACCA GAGAGARG GECCAGART OTTTCCCOAC AGTTCCAGAC AGCATCAGA GAGAACGGT AGAAAGGA AANTGTGA AANTGTGA AGATCCTC
35	AGANCTICET TECCOTGATE TECAGONAG CETECAAGA CITOCHOCTO TOCAGOTAGT GALADAGATE CECATOLOGE ACTIOTACAT CETTOTACAC TETECTACA TOCETACAT GACACAATE AGGICATACE CALGACAGO
40	TOTICAGE CATATOGS ATALGGGG ACTITICACE ACTUALTY OTTOLOGY TITLOGGGG GGGGGACO GGGGCTC TO TOTOLOGY TITLOGGGG GGGGGACO GGGGCTC ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCTCA ATACCA
45	Seq ID NO, 206 Protein sequence: Protein Accession #: M−005352 ·
50	1 11 51 51 51 61 61 61 61 61 61 61 61 61 61 61 61 61
55	MOPRALIE TEVVIVLHIT LKIGGEPHIS
	Beq ID No. 207 DNA sequence Nocleck Acid Accession # 1 No. 201115 Coding aquince: 74-2891
09	15—
65	Амальмая масямазыя ммерамы ттатттым ессиясска каментто во осемствост тимамаса сысстема атстакам катамат стимитетс 120 ссемилсям статактет этстемтет самамате стиссама выальтаты 180 ссеттатовт статактет стасство выеста до подости стиссама выальтатам 180 состатам димантет этментет семешется стальтатам 180 сположения димантет этменение семешется стальтатам
20	TRETTERANTO GRACODCIOC CTETERALAY CACALCANTO COGOCUTATA COLABARDAS COCOCOCOCOCOS, BANACATEC COLABARDAS COCOCOCOCOS, BANACATEC COLABARDAS COCOCOCOCOS, BANACATEC COLABARDAS COCOCOCOCOCO COLABARDAS COCOCOCOCO COLABARDAS COCOCOCOCO COCOCOCOCO COCOCOCOCO COCOCOCOCO COCOCOCO COCOCOCO COCOCOCO COCOCOCO COCOCOCO COCOCO COCO
75	CTTTGGTTG ACCULANGO, GANTGGGTG CTTACAUCK CCCTTCACTT GICAGCCTA, TOTOGGCCA, CACATCCCC CCTGGGCTG ACATGGCCG, GANGGGACK CAGAMAGTTA ACATGGCCG, GANGGGACK GACANGATTA ACATGGCGCG, GATGGGTCA, CCCACAGAG TCCACCATTA, TCACCACCAC, GATCATCACC, ACCAGAGCAG
80	METHYTER ATTOCKEN GENERAL TECHNOLOGICAL MANAGEMENT CONTROLL OF THE CONTROLL OF
88	TRALCTION CTRANTOR OFFICECATION CONTROL TICOTORY CONTROL TO CONTROL TECHNICAN CANADAM

9
~
-
~
=
~
0
S
=
>
-
C
حَم
_

1620 1680 1740 1800 1920	2220 2220 2220 2220 2220	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2760 2760 2820 2860	2940 3000 3060
CTCTTCTCTA GCAACACCAT TCCGATTTGA TCACTACATC GCAATCACC GGAATGACAC	AGATCCACGT ACAGTGACAT ACCTTGGGAA TCCATTGGGA TAGAGGTATC	ATGACATOS CCCATTITO CCTATATIC GTTTOTOCT	GOGGAACAT GAGCCTACAT ACTCCCACCC	TTOTOGOGO TTOCCCOOK
		GACCCGGGCT A GACCCGGGCT A GACCCGGGCC G CACTCGACCCC G TOCAACCCCG G GAGGGCCC G		AAAAAGGGGC T GGCCTTGATT T TACGGGTTTT T
		CTACCAGION GA CTCCAGTOT GA CCTCAGCTOG AG AGAGGTGGAT CA CCAATACACC TO		GOTACCCTTT AN AGGCCTGGG GG AACAAAGGGT TI
		CCACATACCCOA UNICOCOA COTOCOCOA COTOCOCOCOA COTOCOCOA COTOCOCOA COTOCOCOA COTOCOCOA COTOCOA CO		TTTAMAAGA GGI ATTTATCCAA AGI
<b>5585658</b>		OTOCOGORANO OTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC		TAGGGATTCA TITY TOCCCAAGAC ATTI GTTTTTTGGT TAA
WO 02/ GCATACAAG CAACTCCCTT CCGCATCAAG AGCOTTTAAG CAACCCAACC GAAGCCCCTG	OTCCCANC GGGAGNGNG CTTGACCATC CAGTGGCCC CCCTGCTGGC	CACGAAGTEAC CACGAAGTEAC TGAGAAGTEAC TGAAGGGAGT TGAAGGGAGT	TOOCTOCC GCCCTOCC TTACATCACA CTACAGCCAO	CCAAAAGTT AACCCCATT AAAGGGGGCT TTATAAATT
ν.	2	15	20	25

#### Seq 1D NO. 208 Protein sequence: Protein Accession #: NP\_066938 20

11 11 11 11 11 11 11 11 11 11 11 11 11
11 11 21 31 HAQDAYOEDT SPALAGOEGIS SCHOOL SPALAGOEGIS SCHOOL SAVETISES OF THE SAVETISES OF
11 10 MACBANGER SPALLENERS PROTESSON PILANELS LIANGTHES CHILDRES LIANGTHES CHILDRES LIANGTHES CHILDRES VPECLLABO MITHERTE VPECLLABO MITHERTE VPECLLABO MITHERTE VPECLLABO MITHERTE VPECLLABO MITHERTE VPECLLABO MITHERTE VI
HAGEAPOEI PROTELVI LANOTELVI LANOTELVI BAYERATIVOS VPFGLLSI TAVEFTCOI VALGRACI VALGR

## Seg ID NO: 209 DNA eequence Nucleic Acid Accession #: NM\_001327.1 Coding sequence: 89-631

တ္တ

		<b>#</b> _	17 -	<b>7</b> –	₽_	<b></b>	
	AGCAGGGGGC	CTOTOTOTA		CCGAGAATAC GAGAATACCT	carocaccer	CACCETICECT	9
;	CTGAGAGCCG	OCCACAGOCT	CCCCAGCCAT	COSCIACCAT OCAGGCCGAA	GGCCCGGGCA	CAGGGGGTTC	120
ç	GACGGGGGAT	GCTGATGGCC		CAGGAGGCCC TOOCATTCCT	GATGGCCCNG	GGGGCAATGC	180
	TOCCOCCCA	OGAGAGOCOG	gTGCCACGGG	CGGCAGAGGT	0000000000	CAGGGGGAGC	240
	AAGGGCCTCG	OCCCOCOLA	GAGGCGCCC	gogggatecg	CATGGGGGGG	COCCTTCAGO	900
	OCTGAATOGA	TOCTOCADAT	<b>GCGGGGCCAG</b>	асвосисти вовессовия	AGCCCCCTGC	TTGAGTTCTA	360
(	CCTCCCCATO	CCTTTCOCCA	CACCCATGGA	ADCAGAGCTG	OCCCOCADOA	GCCTGGCCCA	500
3	GGATGCCCCA	COCCITCODO	TGCCAGGGT	<b>OCTTOTOMO</b>	GAGTTCACTO	TOTCCGGCAA	480
	CATACTOACT	ATCCCACTOA	CTGCTGCAGA	CCACCOCCAA	CTGCAGCTCT	CCATCAGCTC	540
	CTOTCTCCAG	CAGCTITICCC	TOTTGATGTG	GATCACGCAG	TOCTITICIDE	ccoronnar	909
	PSCTCA0CCT	CCCTCAGGGC	AGAGGCOCTA AGCCCAGCCT	AGCCCAGCCT	0000000011	CCTAGGTCAT	9
,	<b>BOCTOCTOC</b>	CTAGGGAATG	OTCCCA0CAC	GAGTOGCCAG	TICATIONS	GOCCITANTE	720
3	OFFIGICACE	GGAGGAGGAC	OCCUTACATO TITIGITICIO	TTTGTTTCTO	TAGAAAATAA	AACTGAGCTA	

## Seq ID NO: 210 Protein sequence: Protein Accession #: MP\_001318.1

# Seq ID NO: 211 DNA sequence Nucleic Acid Accession #: Eos sequence Coding Esquence: 52-459

		•	;	;	-	70	
	_	_	_	_	_		
	CCTCOTOGGC	cercorogoe ecroneerre reresanda ecogocada gerecogade exrocadece	TCTCTGAGAG	CCGGGCAGAG	OCTCCOGAGC	CATOCAGGC	9
į	GAAGGCCAGG	GAAGGECAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT	TTOGACOOGC	GATOCTOATO	<b>OCCCAGGAGG</b>	CCCTGGCATT	2
ŝ	CCTGATGGCC	сстантвасе сидаваесым таставсава ссыванана совятаесыс ванаваемам	TOCTODCOOC	CCAGGAGAGG	COGGTGCCAC	<b>aggeogecyda</b>	2
	00100000	NICECCODO OCOCIAGODOC AGCAAGGCC TCDBOGCCDA GAGGAGGCGC CCCGCGGGGT	AGCAAGGGC	TCGGGGCCGA	GAGGAGGCGC	000000000	7
	CCGCATGGCG	COGCATODOS GIGCOCTIC TOCGCAGGAI GGAAGGIGCO CCTGCOGOGC CAGGAGGCG	TGCGCAGGAT	GGAAGGTGCC	CCTGCGGGC	CAGGAGGCCG	ន

6 4 4 8 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. 021		1200	20000	5558	1200	1200	1680	2220 2220 2220 2220	22222222222222222222222222222222222222	10000000000000000000000000000000000000	000000000000000000000000000000000000000	33460 3720 3720 3720 000
GCAGCTCTCC CTTTCTGCCC CGCCCTTCC CATTGTGGGG GAAAATAAAG	S1     ARAGOPROGA   LIBLIAMITOC		\$1 	MANTATGGA GAGGCTCCGG GAACCAGAAC GCAATGGGGA		TOTATORANA AACTOORONC TOCATORITT ATOCTCAGOA			TCCAAATT TOGAAGACA TGTTOTCCAG TGACACCAGA AATACTGCAG ACTGAGGCAA ACCTGATTCC	CATCTATCTC TATAMANT OTGATTTTCC CCCAMGANTA AMCAGANTA	ACACAGAMAT TCATTTGAMATA TCTATGATTG TTTCGAMATG TTCCTCCACT TGGTCCACT		CCANTGACTC OTTGACGAAG CTTGGGCCTC AATACCAAT TAGTACATCT
ACCICANT TANCOCATO CCCAUCCTO GTOSICANT TOTTTCTOTA	41       GGRGPRGAGN   GLETSSCLOO		41 GOGGAAAGGG AAAGGAGAATA GCTTCCTAAGC TOTCCAAGCTA	AGGITCCACC AGGITCTACC CUTITCTACC		COTOTOCTIC GAAGCCATCA GTAACTTGTC AAATTTCGCT		CTGTGATTTC ACCATCCTTT GAAAGCTTAG	CATTORCAGA TOGAGOGACC GGCCCGGGTC CTTATAGTA ADACTTGGAA CAATCTCCC GACTTCATAT	OTATOGRAIC ACTOTORORA ATATCCTETT TATAMACTO AMMANIMA CTCCAGGAGA	CATACTORANG TATATATACC TOCTTOCCAN GOTOCAAATA CTTOCAOTO	ACTOTOTIAGO GATTCTGOTA TTTTOTIAAC AGAAGCTCAG	GCCAGACCC TTTATTITAA TTTCCTTATG ACTACTAGA TCAATAGAA
GCTGCAGACC TTGATGGGA AGGCCTCAAG CCCAGCACAA CTTACATGTT	31   AOGPGEAGAT RLTAADHROL	\$5 \$5	STATESTANDA CCACCTTOOT CTUTCCCTTT ACCALAGAGG GCALAGAGG ACCALAGAGGG ACCALAGAGGGG ACCALAGAGGGGGGGGGG	TOAGTCTCTO	TACACATE GATESGAAGE CTTTAAAAG	DAAGOCTOTO TOATATCACA TOGANAACAG TOGTCCTOAA			AAAAAAACT TCAAGAATGA TCCTGATTGA AAACCAACA GAGAATAGAC AATTCCTGGT TGGAGTAAGG	TACATGAACT CACTGAAAAC CAAGAAATCA GOOTCCTTTT ACCAGAAAAA			TAMATTOM OTCCATCACC AGAATCCAGA CGGTATATOT CCAACAATHT
CCGACTGACT GCTTLCCCTU CTCAGGGCAG AGGGAATGOT AGGAGGACGG	ain sequence: Dos sequence: 1		21 GATAGCTGCA TCCCTOGAGG ACATTAGAGT GTACTGAAAT	OGNOCCACTO ACGNANGAGA CCACTCACAG AGNAGAAAGC		TOARDCCTCAC ANGTCCTCAC ACACTCTOGA TTATTGCCT			TCTCTGGGAA TCTCTGGAACC CACTCTTCAC GGGGAGAAAT GGTTAGCTAA AAGCACAGTG	ACCACATGAT TAACAGCCAA CTTTTATATA AAACTCTTCA AAACTCTTCA AGAAAATTT TOTCACTGCC TAGAATATATA	TATCTATAAT TAGANAGGAT TACAGGATTAA CTACTTTAA TTCCTTTAA GCTGTTTAGG GCTGTTTAGG		GOCCTGATTT OTCTCATTTA GACCAGAGGA TCCTTGATTG
086443 recretair orcressor creaserce creasece	212 Proteston #	SOGRR 213 DNA sequence 1d Accession & NA_DO sence: 4161498	ATGAATGGG CACTGGCTGT GGGGATGCAT CATAGTCATT	CAATTGATA GGACACTTTG TTGCCTAGC CTGAGTAATG		COCAGOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	OCATCCCAACTO TCTCCAACTO CAGTCTCCCA CTGCCTCTOT	ACCUACA CACATTACCA CACATACCA CACATTACCA CACATTACCA	TAMANGTET TOCCCAGCE TOCCCAGCE GGCTOTCAAT CCTGGTGCTG AGAGTTTATA ATAAGCAATT	TOTCTACAT ANTOCCTOT CTTTCACATCT TTTCACATCT ANACACATO CANATATIC COCCATTCACA	CACTETATA TCTTTTAGA GCAAAACA AATATAAAA AAACAAGCT TGAGCTTTT TGAGCTTGCT		ANTOCHOGOA NTCACTITAG TANGAGGAG THYGAGTATT TCITTAGGAT
WO 02/086443 accessors rectro accessors oreno another oreno another exerc exercise exerc exercise exerc exercise exerc exercise exerc exercise exer	Seq ID NO: Protein Acc	PLEVELAGAR I Beq ID No: 3 Mucleia Acid Coding seque	CTTATTTTT AGCACAMAN TCTGGGGGGA ACTCCCCCTT	CCCGAAGTTC ACTGATTTT GATGAATGGG CTTGCAGGCA	CTTGCTGGCT TTACATTTAC GGAAAGCTAT CAATCCCAAC	TACCATCATC GACAGCCCAC CGGGGTTGTC CTTTGGTGAT	CCGAGCAAG CCGAGCAAG CAAGTCTAAG GGACCTGTAC	TATTTOAA CACTGATCCA TCCAGGGATG	ATACAGCAT ACAAACACA GCAAGGCAG CACCATTCT TGCTTAGAAT ACATTTCGAA	TCTAGAAGGC TOTTCTATTO GOTCTGACAC CATGTCTGTA TTTTTGTCTAA ATGTTATTA	ATATTTAMO CTTTCACTO GAGTITICAO GCCATAATO GCTTTWACCA CACAGCATCC CTAAATOGAA GTAAATOGAA GTAAATOGAA	OTATOGRAT OTGCTGCTO ACATTTTCO ACCCCAATO CCATTAATA	GGGCATAAAG CACCCATAGT TGGAGGCTUG ACACTAGCTC GGATATATT
<b>~</b>	0 ;	2 2	25	30	35	40	45	20	55	63	07 27	. 08	82

<sup>2</sup> 2

<del></del>

S

9160 9240 9360		2820	90		120 120 140 140	2 6 5 5	78.0		9		120 140 140	2 0 0 0 7 0 0 0		9			25 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
TCGGCATTC GCCATGTGT GCAGCCAAG CTCATTCTT TTTCAAT		51 	ОКТВАКВРОР Воврвілови		S1 	GGAAATGACC GAAAAACGTC ATCAAAAATG CTGGCTCTGC	CTGCCCACTT ACCAGACAA AACATTCTCT		S1    - 		S1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOGICCIOAT AGGICAAAAG TOTICCAAAI	2	QDPAAAQEGB GEKQSQC		<b>18</b> —	
CCCCACCCC AAAAAATTT TCATACCAA TCATCCAATTTAA		41 	TAGPKASPTP HKDLYLPLSL		41 TTCTTCCC CCCOGTAGT GCCAGCGCC GCCAGCGCC CCGGCTGCC CCGGCTGCAC	CTCAGAAAA GCCACTGAG TAGTGGGGAG TCACAGGAA	OGNOGORCT ATAGGTTTAA TTTGACTGCT AAA		41   PPTDMQGIAP KVLEAGEOQL		41 CCBOACTCTT CDACCTATTA TRONGCCCBA CLACTCAACO	AGTGTGAAGA CGCCTGAAGA OCTGCTCCTA TGCAAAA	5	PEEGEPATOR NPERVKTPEB		₽_	GGCAGCAACC CTGGCTGGG GAGGAAGTC CAGACAACT CTGCGAGAG CTGCGAGAG
ACCCICTIC AGGINGIC TICGCAGUS GCTCTGTTCT TITCCAAAA		11 HRAHCSFYRT LEDNINLPQG KTSANMKAPQ LTDITEAIKL	CRVMKGHPSA TPTSPGSLRK	49	11 10101CTTCS CCGAGACTCA OTCTGGAGGA AAAGGGCTC GTAATCGTGG	GATCCCAATC TTGTCCAGCA GTATTGCACC TGGAAGCTTT	CTGATOTCAG AAGGCCACT ATGCTGGAAA AAAAAAAAA		31   PTEEKRQEER EGTLPTFOPT	476.1	TECTOCOT CONCOLOR ATTOCOCTA GUGGACCAG GCATCTOCAG	ACTGGGTGTG GAGGTGAAAA AATGATGCAG TACAGCCTTC	ı	OPEDEVEPAT GPDGQEVDPP	• 1 •	ñ.,	COAGGGCCG TGCCTGCGCT CCACCTCCAG GGGAACTTCA ATGGCATTCA OTTTGCCCTG
TOCCHOTAC AGAGACTIC OTOCTGAAGA TOGCTCTCAA GTAATOTCAT	n sequence: NP_000546	21 BRACKGLPSPT DALLADLTRS NVNPNMSVNV KKTAHSPEQV	QODF8LDENE TPK8KQ5P18	nde M4_130-	DGAGAGOT CTCACTGA GAGTGAAT TTGAGGGA	CATGINACAA GGACCTOTGA GATAATCAGO GGGACTGATG	GGAGATGOTC GAAGCAGOTG TATTOTTCTT CTGCAAAAA	n sequence: NP_569734	21 -  QPVGPVIVQQ DAPGDGPDVR	sequence sion #: BM_0014 1435	21 	TCACCCACAG AAATCCAGAG GACACGTTGA AATAAAGCTT	eequence: ool467.1	PEVIOPHRPE	#: NM_001-	<b>#</b> _	AACCACCAAC GGCACCGGCA GCACCCGGG ACCTTGATC ACCAACCCTG
086443 TCATCOCTO TCAACTOTOA GCAATTATTT CAAGATOTOT	MO: 214 Protein , Accession #: Hi	11   	accdeek prya Ancteseols	NO: 215 DNA seque c Acid Accession () geoguence: 31264	11 AAAACTCTGC TCTTCOTTCT TAATTAATT CAATCCGTGG	CCAGCCAGT ACCACCAACT TGCTGTTCAA	GGATGCACCT TAAAGTGCTG AAACCAAGAA TTACAGTTTT	Protes	11   SERGNDQESS QQELALLKIE	NO: 217 DNA sec 2 Acid Accession sequence: 824	11 † TOTGAGGCAG CLOTGTGAAA ATGTACAGCAG AACCAGCAGA	AGGNACAGG TOGNCCCGCC GTTANAAGAA AATTCTCCC	218 Protes	i HPRPRRYVOP KPEADSQEGG	219 DNA d Access ence: 90	<b>:-</b>	GCAGAGTGAG TGAGCGGCC CCTCCTGCCC CAGGCAGTGT CAACTGCAT GCACAGAGAA
WO 02/086443 coaccett transferor Antiodes transferor Independent gransferor Acceptes g	Seq 1D NO. Protein Acc	MELDFORFDE ODRYFAGIVY EGESTVCSED LVTI I RSGVK	DPPODDOVFI	Beg ID NO: Nucleic Act Coding sequ	1 GOCACGAGGC CTTTCCAACA OTCTTCCTGG TCCTGTGGCA CCCAGGTCGT	AAGAGCTTC AAGAGGGGA AAGAGGGA AAGAGCACC	TTGATCCCAC ATGAGGACTG TAATAAAGTT	Seq ID NO: 216 Protein Access	1     MSBHVTR608   AVQGTDVBAP	Seq ID NO: Nucleic Aci Coding sequ	1 dccagggage TGAGATTCAT CCAAGGCGCT GATGAGTGG GCAGCTGCTC	GCTGATAGCC GGGCAGGAGG CAATCACAGT TIGITCATTA	Seq ID NO: Protein Acc	Swrcretyy Egasaggep	Seq ID NO: Nucleic Aci Coding sequ		ACAGCGAGG AGACAGAGAC GCTTCCCGCT ATGCGAAGTC TCCGCTOCCT GCTTTTACCG
~	01	15	70	٢,	£ 8	35	40	45	80	ÿ	3 6	69	92	75	:	80	88

WO 02/086443

иридиское образования извидуесь на развидуест образования образ

10

13

2

Seq ID NO: 221 DNA sequence Nucleic Acid Accession #: NM\_016529 Coding sequence: 13-1854

25

	9	•
;		į
١	,	į
į		2
į		į
•	١	•

WO 02/086413

							,	;
	CCAGATGCGA		AACTCTODAC	OCTUCAGETO ACATOCTEAC	TAAACCAGGT GGATGCGGGG	OTGACAGGAG TOCACCCAAG	420	
ν,	ACOCOGOCCO	CTOTOTCTOC	AAGCCAGCTG	TTACTOGAGA	ACCEPTANT	AGGREGATA	0 0 0 0	
,	GCATTCAGC			AATACAGTGT	CCATAAGATC	ACCTUTACUT	780	
,	AATOOTCACA		CTTOGGAATC	ACAGOTOA	ACCIACTACIAC		000	
0	TTGACTACCG		<b>GONDOCADAC</b> GCTCCCTTGA	ACCCATCTGC TOCCACTTGG	CCATGATOTO		960 1020	
	TCACCAAGAC		AGGITAAATG	AGCATCCAAG GGAATCTCAC	ASCCCTCCSC	ATCCCAGCTA	1140	
2	TCTCTGGAGC	CCCAGCACCC		AGAGAGATTC	TCCTGTTGGG	TACAAGGGC	1260	
	GCACCTOTAT	TCCTTGTAAC		AGTGTGCTGA	TOCCCATT	ACAGGAGATT	1380	
0	ACGATCCGCA CAGTGATGCC			CATGROCCEG	TCATACOOD	TTCAGCTGCT	1560	
	TOROGECT TO	TCAGCCCTGT		TTGGGGACCC		TCTGGGAATT	1620	
	OTGACCOGCT ACCAGTGCAA	GACAGGCAGG AGCAGGCTAC		OTATCCACAA CATTGGCTCC	CACAGCCOGC	ATCTACTOCG	1740	
^	OTOTITIOCAA		ATGGGCTCAG	AGCCTGTAGG ACTGTGAGGA	ATGREGAMOT	AGCTOTCCAG	1860 1920	
	CTTGCTATAA		ATTCADATOG			CAGAGAATGG	1980 2040	
0	AAGGTGCTAG		CAGGCCTTC	TOOCCAAGOL	GAGAGACCAA	CAGATTICAG	2100	
,	ACCAGAGCCG		CTCAGATGA	CTOTOGOMAG	AGTTCCOGCT	CTGGGAAGTC	2220	
	CAGAAAGTGA		DOMANCACTA	ACATTCCTGC		TACGTGGGC	2340	
S	CAGCCAGTA			AAACTGAGGA	CTATTCCAA	CARGOCCTCT	2460	
	CACTOOTIGO	CAAGGCCCTG	CATGAAGGAG	TOGGAAGOGG	ANGCOOTAGE	CAGCAGTTOA	2520 2580	٠
	CAAGGAAGC		CANATTONA		TTATCAGCAC	AGTCTOCGOC	2640	
0	CAAAGAGGAT			TCTCACGC		CATATOCATO	2760	
	AGTICAAGCO	TACACAAAA		ACTOGRAMOA		CAGCTCTTAC	2820	
•	AAAGCAGAGC	ACAGAAGCA		GCAATGCCAC		CTTGAGAGCA	2940	
Ś	AGCCATGAS		TACATCAGC	AGAAGGTTTC	CHANANGCA	GACAAGACCC	3000 3060	
,	AGCAAGCAGA			стастактас	ACAGAGGGA	AAGAATGGGG	3120	
	ANGCCANTOT	GACAGCAGAT	DOAGCCTTGG	CCATGGGAAA	GATTGGGAGT GGGACTGGCC	TCTCTCAAGA	3240 ·	
c	OTCACATOAG TOCATOCAC		OCAGAGCTOC	AAAGGAAGGA	OCTOBAGETTE ADATACE	GACACGAATA	3300	
,	CTGGGGTTAC		ACACTCACA	CATTAGACGG	сстествелт	CTGATGGACC	3420	
	AGACCTCTCAG	CAACAGCCAA	CTGCGGCCCA	TCTTACTOCA	OCHORANGETT OCTORANGAG	TCCCGAGCCA AggCACGTC	3480 3540	
٧.	AGCAGAGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TOCCATTICTO	CAGGGTGTGTGA	3600	
,	AGCAACAGTG	AAGCTGCCAT		CACTCAGGT		CAGATCTCAG	3720	
	TATCCTCAGG	TCACTGACC		CCTGATCCCA		OTTOTCTIAL	3840	
0	ATGACCATAC		CAAAGAATAG	OCAATGAGGC ACTGGATGGA	AGATAGCACT	GOOTOTGAGA	3900 3960	
	ATGTTTGCCT					CTOTTGGGAT	4020	
	ATGAMITET	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT			4140	
55	ACCCAGGGTG				ANGTONGONG		4260	
	AGGACCTOTA OTTCTGGACC	TOOGCATOAC	ATTCAGAGCT	ATGGTGCTTG TTAATGATGC	CATGGCAACT		4320	
	ATTITITATION				AGGLAAAATT	TACHTETECS	4440	
0	ATTAGECTA				GATGCGCATC	AATGTATTT	4260	
	CACACTTCAG		TCCATCCCTC	CATTCATCCT	TCCATCCATC	TTCCATCCA	0790	
,	TTACCTCCAT	GOTGACATAG	~ -	CATAGAGTAC	CTACHETETO ATTESCHAST		4800	
^	ACCATTATTA GCAATAACCE			CTCAACAGAA	CATATOTTGC	MAGACCCTCC	4950	
	CATTOCOCCA		GCCTTCTAC	ACAGAGETET	ACAGACTOT		4980 5040	
0	TAACACCAGT TGGTGCTGCC	GGGAATTGCT TTGCTTCTGT ATGCC	GGAGGAACCA ATTICCTTOG	ATTTCCTOA	CACCTTOGCT	GGGAAGACTA ANATAAAGAA	\$160	
	Beq ID NO.	Seq ID NO: 220 Protein sequence	n sequence:					
5	Protein Ac	cestion #:N	005553					

10 COLOMANA AUTOTECT ANTOTICA ACCENTION DECORATION TOTAL ANTOTICAL ANTOTICAL ACCOUNTS TOTAL ANTOTICAL ACCOUNTS TOTAL ANTOTICAL ACCOUNTS TOTAL ACCOUNTS TOTAL ANTOTICAL ACCOUNTS TOTAL ACCOUNTS ACCOUNT

Seq 1D NO: 221 DNA sequence Nucleic Acid Accession #! BC017001 Coding sequence: 1-394

82

и 21 и 41 81

37.5

WO 02/086443
sectricist persenance reposacia co quidosesso redigento impliatro re sculatorio versorcies fultificate terminale redigento in analysis and redigente il regionali di radefente

WO 02/086443

2	
124	
<u>S</u> 02	
E	
<u>~</u>	

																		٠																						
9 22	180	240	300	360	420	480	240	009	099	720	780	840	900	960	1020	1080	1140	1200	1260	320	1380	1440	1500	1560	1620	1680	1740	1800	0981	1920	1990	2040	2100	1160	2220	2280	340	2400	2460	
COMOCOOCOGO 1			_			AAGGGATAGC 4		CTGTGACAAT 6	<b>GOCTTCAAGA</b> 6	r presented 7	rocharcorr 7	TOOCTAATOO B	OCCITAATOR 9	CATOTOTOCO		CATATOTTCA 10	_	TACTGAGACT 12	TOCKOALTTO 12	FACANACAM 13	CAGGGCAGTT 13	CAGCTOGGCC 14	POCCIOONAT 15	PCACATOLATO 15			-									_			OTATCATTCC 24	
ODDCCCOORC CD	_		_	_	cerroacace to		CTOGGGACCC CT	_	AACAGAGATO GO	CCTCTGCATT IT	AAACCTTONT TO	DCCACATOCO TO	GOATCETTT GO	CCCCAAGAAT CA	_	ACTOCCUENT CA		STOTTCCATC TA	AAGAGAGAAA TG	ACTTOGGAGG TA	CTGGGCTCAA CA	OCTOTANCET CA	CACAGGCTOT TO	TCAGGCTTAT TC	•	_		•	•	•			CCTCTAAGGG AA	NOCIACANGAG CT					<b>LAMICTA</b>	
ODCOCCOOND OC		-	-		OTAGCAGCT CC	CAGCAGGCTG GG	ממחכדמער כיו	DOGRACOCCA OT	CCANDANGCING AN		AAGGAAAGGA AA	DCATGOATTC TO	OFCACOTOTE GO	_		PITCCIOCIC TO		TAGACCIATC OF	TCCCATTACC AN	-	-	OCTANGGTCA OC		-	AAGCTGAAAG AC			MATATTIT OC			TAGTAGGAGT OC	AGAGGGGGTT CI	TICTCACTEC CX	TTCAATAATA AC	DOTORCCAGE A			_		AAAAAAAA AA
COCOTCOOO &				-	CADACTTOCA O	-	CCTGGGGAGA G	DIACAGIGE OF			ATTCAGCTGC A					CAGAAGTOTO T			AMACTOGGA T	_	_			_		STCACTTCTO C		CACCTATCAC A	CCTTTCTCTC 1	CTGGCCCTCA 0	GOACCCACTO T	ADDACATTCC A	GCAGGCCTTG T	OTTICICOL 1	AUTTOACTOR O	CATCCTGGAT T			TACTATCTCT 0	TTAAAAAAA AAAAAAAA
AGGGCCGGCG C			CACTACTTCT A	_	DCATCCACAC O	-		•		-	TATCGACTAC A		-		_	AAAACCTCGT	_			_	_	_	•	_	_	TAGGACAGT O		OGCCATTITI' (		_	recardager (	TAGGCCAGGT A	ACAGAGTAAG (	TTARGECTER	TCCCCOGGAA A	DOCALTOTOS (				THATTATA
AACOCTOOOC A		_	CCAGGGGGGT (	ACTOCAGOGA (	OTACCTGGGA (	_	AGGGGTGCAT 1	•	_	-	TACCICITA	_			_	ATCAGAAGT )	_	_	_	_		_	_		•	GGAACTGGGA (	OCCULIANCE A	AAGAGCTTGT (		GAAGGCACTA	AGTGAGTCTC .	GGTATGGGGT	COCANAGOGA	CTCCCCACTT	GCATTCTCTT.	OTOTOTOM				MAATAAAG
		'n			_		0					2	:	-	-		200		-			2					2					33				:	5			

Seq ID NO: 224 Protein sequence Protein Accession #: AAH17001.1

45

11 21 31
LIGHADAGRO APEDPOPSOO AQUESTISCRI IAL
TIZRADESSP PIPULATIKOA QCODPTYSPO GCC
YLOAGTPOLO 8

Beg ID NO: 225 DNA sequence Nucleic Acid Accession \$: NM\_021048 Coding sequence: 1..1110

55

ANGECTION CECONAGE TEACCORE ANCOCIONA MAINTENA ANCOCIONA ဗွ 65 2 75

Seq ID NO: 226 Protein seguenco: Protein Accession #: NP\_066386

8

15	888888888
7	 STBTSSSFPB
31	PLAVEDASS
11	 Etogleboada
11	NPBEDLOSOS
-	) MPRAPKRORC
2	

9	Seq ID NO: 227 DNA sequence Nucleic Acid Accession 1: NN_005028.1 Coding sequence: 82-1314
15	1 11 11 11 11 11 11 11 11 11 11 11 11 1
20	TOGGANTAN GOMETTOON OCCOMBINE TRICCHANA GRANDEN TRICTETT TAKTOCTAN ANABORCAN TAKTOGTAN ANTOCCAN ANTOCAN ATTOCAN TAKTOCAN ANTOCAN ANTOC
25	ARACACAN CANTENDO AMANTEN ANGORACO ANANGECE CATANDE DECEMBE ANANGEMA AMANTACHO ACCTITECT TECHCIMAD ATUNDAMO TOTACIONO AGAINST TATALAGGO ANTINOTA GRATCANCA AGRICADA ATACANAN ANGORANTA
30	TOTICISACIA GRADATICATO TROCACITA MANATOGIC MACTETATO MANACOM, MATANTA MANATOTA TRANSCATO TOMOGETE TOMOGETE TROMARTIC MANATAGIA OFFETETICA MANATAGIA TECANATIC CITETINAM GITTATICA MANATAGIA TECANATIC CITETINAM GITTATICA MANATAGIA
35	TOTTICTHE COMMENDED GENERALE ANTICHATE CONMENDE GENERALE CONMENDE GENERALE TOTHIGHNER TOTHIGHNER MACHIGAN RECORDANT OTTICHATE TOTHIGHNER MATHEMATE MACHIGAN REPRESENTE ANTICHAGE ANTICHATA ANTICHAGE ANTICHAGE GENERATIFA ANTICHAGE GENERATIFA CAURITHAGE ANTICHAGE GENERATIFA CAURITHAGE ANTICHAGE GENERATIFA CAURITHAGE ANTICHAGE GENERATIFA CAURITHAGE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATION CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERALE ANTICHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERALE ANTICHAGE GENERATIFA CAURITHAGE GENERATIFA CAURITHAGE GENERATIFA CAURITHAGE GENERATIFA CAURITHAGE GENERATIFA CAURITHAGE GENERATIFA
9	TOTTATIONAL TRUTOTION OF OCCUPION TANANTANA AGRACTANT GAMONOMO Seq ID NO: 1218 Protein sequence: Protein Accession 8: NP_003016.1
45	11 21 11 41 41 41 41 41 41 41 41 41 41 41 41
20	ERECHORY TRANSING PERMANAT INFORMETH HAVDUREDS PROAFTIAL, IRANTROMS RECIPIESTO GESENGATION INFORMATION OF STREET HAVE AND STRE

YLPRPTVEOB AAAVEGMIAI		51  -  -  - 	CAAGGCCAGG GAGAAGCTGC GGGCTGGCCC GGAAGGCCCC	TCCAGOTACO AGGCACCC TGGATCCCO TACATGGAGA
VERTPEEDE INGLYLERQ EYPLÄLTER, VARLYERAN EYREVREGER AANSGHIAT IDLEOVLAAL GITRIFIKDA KLYGLEDKE IFLEKAIHER FLEVNEGER AANSGHIAT SRMAVLYRGV IVDRPFFLI BRRIGTILP MERVRIPETH FYSCHDFEEL		41 	CTACACCCTO CCTGTGCAAT CCTCAGCCTG TTCCCCCCAG	TACANCIE TETTECAM COMBANDO COCCUMANTE TROBACCHOR COCCUSATION CACAGACOCC ACAGAGATO MACCACCC GATRAGACA MANACCCTO TRANTCCOO THATTITI CTCANACCC TACATGARA
VJATPYZODE ÍSGGUVLÁRQ EYPLÁTLER, VKAGJVERA, HEKKGYVEY IDLKOVLKAL GITBIPIKOA NITOLGÓNKA IPLGKAJHKA FLEVNEGOSB BRAVLYRQV IVENÞPPFLI RRRAIGTILF MGKVKHPFTH KTSCHOFEEL	8	31  - TCCTTGCAGC CCAGCTCCAG CCAGGAACAC		
ULBIPIEDE ISMULIERO EVELATUERI IDLEOVUKAL GITBIPIKDA NUTGUSCHKE BRHAVLYROV IVDHPPPPLI RIRRIGIILP	Beq ID NO: 229 DWA sequence Nucleic Acid Accession #: NM_D03699 Coding sequencs: 12-398	1 11 21 CARCATOR OF ANTAGENCE CONTROL OF CANCERTOR CANCESTER CANCESTER OF THE CHARACANA.		
ISMMLVLGRQ GITBIFIKDA IVUKPPPPLI	8eq ID NO: 229 DWA sequence Nucleic Acid Accession #: NA Coding sequence: 12-398	11 	GAAGGACTOT CACCAGCTCC ACCCACCCGC GGCCGTCATC	AOCCCCAGGC TGATGACTTO CAGCCCCAG TCCTTCTGTT
VLRIPYEGDE IDLEDVLEAL SRMAVLYPQV	Seq ID NO: Nucleic Aci Coding sequ	1  - CGACATCAGA CAGCCCTTAC TCTGCCGGGC	ATCTGGTGAA TCAGCAGCGG ACAACGCTGC TGAGCCTCCT	CATOGRATOC CATOGRATOC ACAGAGATO GATTICACAC TAAATGATIT
S	55	99	99	70

6660 6660 720 720 720 720 720 720

92220

Seq ID NO: 230 Protein sequence: Protein Accession 8: NP\_003686 75

200 8

Beg ID NO: 131 DNA sequence Nucleic Acid Accession 8: Dos sequence Coding sequence: 126-752 83

<b>S</b>
≍
·+
rie .
-
==
~
=
S
$\rightarrow$
5
_
Ĉ١
_
<b>P</b>
ρ.,
ρ.,
ρ.,
<b>D.,</b>
Δ.
Δ,
ρ.,
ρ.,
Δ.,
<b>D.</b>
Δ.

WO 02/086443

	-	<b>a</b> _	<b>12</b> –		₹_	-21	٠	
	CCGGGGGGGT	COCTCATOCT	COCCAGCOTO	OTTOAGCOOC	TOCCCCOTT	отоставлас	. 09	
	AGGGGGGCAG	DANTICTOAT	OTGANACTAA	CASTCTSTOA	GCCCTOGNAC	COCCACTOCA	. 021	
^	ADANGATOMA	GCATATCCAC	ATAGGAAAG	AGTATATCAT	CCCCAOTCCT	<b>GGGTATAGAA</b>	180	
	OTOTOAGGGA	CAGAACCAGC	ACTICTODDA	COCACAGAGA	CCCTGAAGAT	TCCMOTTCA	240	
	<b>OCACALCTCO</b>	ACCOLLOGAA	TOCCAAGATO	CCTTOGAAAC	AGCAGCCCA	OCCOAGGCC C	300	
	<b>TCTCTCTTQ</b>	TOCCTCCATO	CATTCTCAGC	TCAGAATCCT	OGNICAGGAG	CATCCCAAOO	360	
	GANAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCATCCG	DACTACTTCC	MACACCADC	420	
>	ACCCAOTOGA	CAATOCTOOD	CHITTITICCE	GTATGACTTT	TOOTOGETT	TOTTOTOT	480	
	cccatotoac	CCACAAAAA	GOGGAGCTCT	CAATGGAAGA	COTOTOCOTOT	CTGTCCAAGC	240	
	ACCASTCTTC	TCACCITCAAC	TOCADAGAC	TAGAGAGACT	OTOGCAAGAA	GADCTGAATG	900	
	ANGITTOGGCC	AGACOCTOCT	TCCCTGCGAA	CONTINUE	DATCTTCTOC	COCACCAGGC	999	
	TCATCCTOTC	CATCOTOTOC	CTGATGATCA	COCAOCTOOC	TOOCTTCAGE	GOACCAAATT	720	
n	TTCAOCIATGO	CTOTATTCTO	COGTCAGAAT	CAGAGAGTCA	AGCTGGGCAG	AATCTCTCCC	780	
	CAAGAGTTCA	<b>OCCUTOCUM</b>	GOAGACTGCT	CCATCAGTGC	CCACCTOTOT	OGGNACAGOC	840	
	TCACTOCAC	CCCCATCTTA	CTGAOTTOCT	TCACGTGAGG	AAAAGGGGGC	TTTOOCCCTO	900	
	TOACTCAGTT	COCATTITIO	GATTGCATAC	TOGMANGAN	GCCAATCTTC	TTGCTAGTAA	960	
	ACCABONICE	COCCIOTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAMMATCTO	1020	
<b>-</b>	AGGGAGGGA	GAGGTGGAAT	ACAGTAGTTC	TTOOMTCTO	ANGTOTOCIA	TITGATCAGG	1080	
	TTATTTCCTO	COACTIGGGA	AAAATCTGAT	TOOTOGGGAT	CTCCTAGGAC	CTAGTGGACA	1140	
	TCTGGTATTA	ATTTAATCTC	ADDAMANCA	AGAAATTAAC	CCAGAGAGAG	100001111	1200	
	DOMNITCADO	<b>OTAGCTACCT</b>	CCAGACCOTO	<b>STOTCTOBCC</b>	TCCATTITIO	TCTOTCATTC	1260	
	AGCTCTGACT	TACAGCTGCA	GICACCTITIO	CTATAAGGCA	CCTOOGTAGA	AGGGTGGATG	1320	
n	<b>BOCTTCACAT</b>	CATTITITI	CTTCCTTTAG	DOTOCOGGAT	TOOTTTOCCT	TICTITION	1380	
	<b>PROTEINT</b>	GTTTTATTTO	TOTCOAGATT	CATTITION	TOCOMOGNET	TOMMAGACC	1440	
	CAGAAGGATG	CCACCAGTTT	TTCCTTGAGG	CCTAGGATTT	TITATICION	CCCGAGCAGA	1500	
	OUTMITTEET	CACACTEMO	TOCACCAGTA	GCACCAGCCA	TTTTGAGCAG	AGTACCTCTT	1560	
	TOOGGAGCTT	TICOTITION	ATTITITION	ATTCTCTTC	CTTAGCAGCA	AGGTCTTTTT	1620	
_	TCCTAGAGAA	TCTACTCCOT	TOCHOMICA	TTGCAACCTC	AGGAGCCCTC	ACTOATTOAG	1680	
	TOCTOTOAGO	CTCATATACT	ACTITOGACT	CTGGALACAG	ATATOGGITIC	TATTCTCTAT	1740	
	TTCTACTOTO	TOTOTTAM	CAACCOTCOO	AGACCAGATO	ACCIGITAGA	TOCCIAOTCC	1800	
	TOTATAACTC	CACTCTOTAT	OTTICALIOF	ATGITACTOC	ATGCTTCAC	CTGCTGTACA	1060	
	GTOTTTOTO	GATOCTCTTT	GAAGATOOTA	CTTTATATT	-			

Seq ID NO: 232 Protein sequence: Protein Accession #: Eos sequence

Seq ID ND: 233 DMA sequence Nucleic Acid Accession 8: CAT cluster AYATATANG TANDERGAR ATTORDERGY AND ATTORDERGY ADDRESSED AND ATTORDERGY ADDRESSED AND ATTORDERGY ADDRESSED AND ATTORDERGY ADDRESSED AND ATTORDERGY ADDRESSED AND ATTORDERGY ADDRESSED AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY AND ATTORDERGY ATTORDERGY AND ATTORDERGY ATTORDERGY ATTORDERGY AND ATTORDERGY

TO CITOGETE CECUTOR CITETERIA CALLINEA CONTROLE

recourder destructed Autrothac treatabath Autracers Interpret 2386

OASTITUTED THEORITE TRYATUMA ANTITUTED TROUBLES CONTINUES 2386

AUACTICAL SECURITION TRYATUMA ANTITUTED AUTRICAL CONTINUES 2386

TITADAMON CITATANA ANTITUTED AUXILIARIA AUTRICAL SECURIARIA 2386

TATADAMON CITATANA SECURIARIA ATENTITUDA AUTRICALA AUTRICA CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC CONTOCARA AUTRICAC ACCACACA.

20 See 10 No. 131 8 NA sequence CONTOCARA CACACACACA AUTRICAC AUTRICAC AUTRICACA AUTRICACA AUTRICAC AUTRICACA

Beq ID NO: 235 Protein sequence: Protein Accession #: Eos sequence

65 Noclair Actd Accession 8: NY 002075 Coding sequence: 406..1428 WO 02/086413

PCT/US02/12476																		•
	1140	1200	1260	1330	1380	140	1500	1560	1620	1680	1740	1800	1860	1920				
	CACCOCCTCG	CHRISTICACC	COCCIACIA	TOMOCOTOTO	POACOGOATO	ACCCTOCAGA		MODOCAOTO		INATGAGGAA				TAGCACCCTG				
	CCCAATGGAG AGGCCATCTG	COGGCAGACC AGGAGCTGAT (		CCATGLAGTC TGAGGGTGTG		CONTINUO	CCCGACCCC	TT-CTCCTTT	Chchadadach	COCTOTOCCT .	DOCCCAGCAG ACTTGAGTCT	SAGCCACTAC CTTTOTCCAG GCCTGGGTGG 1	MOGGICCIO OCCUPATOR	CAATAAAGTG 1				
	CCCAATOGAG	COCCACACC	TOCCCTICE	TCT000ACT	MACTICCTICA	CTCAMATCT	DCAGCCCCT	CCCACTANGC	DCATCAGGGA	AGTOCTORON	ООСССАОСЛО	CTTTOTOCAG	TAGGGTCCTG	MONCACCTIO				
	CTOTTTCTTC	отттолосто	CATCACGTCC	CACTGCAAT	TAACAGGGTG AGCTGCCTGG	GOACAGCTTC CTCANANTCT	MCACACTCA	COCTOCCATT	TTGGGAGGCA GCATCAGGGA CACAGGGGCA	CCCTCCCCAC AGTCCTCACA GCCTCTCCCT 1	OCCUTTION 0	GAGCCACTAC	CTGGCACCAC	THOUGH			sednence:	9 00 00 00
086413	COACCCAT	CCTOCCOCTT	CATCTOCGO	ACCIACOACTT	CTOGCCACOA	CAGGITTCCTG	SAAGGCAGTG	TCTATATTCC	GACTOTOCCT	CCATGOCCTT	COCCTCCCCA	TOCTCCCCA (	SACTATOOCT	TCTACCTTTT		•	237 Protein	N . I worse
WO 02/086413	GAGTCOGACA TCAACGCCAT	GATGACGCTT	CACCACACACA	TOOCTOOCT	OOCATCCTCT (	GCT0T00CCA (	AAGGGAAGTG	OCTOTACTOT	CCCACCATGO		COACCACCTO	<b>GCCCTAGGAT</b>	TOCCCCTOT	TICTCCTTTT TCTACCTTTT	ŧ		Seq ID NO: 237 Protein sequence:	Protein Accession 8: NP_002066

Bag ID NO: 238 DNA sequence Nucleic Acid Accession #: CAT cluster ဓ္က Beg ID NO: 239 DNA sequence Nucleic Acid Accession #: NM\_001786.1 Coding sequence: 130-1023 

Seq ID NO: 240 Protein sequence: Protein Accession #: NP\_001777.1 

S1  -  -   EISLINELRH   QILQGIVPCH
41,     EESOVPETA1   DEBLUKSY1
21 11 
11     GEOTYGVVY    MQDSRLYLI
MEDYTKIEKI G PNIVELGOVL P
82

WO 02/086443 SERVIZEDLE PRINCIPAL STREAMENTS PRINCIPAL STREAMENT RELIGIORED SERVIZEDLE OLICIBROLIT SEQ ID NOT 341 BRA SEQUENCE OCCUPANT SEQUENCE IN 132-64  13 13 13 13 13 13 13 13 13 13 13 13 13 1
VYK NEL N
ACMANCAM TATCTTATT TATCTCATT TATCTCATT TATATATA TOTATATATA TOTATTACT ANGRATOTT TOTATTACT ANGRATOTT COTATACT COTATACT COTATACT COTATACT ANGRATOTT COTATACT ANGRATOTT COTATACT ANGRATOTT COTATACT ANGRATOTT COTATATACT
CCTOTTGACC AATATTGT TTGATTGAT TTGCCATTCC TAATAAGGTG TGACAATAT ATCTGCCAT ATCTGCCAT ATCTGCCAT ATCTGCCAT ATCTGCCAT ATCTGCCAT ATCTGCCAT TCACTGCCT TCACTGCT TCACTGCCT TCACT
ACCURACT TCATGGGTT CAGGGCTC  AAACCTAGG ACATACCTTC ATGTGGCTCA  ATTCTTTCATGG CTGGTGGTCAAAACTCAAAAAAAAAAA

9 2 2 9

нимацаца телетан атупталера втивтиры телемитель месуверо посучеры изветнул вымующь отзетулу опсоледые векороваму едометьще сытиятия опеторето регенвате горметота мысседова съссеряй твутрате калеводог у

Seq ID No: 244 Protein sequence: Protein Accession 8: AAD16433.1

2

22

2

15

Beg ID NO: 245 DNA sequence Nucleic Acid Accession #: CAT cluster

30

35

		WO 02 Seq ID NO: Nucleic Act	WO 02/086443 8eq ID No. 248 DRN sequence Notaliste Acid Accession 5: NN_003392 Coding sequence: 758.:1855	uence \$: NM_00335 1955			•	
	S		=	<b>.</b>		s.	<b>5</b> -	
	9	TTAGGAAT AACTGATTAT CGCGCTGGTC CATCCTCCAC	COBOCTOCT COCCOCCCCC CCCCCCCCCCCCCCCCCCC	ATOTTANTE OCCOCCOAC OCCCCCOAC	TOGAAGTOOC GOAGCTGCAT CCCCTGCCCT CCTCCTTGGC	TTTCCCACA TTCCCAGCTG TCCCTCCGGC AGCCTCTGGC	TCGGCTCGTA GGCACTCTCG GGCAGCGCCC GGCAGCGCGC	
	15	GOCCCAGOTT GAGGACTGA GGAAGGAGC TCGCTGGCOT TGGTGGCOT	OGGCAGAGA GCACAGCACC AGCGCCTGGC GCCCGGGCA AATTTGGAAA		CCCCAGCOCO CCCCACCACA TCACTCACA CCCACAAATCA CCCACAAATCA CTATATCTTO		ANTTACCEAG COAGCOAGCA ACOTTTOTAA TOAGOTTOCO ACTCACOGAG	
	. 8	GAGAAGCGCA TOTATGCTTO OTCCATTOGA CAATTCTTOG	OTCAATCAAC AAAATTATCT ATATTAAGCC CTAGTGGCTT TOGTGGCTAG	AGTANACTTA GAGAGGGAAT CAGGAGTTGC TGGCCATATT GTATGAATAA	MACATCTTT TTTGGGGATG TTTCTCCTTC		TOUTTTAACT CTCTCCAGAA CAATOTCTTC TAATTGAAGC TATATATAT	
	. 25	AGGAGCACAG CCACTTOTAT ATGCCAGTAT TTTTGGCAGG AGCAGGGGTG	CCTCTCTGCA CAGTACCACA CAATTCCAAC GTGATCCAGA GTGAACGCCA	DECADENCAL TECAGENCAL ATCACOGTO TAGGCACCO TOAGCCACCO	AGACTITET CREARANGE CRACTICAGE CRACTICAGE CRACTICAGE CRACCOCORIO FICCOCORIO	CAAGGACAAA GCGAAGACAA ACTGTGGATA TTCACATACG GGCGACCTGT TGCCTCGGG	ACACCTCTOT CCATCAAGO CCACCTCCO CCACCTCCO CCACCTCCO	
	30	COACAACATC GCGCATCCAC COAGGCCOGC GTCCGGCTCA	GCCAAGGCT GCCAAGGCT CCCAGGACGG TGTAGCTGA	ACCOCTTOC CCTACGAGAG TOTACGACCT AGACATGCTG	CAAGGAGTTC TOCTCGCATC OOCTGCAGTGT OCTGCAGCTG		GCGAGCGGAA TGCACAACAA GCCATGGGGT GCAAGGTGGG	
	. 35	OCCAGOCCT OCCAGOCCT OCTOTOCAC	GTCAACAGCC GACTACTGCG AAGACGTCGG TTCAAGAACGT	GCTTCAACTC TGCGCATGA AGGCCATGGA TGCAGACGGA	OCCCACCACA AAGCACCACA TAGCTGCAA OCCTGCCAC	CAAGACCTOO TCGCTOOGCA CTCATGTGCT TGCAAGTTCC	TCTACATOSA CSCAGGGCCG GCGGCCGTGG ACTGGTGCTG	
	40		ACTCAGCCCC TTTTTAGAAA TTACCATCTA GGGGTGGGAA CTTTTGGAAA	OCTCCCAGA TATTITIAT AGACTCTOT CCACGAMA GTATAGAMTO	CCCGCTTATT TTTTCCCAA GGTTTATTAT TATTTATTT	TATAGAAGT GAATTGCAC TAATATTATA GTGGATCTT TAACACATAC	ACAGTGATTC COGNACCATT ATTATTATTT GNANGGTNA CCTNACTTNG	
	45	CTGTGTGGGA TGCCATCT TTCAGCTTCT AAAACAAAC	CATGGTACAC TOGGATGGGT ATGACCAAA AAAACAAAAC ATGATAATTT	ATCCAGNAGG AGGTTCCAGT TGAGTTGTAA AAACCTCCCT ACAATGGAAG	TANAGAMATA TONANGAGOO ATTCTCTOOT TCCCCAGCAG GACAAGATG	CATTITICITI TOGINAMAT GCANDATANA OGCIGCINGE TCATATICIC	CTATTCACAA CTATTCACAA AGOTCTTGAG TTGCTTTCTGA	
	20	GGTATATCAC AATAGCTCAT CTCTTATGTC AAGACCCCCA ATGAAATATC	ATOTCTCATT GAAATTTGGG AAGATGTTGA ATGATTCTGG CTOTATTTC	CTCCTCAAAT TATGAAGCTG ACACTAGATT TTAGGGATAC	ATTCCATTO GAAGTCCCC TTATAGAT TTTTGTTTGG TTGGTTAGTA	CAGACAGACC AGAAATTAAA TGGGATTCCA GGAGGTTGGC AATTATAATA	GTCATATHCT AAATTTAAAA GATTTOTAAA TTGAACATAA	
	55	TACATGAATC GCACTGCACC ACACTGAGGC GCAGCTCCAC TGGAAAACAG		GTTTCTCAGC ACCTATTIGA CCTCCGTGTT TTGGTTGTAG AGGGATTTTT	CCAAGCAACA GGAAAAAACAG GTGATGTGAT GACAGGAAAT GACAGGAAAT	AGGTAATTGC TGAAATGCAC GCTGGCCACG GAAACATTAG ACTTTAATTT	CHECKTICA CHECKTOCHE THECKANOS ONSCHENSEN TONOSAGONS	
	8	TAGTETTCTA TATCACCTTA GTGTACCTTA GGTTTAATG ATATATAAAT	ATANTCETOT ANACTOTICC ANACTOTICC TOCCTANTA ATANTATA ATANTOTICT	ACAGAACTTO GETTAGATTA CAGTGTACTT CTCAAAGTCT ATATATCTCA CTAGAGCATT CTAGAGCATT	GCTAATGGAA TCCACTCATG GAACAGTTGC TTTGTACATA TTGCAGCCAG GTTGTCCTTC			
	8 8	ATTCCAAAG GCACGACGAA TOTTGGGTTG TTCTGTTCAC ATTCAAAACT AACCCATGCC	TTTTTTGAGT GCACCTCGT ANGATATCTT TTTGTGGAGA CAGAAGCATC TATTAGAAAT	CTTGAGCTTG TTCTGAGGNA TTTTCTTTT GGGCATTACT AGCAATGTTT GACAGTACT	GOCTOTOGO GAAGCTTGAG CTGCCTCACC FOTTCGTTAT CTCTTTTCTT ATTAATTGAG	CCGCTOTAT TTCTGACTCA CCTTTOTCTC AGACATOGAC AGTTCATTCT TCCCTAAGGA	CATACCETAA CTGAAATGGS CACCTCCAT OTTAAGAGAT GCAGAATGGA ATATTCAGCC	
	75	CACTACATAG CAGGCCATCA ACATCTTATC CTCTTAATTT ATAATGATAT AAAGGACTAA	ATACCCCCC ATACCCCCCC ATACCCCCCC ATTCATAAT TCACATCCCC TTAGTTAAA	THITTITIT TATCTCAGAC TTAGGAGGIT GATATCCACA TCAGTTGCAGA ATGTCACTTT TCAGTTGCAG	TTTTTTTAM TTACOTTOTT COSCUTTCAT TCACCCACT TCACCCACT TCACCTTTTAT	TAMBGACACC TTAMAGTTT ATCACCTCAG GTGGCTCTTT OCAAAGATC ATTATACAAA GACTCATGTT	TCTTCCAAA OGAMGATAC CCACTOTOG AATTATTOC TTGAAGCAA AACCATGAAG	
-	8	GTTGAGTTA CATTCAGATA GTCTTGCGTG AATGGAAGAT	ACATICETAG TTATOTATAT ATTTOTATAT AGAATATAAA	CTTTTAAAAG CTTCTAGCCT TTCACTGUTT ATAAAACGTT	AMACTATTA TTATTCTGTA TAMAMAGA ACTTGTAMA		TTCTACATOT ACATATTCT OCTTATTCCA	
	82	Seq ID NO: Protein Acc	249 Protes	In sequence: NP_003383 23	#—	<b>7</b>	<b>s</b> —	

Seg ID NO: 246 DNA sequence Nucleic Acid Accession #: XM\_058553.2 Coding sequence: 897-1400

45

<del>6</del>

AATTTTCAGA A

S

ଓ

65

2

9 27

KONIQIRACRP PYHLIKCRKW VVNQTRELRQ ETLABSTWGC KONLASGKRV PKELPYVLPW

PEKLLOCPYD Y CODRECIEDD V SPASNIVTEN P

MESTYTDSLD P RAZIGHHISS C MOTTHYSDNN S

82

Seq ID NO: 247 Protein dequence: Protein Accession N: XP\_058553.3

8

75

ORGENTORIA CHEGOSCO TOLCOTTOS GEGENTOS COLONOLOS ACACETOS A CARONARIA ETITITADOS GEGETTAS ANGOLOGO GUAGOCAS CENCORDAS GETOCLOS CHITTOS ETICINAT TOLCOTON A GEGOGAS GEGOCAMENT PETOGACO CHITTOS ECUTORES GANTINI TETOCOLOS TOCCHITA ATTINITAN CYGOTITOS TETOCATAS ANTINICA CHICATINA GANTINAMA COLITITAN TRANSAMA TETANTITI AGGETOSTE CECANAMA MANAMAMA MANAMAMA A

و
Ξ
Ξ
.8
S
Ξ
Ç
-

WO 02/086443

	9	120	780	240	900	360	
	OPLCSQLAGL	RVMQIGBRET	IDYGYRPAKE	<b>BCBLKTCHLQ</b>	POYCVRNEST	KCKKCTBIVD	
	MELCHRIPV CHEEVYIICA CPLCSCLAGE	STVDNTSVPG	DWINGGCCDN	GRRTVYNLAD VACKCHGV60	TODLYYIDPS POYCVRNEST	OPKTVQTERC HCKPHWCCTV	
	VARIABADIENN	GALTITICO YOPRHRANIC	RAARPKOLPR	<b>GRETVYNLAD</b>	OVNERRENSPT 1	OPKTVQTERC	
	FAQVVIEANS 1	CANTTOINGO	EGELETOGCS	ILMWLANWEA (	MRLMERGKLV Q	SLACCGROYD (	
WO 02/086443	CAGBAMBERP PLUALAIPPE	POCOULCHL YOURNOYIGE	WANAMERACK	PUDARERERI HAKGSYESAR	LICERYDSAAA	BLOTOGRIC NKTSEGNOGC	
WO 02	MAGBANBBILP	BOODINGH	APTYAVBAAG	PVDARERERI	LADPRIVIDA	GBLOTOGRIC	QPVCK.

86q ID NO: 250 IIIA pequence Nucleic Acid Accession \$1 NM\_014056 Coding sequence: 56..1324 2

	CAATGATGTA 6	TATCGGCT 120	ITCATTATOT 18	CACTGACA 240	DCCAGAGACT 30	PTOTCANOTC 36	DETTOATTTO 420	TOTTTACA +8	TAMATTA S4	CACCANDANG 60	ACCOTGAATO 660	CCTTAATTAA 72	CTGCCAGATG 780	PCCGGAGAAT 84	PTGCAGAGCT 90	ATGCATCCTA 96	AAAATGATGG 102	CARCTTOCAA 108	DETECTIVOA 114	CAGATGCTAG 1200	ACCCARCA 126	WACTGGTAT 132	OCTUTOGRADO 1380	DACTGATCTC 1440
41 51	TOCTOGTTOO CA	GACCCTCOO TT	DOACTCACTO TT	THORATTA OF	ACADAMATON OC	ACCOMMONT TO	OCTICATATOC TO	ATTOTTCAAC TO	OCTURACTORS TH	TOCTOCCION CA	CANGTAGAAG AG	TOTOGRADON CC	TATAAGAACC CT	AACCOCOTC TO	DATATTICE TO	TOTCT CCCTO AT	DONOCACTOR AN	ATACACCCTA CA	TTATOTOCTO OC	CITOCITAOTI CA	GAATOTGCGA AA	ATTACTTCAA AA	monther 60	ACCTAGATITE GA
<b>1</b> -	OACTCTTCAT .	Agritoritos	AGTOTOCATT	CTATAGGACA	TANCARTET	ATCCCATTA	TOGAGTOTTO	TOTAGATAAA	TAAAGTAGAT	TCTAMACCAT	TCGTCGGACA	DAGTCATCGC	TITACAACA	TTCGARATC	ACATGACTAT	ACATAGAGTT	GACAGGATTT	COTCACTCTC	TCCTAGAATO	TOGAGGACCA	CTGGGGAGAT	GCGGGACTGG	ACATTATATA	CTTGCWAAG
<b>1</b> -	ACCTTCACAG	CTAGGAAAAG	TTOTOCTOOC	CCTACAATTA	GAGAGGCTTC	CATTITATA	_	ATCCTGAAAC	TAGGACCCCC	CAGACAGCTA	TCAGGATCGT	AGTGGGATGG	CTGCTCACTG	CARTANACC	AACACCCATC		TOATOTTO	GACAAGCACA	OCTTACAATO ACOCCATAAC	GATGCATGCC: AGGGTGACTC	TACCTTGCTG, GAATAGTGAG	INTACTAGAG, TTACGGCCTT	GGAACAGATA	TTGGAGAAGA
<b>1</b> -	GTAGACCTCG	GTOGTGAGGG	ATATCCCTGA	CANAAGAAGA	CAGTITIOGCA	OTGAMMATG	AMOTTCAGTC	TCTACTGAGG	CAAGATGCTG	ANGACAGAAA	GOTCAGAGTC	OCTAGCCTOC	CTTGTGAGTG	TTTGGAGTAA	GAMAATACA	GTTCCCTACA	CCAGGTGATG		-	-	-	TATACTAGAG	_	AGATACAGAA
<b>-</b>	TOACTTOGAT	TOGGCCAGAT	COTCATCTTC	GAGATATAAT	ACTATATGCT	TGAATCAATG	TCAGGTTATC	TAGATTTCAC	TCAAAACTO	AAAAATCAAC	TAMAACTCTA	OCCUTOBOAG	TOCCACATOO	CACTOCTTCC	AATTOTCCAT	TTCTAGCCCT	TOAGITICAA	TTACAGTCAA	TOAACCTCAA	AGGAAAACA	AGATATCTGG	OCCIDIOTOTI	CTAAGAGAGA	CCATTITAG
	15				;	20				٠,	52				;	2				;	35			

Seq 1D NO: 251 Protein sequence: Protein Accession #: NP\_054777

<del>수</del>

20 45

Beg ID ND: 252 DNA sequence . Nucleic Adid Accession 8: NM\_003504.2 Coding sequence: 71-1771

55

	2	021	9	300	360	2	8	55	2	099	2	96	•	2	960	2	2	2	2	0	2	2	2	2	2
	٠.	3 3	~	×	ř	÷	Ŧ	ž	9	ĕ	2	۳	840	800	ă	1020	1080	1160	1200	2	1320	Ξ	2	1500	1560
<b>.</b> –		ADATECTICA		TCATAAACTO	TATTCTTTGT	AGATCAAATT	TCAGGGATGA	CTCACAAGCG	GOCCAGACTO	ATGGGACATC	ATGACATGCT	CTCAAATGAA	ACCEDANCE	ATGACCTCCG	GCTATACCGC	TCCTTGCAGA	TCTCCTTGAA	AGGACATGCG	GCGACOTOGT	CAGATCACTT	ATCCCCTCCA	TTTGCACCCAA	CTCCAGATGT	TCMGTCCTT	CTGCCCCCCT
<b>\$</b> _		TOTECOTOCA	_	TATTTTATT	GANDACACTA	ACCATACCC	CANGACATCT	TCAGAGCCTT	AGGAGGCAGC	TATGAATATC	AAGGACCTGA	GACCAGATCA	COCCACACC	TOCHTHONOT	TOCANCACCA	CTCCAGGAGT	<b>OCCUTODACA</b>	TTCCCATOA	11C1000CA	<b>GGCTCAGGGA</b>	ANGCTOTACC	_	ATOGAGGGG	MACACCTGC	CTOOTGATOR
<b>#</b> -	GTACCTCAGC	CAMBRAGITIC	TACOCTOOTT	ACAGTTTCAT	TCACCTGAT	CAATGTATAC	TCCCGCCTAT	CACTGATOGO	AACCATGCGG	CTACGAGCAG	<b>AATOCHOTOC</b>	<b>OTGGGTGCAA</b>	CCACOTTTCC	CCCCCCTC	TCACAGCCTG	ACAGAAGCGG	GANGTICCAG	TGCANATANA	CARGACARA	COAGAAGGAT	TAACCTOGAC	GCAGACCATT	COCTOTOCIC	CCTGCTCAGC	ACTGCTGCCC
12 _	CGGGCTCTTG	CCTCGGACGT	ACCTOCATA	AGCATAAAGA	TOGATATICE	TCAATGTCGT	ACCTTONAGE	CAGGAAATGA	TAOTOGAGCA	TOCTOTATION	ACCTOCCTTO	TAACAGACCA	TCCTGCAGCG	CCOTGGACTG	CONCECTORA	CTOTCCATGG	AGGTGAAGCA	TTGAAGAGTC	ATTITIOGETT	TOGAGAGCCC	TCTCCAGGAG	GAGCCACCCA	CTTTCCTGTA	CATCCCTANG	GGCGCTGCAA
- <b>:</b> -	crearaceac	CTCTTCGTGG	CAGTOTOACC	OCATATIONS	GTAGACCTAT	CATAGGCCAG	CAAGATGATG	GAAGAGCATT	DAAGAGGAGA	AGAAGAGACA	CTCATOTITO	ATCCTTCGAC	CATOTTOOTO	AACACACTCT	TACCAGCACT	AAGCTGTGGT	CCCCTGAAGC	COOGNAATGA	TTCAGCATTC	ATOTOTITIGA	CTGGACAGCC	AGCAGCTGC	TOCCAGGGC	TCTAGGCCGG	ACMAGNACC
	OCCACGAGGG	GAGGGTCCTT	OCCUPATION	ACTTGAAACT	TOGAGCTAAT	OTOTOACACC	ACTCATTANA	AGAGGAGGAT	CACACOGTTA	GGAGGCCCGG	STCAGCCATG	OTGGTGGGC	ATACOTGACT	COATGADOAG	ceroordere	AGCCAOGTTC	CATCCONCT	DOAGAATITO	COTOCAGACT	CTTTGCCACC	CATCCADGCT	ACTCGCCAAG	<b>CCTCOTCATC</b>	CATOCTOTTC	TGTGTGTTCO
09			9				É	2				è	c				8	2				è	ŝ		

S	
~	
⇉	
ä	
ネ	
ë	
s	
₽	
≥	
Ε,	
×	
_	

WO 02/086443

TOTALINEAR GEOCOCATO GEOTOGRAPE GALOGRAGE TECTACOCAT TRANSPORCE TOTALINEAR GEOTOGRAPE GALOGRAPE TOTALINEAR GEOTOGRAPE GALOGRAPE
11. 11. 11. 12. 11. 11. 11. 12. 11. 11.

25		1-	. 17-	31	<b>\$</b> _	2.	
}	MANNTHURME		PETCLILLOV INVILEDOVPV RYDPEADAHN WEERTHRATE D	RYDPEADAHW	WBERTHENIS DMENEFYYRY CMALLACGNP HFLODRYIVV	DMENGFYYRY HFLQDRY IVV	
30	GVENLINADP GWITHTPGAY YHGDSQHRAA I	CVASVCVAPO PGLTVTRILY INTYCBLAAC	CVASVCVARO AVLGRVSRIQ LLIMTRROVT LRANKERILL KILKVKDAGO POLTVTRILY RANLEGSKER GNSVYGSDLP ANIOTLRUM YMPRÝNSAIR INTYCELAAC VLTGVAISSA LHKKGKLDMY HIGNATLAGO VAVOTAABON	LLIMTFFQVT QNGVYQSDLF LHKKGKLDMV	LPAVNEPILL AMIGTLFLWH HIGNATLAGG	nllkvndagg Ywrbpnbaib Vavgtaaed	
	LMPYGALI 1G SAELEVYGKE WGQPSDENCP	APYGALIG PYGDIEGLIA PYLYEPEB RIALIGOGOGO INMEGROTO IGOLOGOIO GOLOGOIO PYGALIGO PYGDYRAY OKYOYIGLAY TANALAGGI IVOLIJALIH KOPBOBICE EDAYYMERPE GIGTYIIPED PTEVEGOSO PGYPHYGPLE KASSYPLVP	PVYLTPPLES PNGDWTARTO GNBTVYIPED	RLHIGDTCGI GKPQIYGLLV PTPKPSCPSV	nnlhgipgii ggivdavtaa Tlamalmogi ivgliirlep Pgvpmvbplp massvplvp	GGIVGAVTAA IVOLILRLPP KASSVPLVP	

Sed ID NO: 256 DNA sequence Nucleic Acid Accession 8: NM\_002358.2 Coding sequence: 75..692

<del>\$</del> S 

Beq ID NO: 259 Protein sequence Protein Accession &: NP\_002349. 

11 41 51
11 LYORGIYES TPETRYOKYO LILLAVITOLS
18 ILYORGIYES TPETRYOKYO LILLAVITOLS
18 ILYORGIYES OFOLINES
25 FOLLIYTOMO LAVPERNESS OPOLITYSES HALQLEREGO TILRGEREIV AFFFETTINS IL LIKYLARIVE GLACMLINKCE VOKLIVVIER IE QKALQDERERS VIRGITATUT PUPLLEVISCS FOI VRLESFTITI HKNISHVAYK IEVID 

Beg ID NO: 260 DNA mequonce Nucleic Acid Accession 8: NM\_001211 Coding sequence: 41.,1195

Seq ID NO: 162 DNA sequence Mucleic Acid Accession #: NP Coding sequence: 365..1507

ដ

WO 02/086443

WO 02/086443

10
≂
7
Ξ
0
23
z
₽
C

	_	_	_	_		_		
	OTCTACTTAT		CTGCCTGTGC	AGAGTGCAGG	CHOCOCCITA	BOACHOCCTT	9	
	TANAACTGAA	TICHCAGAAT	TTTAGAACAA	ATTITIBLE	AGAMATGCTG	ACTITIOGITIC	120	
	ATTAGGTAGT	GOTAMACAG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTOCA	180	
^	TOTACAGGGA	ADCTOCOTT	_	CTAAGTOCAT	COCCCAAAT	ACCTAGOGCT	240	
	CACCOCC	GAGAMOTOTO	GAMCATTIT	CTTTOTOTOTO	GAGAACAGAT	CACCTAGAGA	300	
	AAGGAAACCA	GATTCCCATC	ACTGCTTCT0	COTATCAGAT	OCTAGOGGG	CACTCCATT	360	
	TOCANTOOCC	TCCCTTGCTO	CAGCANATOC	AGAGITITUC	-	TCAGAGAGAT	430	
•	OGATOACAAT	CAAGGAAATG	GAAATGTGTT	CTTTTCCTCT	CTGAGCCTCT	teachacect	480	
2	OCCUTOTIC	0000011000	CTCAAGATGA	COCCEPCTCT	CAGATTGATA	AGTTGCTTCA	540	
	TOTANCACT	<b>GCCTCAGGAT</b>	ATOGAMACTC	TTCTAATAGT	CAGTCAGGGC	TOCOMPCTO	909	
	ACTOMANDA	GTTTTTTCTO	ATATAAATGC	ATCCCACAG	GATTATGATC	TOGGCATTOT	999	
	CAATGGGCTT	THOCHOANA		CTITICATANG	DACTACATTO	AGTGTGCCGA	720	
	AAAATTATAC	GATOCCAAAG	TCCAGCGAGT	TOACTITACO	AATCATTTAG	MGACACTAG	780	
2	ACCTANTATE	AATAAOTOOO	-	AACACATOOC	ANATCANGA	ACCITIONATION	940	
	TOAAGOTOGC	ATAAGCTCAT	CTOCTOTANT	ogracioana	AATOCTOTOT	ACTTCANAGG	900	
	CAMOTODCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TOCCATTICA	AATCTCCCM	960	
	GTGCTCTOGG	_	CCATGATGCA	TCAGGAACGG	AAOTTCAATT	TOTCTOTTAT	1020	
;	TOAGGACCCA	TCAATGAAGA	TECTTOAGGE	CAGATACAAT	DOTOGCATAA	ACATOTACOT	1080	
2	TCTGCTGCCT	GAGAATGACC	-	TOAAAACAAA	-	AGAATCTAAT	1140	•
	GGAATOGACC	AATCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTT	TICCICABIL	1200	
	CARGATAGAG	AAGAATTATO	ANATGAMACA	ATATTTGAGA	<b>GCCCTAGGGC</b>	TGAAAGATAT	1260	
	CTTTGATGAA	TCCAAAGCAG	ATCTCTCTGG	DATTGCTTCG	COCOGNOTIC	TOTATATATC	1320	
;	AAGGATGATG	CACAMATETT	ACATAGAGGT	CACTGAGGAG	GGCACCGAGG	CTACTGCTOC	1380	
ន	CACAGGAAGT	DATATTOTAG	AAAAGCAACT	CCCTCAOTCC	ACCIONTINA	CAGCTGACCA	1440	
	CCCATTCCTA	THOTTATCA	COAAGGATGA	CATCATCTA	TCAGGGCA	MOTTICITIO	1500	
	CCCTTGAAAA	TCCATTOOT		OCAGTCCCCA	CACATCAAA	GRACCACCAC	1560	
	ANGTOMING	ATYTOROTTT	AATTOGAAAA	ATGROGIGIT	TOCTTTGAGT	TTATTTCTTC	1620	
	CTAACATTOO	TCAGCAGATG	ACACTGGTGA	CTTGACCCTT	CCTAGACACC	TOGITICATIO	1680	
ವ	TOCTGATCCC	TGCTCTTAGC	ATTETACCAC	CATGTGTCTC	ACCCATITICS	MITTCATTG	1740	
	TOTALCITICO	COCCCIT	TCTATCATTC	TCCCCCATGA	CCCGTCTGGA	AATTATOGAG	1800	
	ROTOCTCAAC	TOOTAAGGAG	_	TAGCCCTAGG	GATCCTTTT	GAAACTCTAC	1860	
	AGTTATOSCA	_	_	AGCAATCTAG	GANATANGCC	CTOCTOCTT	1920	
	CTAGAMATAA	GTGTGAAGGA	TAMETETECT	TTOTTOACCT	ATGRAGATT	TAGAGITTAC	1980	
35	CTTCATATOT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAMAMATO	TGAAATTGGG	2040	
	ATTAGGGACC	TACCMAATA	TITCATTAAT	<b>ACTITIONAL</b>	CACCALATTE	<b>GOCCTITICIT</b>	7100	
	TOATAAGACA	ATATOTACAT	GTTTTTCA	ATATTAMAGA	TOTAL	GTTGGCAGTT	2160	
	<b>STEATCTACA</b>	GAATCATATT		TOTAGETTAE	AAGTTTTOC	TCTATTATC	2220	
	AGAATAAAGA	AATACAACAT	ACCTOTAAA					
5		•						

Seq ID NO: 263 Protein sequence: Protein Accession #: NP\_003775

**\$** 

HOSTANANA PURILED HOROGONYP SELENANA WARDANDE LADIDICALEY PROFESSION PROFESSI S 45

Beg ID NO: 264 DNA sequenco Nucleic Acid Accession #: AB052906 Coding sequence: 74-814 55

MANCETTA GOTALITOR CITCELAGET CICCITICAN CAUGUTECT CICCCTAGG 6
GOTCOGGOTO TRANSCOLO CACCOCCOC FACAMARIC CITTEGROE CICCGGOTO 1
GOTCOGGOTO TRANSCOLO CACCOCCOC FACAMARIC CITTEGROE CICCGGOTO 1
GOTCOGGOTO TECANICACE ACCACATOR DESCACADO ESTRECOLOS TRANSCOLOS TO CONTINUE ACCACATOR TOCANACOC CITCAGACA ACCACATOR TOCANACOC CITCAGACA ACCACATOR TOCANACOC CITCAGACA ACCACATOR TACANACOC CITCAGACA ACCACATOR CACATOR TOCANACOC TRANSCOLOS CAGARCEOLOS TRANSCOLOS TACATOR ACCACATOR TOCANACOC TRANSCOLOS CAGARCEOLOS TACATOR ACCACATOR CACATOR TOCANACOC TRANSCOLOS TACATOR ACCACATOR CAGARCACOC TOCATOR ACCACATOR CAGARCACOCA TOCATOR TATANACOCA ACACATOR CAGARCACOCA TOCATOR ACCACATOR CAGARCACOCA TOCATOR ACCACATOR ACACATOR CAGARCACOCA TOCATOR ACACATOR ACACATOR CAGARCACOCA TOCATOR ACACATOR ATACATOR ACACATOR 8 8 2

75

8

85

		. :	_	_	_	_	;
S		UCLPLILLIS VTPV8PLOKK AECHSEGSWO	CHSRACKADP LHVTTANKAQ PSPDQQIPLL	HBLCTO I TVI HPVLRBVVD I FDGEKRAMTT	LTEQLEDIQUE VHPCARIONES	AVQSQVDEKT ENTTPKEPLT KMENDKVVAN	2223
	PILPGI	IGNUEDFLAIG	MUSTLEPSAG	APLANSBUTT	QUENTALLE	DCCDD1 1DPC	
01	Seq ID NO: 266 DNA seque Nucleic Acid Accession # Coding sequence: 127-444	MA eeq	eequence ion #: XM_064853.1 7-444	. 1883.1			
~	11 11	11	1.	11	11	51	ş
?		ACTTACCAGA	TTCCTAMA	ONOTACETTA CAGOTOCTC	ACCACAAGC	CTCCAAAGGG	180
70		AGATOTTOGA	TTOCTTTOCT	TCACTOTTTO	GCCTGAATCC TTTGCCTTGA	CGAGGGATGG	
25		ADGACATOT ATCCATAGA ATCTTTAGAA	GTGAAGTTAC GTGTGTTTTC. CATTTAGACA	CAGGAATGTT	TAAAGCACAA TOCTTTTTAT TTTCTGGTGA	AGASTTCCCT GCASTG	33
	Seq ID NO: 267 Proted Protein Accession B:	Protein on 8: XE	n sequence: XP_084853.1				
. 08	1 11   HYDIHKSFEV LQYTH EPATCSVKGS BICLE	11    -  -  -  - 	21   AIRREDFURD EITABIPATB	11   LVTKQEHMTB   ILQLT  SEDS		41 51         BEMILDCFASL FOLKPEGWK8 GODOQ	3
35		268 DNA sequence d Accession ≨: N ence: 57-482	uence #: RM_0011				
04.		tt    -  - 	21  -  -	31   CTTTOTOCTC TOOCCACCCT	41     TACCTCTGAG   AGCTGTGGCC	sı     GAGACCATGG   CTGGCCTGGA	8 2
45		GGAGGATAGG GCGTGCCCTT ACGTCCGCTG CGACGTAGAG CTTCCATGAA	ATAATCCCGG CACTTCGCCA CGGGTACTAA OTGGGCCGCA	OTOGCATCTA TCAGCGAGTA GAGCCAGGCA CCATATGTAC TGCAGAAGAA	TAACGCAGAC TAACAAGGCC ACAGACCOTT CAAGTCCCCAG ACAGTTGTGC	CTCAATGATG ACCAAAGATG GGGGGGGTGA CCCAACTTGG	2000
20	TCTACAMAT TCCCTO AGGATCTOT OCCAGO CCACCCCTGA ACTGOT GACAGACAA GAMGO CTTCCTTCTT GCTTCT ANACAGTAGC ATCGCC	TCCCTOGGAG GCCAGGCCAT ACTGGTGGC GAAGGCTGCA GCTTCTAATA ATGGCC	AACAAAAGT TCGCACCTGC CCCACCTGC GGAGTCCTTT GCCCTGGTAC	CCCTGGTGAA CACCACCCAC GGGAGGCCTC GTTGCTCAGC ATGGTACACA	ATCCAGGTGT TCCCAGGCCC CCCATGTGC AGGCCGCTCT CCCCCCCAGC	CANGARICCI TOTACTOCTC TOCTCCCTC TCCTGCATT	7000
55	Seq ID NO: 269 F	Protein	269 Protein sequence:				

	51   AIBEYNKATK ELQKKQLC8F		51    -  - 	TAGGCTGAGA TTCTAGCACC GACGCAAGGA	AGCTCCGG ACCAGGCAAA CGCCCAGATC GGCGTCCTGG
			ADAGGTACCA (ADAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		TECCUACO OCCUACOOC CCCCTGGTCC CCAAACOGCCC
	11 41     PODIYHADLA DEWORALHF RIICTKEOPH LOTCAPHEOP	9	OTTTCACAAA		GCTGCCCAC GCGGAGGCCT TTCCTGTCCG
sequence: 001889.1	21   Wepkeedrii Unyppovevg 8	uence 6. XM_0932: 54	21 	OTTGGGGGGT TGCACTGAA TGACTCAAG	CACACCOCA GTCACCCCOO AGGCTCCCTO AAGCCATOOC
169 Protein	11    LLATLAVALA  LRARQOTVGG  RELVKSRCQE	170 DNA seq 1 Accession ance: 13-18	COGGNATCTC ACANGCAGCA		COCCANGCCC COCCANGCC CCCCANGCCC CCCCANGCCC CCCCANGCCC CCCANGCCCC CCANGCCCCC
8eq ID NO: 269 Protein sequence: Protein Accession \$:NP_001889.1	HAQYLBTLLL I DDYYRRPLRV I	Beq ID NO: 270 DWA sequence Nucleic Acid Accession #: XM_093210 Coding sequence: 13-1854	TATESCANGES CANACCACACACACACACACACACACACACACACACACA		CACTOGOAGT GCCCAAGACC CTGCCCAAGA ATGGCCACCA CTGTCCAACT
55	09	\$9	2	75	08

ខ្លួន

Seq ID NO: 271 Protein sequence: Protein Accession #: XP\_093210

85

51

Ţ

PCT/US02/12476

120 180 240		120	\$2500					60 120 180 240	360	600	940	11080	1320	•	120		8238	20020
LKTPDTPBTB POACSVADGA QKVB18QALP RTQLEPSPRL 88		SI   	ANGICTITT TANCACTOAT GOCTTATATA TGCCTGANG		15 —	٠.	15 ~	CCATTACCT CCCAGTGCAG GGAGAAACTG	TGATAGAGAT GOCGGCAGCC AGGCCTCCCT TGGCGTCCCC	CTCTTCCCC0 CTCTTCCCC0	OCCACOUCTC OCTCTCCACA COCOCTCCCO	GCCTGGGCTG TGCCTGGGAC CAAAGCTGAA AACTGACTAA	AACCTGGGAC CCCTGTAGGG CTGGAACTGG		S1   RECOPPVIAS PGERARAGA AGALRPPPGS		S1 GCAGACAGC GGCTTACCC CTCTCTACTT	MANGOTOGO MANGOTOGO TOGANTTICA GCCOGCCC CTCGCTOCCA
LECOGEDAHE TOMMOSALLT ANVETERPOP LECHOPASHL		41 	AGCANANAT AGCATATOT TOMONACON		₹_		<b>3</b> _	GOGGATTAAA TAGTAAGGTT TTGCTCAGGT TAGTTTGCAA	CTCCTGGTGT CCCTGGCCTA AGCGTCGCAG CCGCCTGTCC	AGTGGAAGAG CCCCCATCTG GCTCGGGCAG	CONCOCCOCC CONCOCCCCC CONCOCCCCCC	CCCTGCGGCT TGGCTCTTCC ACGAAGGCCT OTGAAGGGAC	CCABGCCT CG CCCGCCCAGG AGTGCCTGTG		41   Lobapredad Rograaragg Hdublaballo		41 CTSCTGCAGG CSCAGGGACC GGCTCCCAG	CCAACCTCGG OTGAGCCCCG ACGCTOGGGC ATGGAGTTGG
 Tervengadr Aagtrangig 81.aea.81ae Ggreseiirer Aatrlesegf	sednence	31 	TTACATCCAT TCTTACAATT TTOTATTTTACAGCTC		====================================	003976.2	<b>#</b> _	TCTGGAAAA ACCTAACACA AGGCCCCTTG ACTCATCTCT		CCGCTGGTGC GCCGCTGCA GGGCAGCCGC	COGCTCCTGC COGCTCCTGC COGCTACGAA	CTCCCCACC CCCTTACCGG TCAGCCAGGG CCCCCAACAG	CTGGCACTGG GGCATCAGCC CTTGGTTGAA		11 NLLEBVARAS PPPAPPEALP SGSCRRARSP	1.160	11 CAGAGAGCAG AGCGGCCCA AGCGGCCCA	TACCCCCTC GAGCAGCCAG GGATCTGGTG CTGTTGAGGG
TCAFKTVBAA QGUT PRRRPA GYLPKAPBPG PAPMATELST EABAGPAQIH	A sequence sion #: Eos se 732	HI MATGGAGG CTTTAACTT TTCTCATTG	TCATATAOT CAGGOTTT	ein sequence:	T. L.	ξ'	17.	TOTTTGCTCA GCTGCAAAGC CTAGCTGTGT ACAAAGATA	TCACACTES TCTCCACTET CCGCTCTGGC CTGCCCCCCC	ACGCACGGC CGCGCCCC TGGGGGCCC	ACTTCTGCAG	IGAACCGCT ICAACCGCC ICCAACCGCC IGAACATCAT	TCACAGACT MOTOGCTGA MTGCAGTTG	in sequence: NP_003967.1	21 PALMPTLAAL PEPQPGRPAP GDELVRFRFC VNSTWRTUDR	Nence   N: NM_0570 445	23 COSOCIGOAG ACCAGCAGTC CTTTCTCCCO	TCCCACCTC CCCACCCCC CCCCACCCCC GGGCAGAGAG
WO 02/086443 HOEDER RAKKODELP SYTAPTO PLUREDAP SODRARS PRLUKEDAP SOURKEE RPOLOGORA	MO: 272 DNA se Acid Accession sequence: 17.	TCACTCAAAG TTTTTTCCCA	CTTOTTTCTG TTATTATCT ANTTTATCGG	~ ~	11   DAPEKAPPPT	Seq 1D NO: 274 DNA sequence Nucleic Acid Accession #: P Coding sequence: 299-961	=-	CTCTGAGCCT TGAAAGAATA TGGGTTGAGT CCGGTCCCCC	GOOGNACAOC CTTGGAGGCC CCCACCCTGG CCCCACCCTGG	CTTOCCOGGGGG CCTTCTCGGC GCGGCGCGCGGG	TGGGCTTCC TGGCCAGCC	CCAGGGCTTT CCAGGGCTTT AGTCCCACTA CGGTGGGTGA	GGACCCACTT ATGAACACTA AAGGACACAT CTCATGGGAG	Mo. 175 Protein Accession #: Ni	11 21 CHICKPARQ PALMPTLALL T ANUGGRARA PEPOFERPA V PYRALGIGH EDELVFREC T TAXEAVSFREC T TAXEAVSFREC T TAXEAVSFREC	NO: 276 DNA sequence Acid Accession #: NM_057/ sequence: 783-1445	11 	AAGGGGCCCC GGGACTGGAT GCGCTCCCAG CTGCGGGGGCCCCCCCCCC
WO 02/ HURNGEDRAK TITENTAPTO BRAEDPARPE PNEGVORKEE LPREGADGEL	Seq ID NO: Nucleic Act Coding sequ	DOGATACTICA COGATACTICA TOGATACACT TAATOTICACA	ATGATTTOT TAGATATOT TAGATTOCAC ANANTTOCAC TTAGGCC	Seq 1D NO: 273 Pro Protein Accession	1     MOGRENREOR	Seg ID NO. Nucleic Act Coding sequ		CATCAGGTT CATCAGGTTG CTACTTCTGC	CAGGAGGTG GGAACTTGGA TGCCCTGTGG GGGCTCCGCG	OCCOCOCOAC COOCOCOCA COOCOCOCO	COACCACAGE	CCTCCGCAG AGGGCTCGCT CCTCCGGCAG AGGCCCCTAG	OGNOCICTIC CCCTCTCTO ACAGCATTTO CCTGTACTCA	8eq 1D 110: Protein Acc	1 MELGLGGLGT PAGHLPGGRT RGCRLRSQLV RPVSQPCCRP	Seq ID NO: 2 Nucleic Acid	ACTOGCOGET OGACCCCCAA TOGCTCCCCA	CTCCATATCC CAAGCTAACO CACCOALCO CACCOALCO
S	01	15	50	25	30	76		6	45		20	55	9	5	. 2	75	08	82

	000000000	GAGCCCCACA	ссовмовала	CAGACTGGCT	accuaacca	CACTTTTOGC	8
	GCCAGCACT	GOTCCCOOGA	AAGOTGCCTA	CANCAROLO	OTOCHOOKCC OTOCHOOKCC	CCOTOCTOCC	2 6
·	TCACAGAA	GOTOGOGAA	CAGCTCACA	ATOCCTOATO	GOOGCTCCTG	OMINIORINA	2 3
•	AGCCTGCCCT	GTGGCCCACC	CTOGCCGCTC	TOCTOTOCT	CHUCCECTUR	OCAGAGGCCT	. 2
	CCCTGGGCTC	COCCCCCCCC	AGCCCTGCCC	CCCCCCAAOO	CCCCCCCCCT	OTCCTCCCT	2 3
,	OCCCCOCCCC	CONCLINE	COOCCOCCC		TOCACCCCA	TCTOCTCTTC	
2	000000000	0000000000	COGOCTOOOO	GCCCOOCNO	CCCCCCTCOO	GCAGGGGG	3
	COCCOCCIO	democratical designation of the control of the cont	TOSCAGCION	TOCKOOLOGO GCAGCOOLOGO	ממת בניתונים	משמעונים	2 2
	CACACGACCT	CAGCCTOGCC	AGCCTACTOO	900000000	CCTGCGACCG	CCCCCGGGCT	3
~	CCCCACCCCT	CAGCCAGCC	TOCTOCCOAC	CCACCICCTA	COMMISSION	TCCTTCATOG	33
3	GCTGAGGGCT	COCTCCAGGG	CTTTGCAGAC		CCOCTOCCTC		2
	OGACCCTCCC	GCAGAGTCCC		COCCTCAGC	AGGACCIAAG	GCCTCAAAGC	156
ŝ	CTAGCAGCC	CAGAGCCCTC		TCCCAGCCTA	AAAGACACCA	GAGACCTCAG	168
70	CTATOGAGC	CTTCGGACCC	ACTICICACA	GACTCTOOCA	CTOOCCAGOC	Стесилесто	5
	MOGRACAGCA		ACATATTGCA	OTTOCTTOOT	TOWARTEC	TOTOCTOOM	1 2
č	CTGGCCTGTA	Credence	GGAGCTGGCC				
57	Protein Acc	177 Protes	NP 003967.1				
	:	<b>s</b> .		<b>:</b> -	₽-	<b>.</b>	
. 8	NELGLOGUST	LEHCPWPRRQ	PALMPTLAAL	ALLESVAEAB	LOBAPRSPAP	RECOPPEVLAB	٠
3	PACHLEGGRT RGCRLRSQLV RPVSQPCCRP	ARMCEGRARR PVRALGLGHR TRYRAVSPMD	PPPQPSRPAP SDELVRFRPC VNSTWRTVDR	PPPAPPBALP SGSCRRARSP LBATACGCLG	rockaarag Holblableg	Posrarlaga Agalrpppgs	2 2
35	Seq ID NO.	No. 278 DNA sequence c Acid Accession #: P sequence: 1-714	Tuence 1 #: NM_057160	1,60.1			
		=	, 12	33	3	51	
ę	_	_	_	_	_		٠
₽	CACCTOGGTO	CCCTCTTCT	CCCTGAGGCT	CCACTIGOTO	TCTCCCCCC	OCCIOCCIO	• =
	TGGCCCACCC	TOOCCOCTCT	остстосто	AGCAGCGTCG	CAGAGGCCTC		12
•	CACCTGCCGG	GOGACOCAC	GOCCCCCTOG	TOCAGTGGAA	ОМОСССОВОС	accaccaco	: :
<del>4</del>	CACCTICTC	OGCCCGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COCCCCCCCC	SCACCCCCAT	Characterioc	COSCOSOGO	2 5
	CGCCTGCGCT		accouracac	GCGCTCGGCC	TOGGCCACCO		= ;
	CTGGTGCGTT	1000011010	CAGCGGCTCC	TOCCOCCOCO	COCCOGGGGGG	COCCCOTC	2 8
20	AGCCAGCCT			avaccorer a	CCTTCATOGA	COTCAACAGC	\$ 5
	GCTCCAGGGC		GOACCCTTAC			GACCETCCCO	2
	CAGAGTCCCA		OCCTCAGCCA	GOGACCIANOG	CCTCAAAGCT	GAGAGGCCCC	2 2
25	AGAGCCCTCA		CCCAGCCTAA		AGACCTCAGC	TATOGAGCC	
	TTCGGACCCA CTGAGGACA TTGAGGACA		TOROGENER	DECENDENCE GRAAGTGCCT	AGGCCCTGTA GTGCTGGAAC	GOGACAGCAT TGGCCTGTAC	121
8	TCACTCATG0	амаставсес	v				
	Seq ID NO: Protein Ac	O: 279 Protein Accession #: NI	.n sequence: NP_476501.1				
65		=-	121	#-	<b>;</b> _	<b>s</b> _	
1	MPGLISARGO APRSPAPRED	PLLEVLPPQA	HLGALFLPEA HLPOGRTARM	PLGLSAQPAL CSGRARRPPP	WPTLAALALL	SSVAEABLGS APPSALPRGG	9 2
5	Raaraggdgs Blastlgaga	Raraagargc Lrpppggrpv	RLRSQLVPVR SQPCCRPTRY	ALGLGHRSDE EAVSPHOVNS	LVR FR FCSGS TWR TVDR LSA	CRRARBPHDL TACGCLG	2
?	Seq ID NO.	280 DNA	sequence	1.000			
	Coding seq	sequence: 29-715	:	•			
75		=-	<b>#</b> -	<b>1</b> -	<b>=</b> _	۲. ا	
	CTGATGGGCG	crecroorer	TGATAGAGAT	CONNCTTOCA	CTTOGAGGCC	TCTCCACCCT	9 :
8	OTGGCCCACC	CTOGCCGCTC		GAGCAGCUTC	GCAGAGGCCT		2 2
3	CCACCTOCCO	GOOGGACGCA	COCCCOCTO	OTGCAGTGGA TGCACCCCCA	AGAGCCOGC	0000000000	2 2
	000000000000000000000000000000000000000			CCGCGCTCGG	GCAGCGGGG	CCCCCCCCTO	2 :
82	action on a	Trecoenter	GCAGCGGCTC	стассассас	acacacacac	CACACCACCT	
	CAGCCAGOCC	MOCCTACTION	CCACGCGCTA	COAAGCOOTC	TCCTTCAT00	ACOTCAACAG	2 %

290

29.

PCT/US02/12476

WO 02/086443
cortradua Acortradua cercitorea concectra octuadeser 72/2
cortradua Acortradua Cercitorea concectra octuadeser 71/2
cortradua Acortradua Cercitorea Concectra octuadeser 71/2
concectra Cartraccada Cercitorea Concectrada Cercitorea 71/2
concectra Activada Inchestrada Acuatrada Cercitorea 11/2
concectra Activada Inchestrada Acuatrada Centacado 11/2
critoria Nada Activada Centacada Concectra 11/2
critoria Activatada Centacada Concectra 11/2
critoria Activatada Centacada Concectra 11/2
critoria Acuatrada Ortologica Concectra 11/2
critoria Concectra 20/2
critoria Concectra 11/2
critoria Conce

HELGLOGLET LENCYMPRIQ APLICISNORY LIFFTLANLIN LESVARIALG BIPRISPAPRE
OPPPYLAREN GHLEGOLFOR NEUGRANIEP POPERARIEP RAPPSALIER GRANARAGOPO
SLANDAGOG CHLEGOLFOR HELGLOGHEBD ELVERIFCOS SCRANIERED GRANARAGOPO
SLANDAGORPO CHLEGOLFOR TENGENDON ETMETYDELS ATACOCLO
BEG ID 100, 100, 100 CCC.

Seq ID No: 281 Protein sequence: Protein Accession 8: NP\_476431,1

2

15

Seg ID NO: 202 DNA sequence Nucleic Acid Accession 8: Eos sequence

2

25

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 2 4 4 5 6 6 5 5 5		757000000000000000000000000000000000000				
51 TOCAGOSTTO GOANTOCACC COCACANCCTO COCACACCTO COTOCACCT COCACACCTO COCCACACCTO COCCACACAC COCCACACCTO COCCACACCTO COCCACACCTO COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCACACAC COCCAC	CANTETCAA TANTGOGET CCCCTGOTCE CCCCTGOGET TOGGAATTCC CAAGGGET CAAGGGT CAAGGT CAAGGG	anachécha gerochere gerechoere characeha ranchera ranchera ranchera reacheace coageraace cracheace eracheace eracheace	CCTGGGAATT CCTGGGAATT AAAGCCCGG AATCCTCCC CTGTAAACT GCCCTCTG GCCCTCTG GAAGCCAGG GAAGCCAGG	CAGTICCTOR GRANACA AACTTGCTT TAAAAACT TCCCTGTGTAT ETGCAGAAA CCTGTGTAT TTTTCCCAGA GCCAGGACGG	GARACCCTO COACHGAGO COACHGAGO COACHGAGO COACHGAGO ACTOGCAGO ACTOGCAGO ACTOGCAGO ACTOGCATO	ACCUSTORCE CECUATOGG CECUATOGG CECATOGGA TECAGAGGG ATETAGAA GCATTTCCA GOMATICAC	ACCAGEGIA ACCAGEGIA ACCAGEGIA ACCAGA ACCACA ACCAGA ACCAGA ACCAGA ACCAGA ACCAGA ACCACA ACCAGA ACCAGA ACCACACA ACCAC
41 A CETECTOGOG CETECTOGOG CETECTOGOG TEMPLETE CTOGOGCET CTOGOGCET TOGOGCET TOGOGCET TOGOGCET TOGOGTET TOGOGTEGOG	AGGACTIGGG TGGGGCTTT GACTGCTCTT TTACTCTCTT TTACTCTCTT AGGACTTCCT GGGGGCCTT AGGACCTTCCT AGGACCTTCCT AGGACCTTCCT AGGACCTTCCT AGGACCTTCCT AGGACCTTCCT AGGACCTTCCT	TCCAGCTGCA AACTOTOTOTA TCCGCCAGC CAAGGGTCCA CCAGTTACCC ACTACACTA AGCCCAAAA AGCCCAAAA CCCTGGCTGCAA AGCCCAAAA AGCCCAAAA AGCCCAAAA AGATAAAAGC AAATAAAAGC	COTORNOCA COTORNATION TOTOCOMAGO TOTTOCOMOCA TOTOCOMOCA COTORNATA		55558888888	2422222244	GEACAATGE GEACAATGE CTCCACCCA TAGTTAGE GTGTTGGA ATGTTTGC ATGCATTGC
	MAGAGETTCC MATCECTA MACCAGATTT TACCTOCCTC CCCATOCCTC ACCATOCCC ACC	CTCATGGGGA ATCCTGGGG CCTGTGGTG CTCGCGGGG CCTGTGGAGG CCTGTGGAGG CCTGTGGAGG GGCATGAGG CTGGCCTGCT	GGGATTATOG GGAGCTTTCC CTTGCCTGAT TCGGGGGGC CCCAGGGGCC ATAGTTCT TTTGTTTCT CCCTTGATT				TECTOCATION  TECTOCATION  AGAGOLOCO  TECCATOMA  TECTOTAGOLO  CALCADATO  TOTOTAGOLO  CALCADATO  AMORTICATO  AMORTIC
CCTTTGCTG CCTTTTGCTG CCTGAGGGGGGGGGGGGGG	CATCTCACCC CAGGCTCACC CTCACACCCAC GCTGCCCCAC GCTGCCCCAC GATCTCCCCAC TCTACCCCCCC TCTACCCCCCCCCC	COTCAATEGC CATCTTCGAT TGACTCGAT GGACATGGAAC GCATGGCAAC GCTAACCAG GCTAACCAG GCTAACCAG CATGTGGC	CCAGGGCTCG CTGGCTCCTGA TCAGGAGAT TGGGCTCCT CTCCCTGG ACTTCGTGG ACTTCGTCG ACTTCGTCG		CTCACATGAT TTCCCTGATA ACCTGATAAT CTCAGAGATG ACCTGAGAGATG ACCTGAGAGAGATG ACCTGCTGAGAGATG TCCTCCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGA	TOCKOGGGA ACANGACAG GCTCCACAG GCTCCACAG TTTCCCTTC TTTTCCTTC TTTTCCTTC TTTTCCTTC TTTTCCTTC TTTTCCTTC TTTTCCTTC TTTTCCTTC TTTTCTTC	
AGCATTATCT AGCATTATCT ACATCACCATA ACATCACCATA ACATCACCATA TOMOMAGAA ACATCACCATA ACATCACCATA	GCCTCACCCA AGGAACTGGC AGGACTGGC ACCTCATGCA TCTTCATGCA TCTTCATGCA TCTTCATGCA TCTTCATGCA TCTTCATGCA GGAGCTGTC TGGCGGCAA GGAGCTGTC TGGCGGCAA GGAGCTGTC TGGCGGCAA GGAGCTGTC TGGCCGCAA GGAGCTGTC TGGCCAACCT			TOGGGATOR GCOTCATCA GCAACCCTTAA AGCCCTTTAA TATTAATACG GTTTGTTTA AGCCAACC GCTTCTAA AGCCACTTAA AGCCACCTTAA AGCCAACC GCTCTCAAC GCTCTCAAC GCTCTCAAC AGCCAACC GCTCTCAAC AGCCAACC GCTCTCAAC AGCCAACC GCTCTCAAC AGCCAACC GCTCTCAAC	AND CONTROL OF THE CO		TANTOCCE TANTOCCE TOCCTCA TOCCTCAGAT ACCTCTGCC CTTCAGCGG
ATGCCACTOA ATGCCACTOA GCCTACCATO GCCTGAGGA GCCCTGAGGA GCCTGAGGA TTCCAGGGC CAGCGGGCC CAGCGGGCC CAGCGGGCC	GCCAGATA  OTTAACTOC  TTCCACCACA  CCACCAGCA  CTGAAGGAC  TATGACATC				TCGCGGTA  OTCCCTGA  TCCCCTGA  ACTINGGGA  GAATCTAGG  GAATCTAGG  GAATCTAGG  CTCCAGGTTA		
10	20 25	30	45	50	09 99	57	8 8

GAMACITTA ATCATETATE CETTOTICET TACICIDACE CIL
AMMATICE AMMATICE CETTOTICET AMATICATOR CETT
CALAMATICA AMATICATOR CETTOTICET AMATICATOR CETT
CALCOSTIVO ETCOLANCIA CONTROLATOR AMATICATOR OFFI
CALCOSTIVO ETCOLANCIA CONTROLATOR AMATICATOR AMATICATOR AMATICATOR AMATICATOR AMATICATOR AMATICATOR CALONIANO CONTROLATOR CALONIANO CONTROLATOR CALONIANO CONTROLATOR CALONIANO CONTROLATOR CALONIANO CONTROLATOR CALONIANO CONTROLATOR CALONIANO CAL

ଞ

65

2

75

60 120 120 140 150 150 150

CHACGACC TOCCTICATO TECETIONA ANTECTIAC CITICATIA GUITICITEC
ANAGANTI CITICATORI TIMAAGUT MALANICH TATORICH TITICATORI ANTECTICATORI TIMAGATUR MALANICH TATORICH TITICATORI COSTINACE TRANSANCE CONTICTION TATORICH CHITICATORI CANTITION TITICATORI CANTITION TITICATORI CANTITION TITICATORI CANTICATORI ANTECTICATORI CANTICATORI CANTICATORI CANTICATORI CANTICATORI CANTICATORI CANTICATORI ANTECTICATORI CANTICATORI ANTECTICATORI ANTECTICATO

39

Eos sequence

Seq ID MO: 181 DMA sequence Aucleic Acid Accession #: E Coding sequence: 564-1481

9

5

S

55

35

23

9 2 9 2 9

WITGILCHG LAGLAAGEN GIVARPROGN SLULAOONAN ÄARMOTFFER
PREFERENE SPINFALMOG GLENNERSPE PLULEGENSIN KRILLEPLANG
DEDEDVIDE STONGENAUS ENKYASIGNE REQUENTERS TERLEPLANG
PREVENT GIR KERDINGLIA, ALESENOOPOS HANDRESERS RETLEKERN
REKROGGIIK SHIRKANAKIL EKTYLORDAN SYNOPHAGN HANDESCHAUGH

83

Seq ID NO: 284 Protein sequence: Protein Accession #: Eos sequence

88

4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		24 4 4 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		;	700 000 000 000 000 000 000 000 000 000		720 780 900		652	3 5 6		120	3 4 4 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
GENERATED GENERA	19	LPWNAMSIQI MYLQVILPIQI HLVQLITKIAIL NQIGILISPOIL PMRNIREIMI NALQDIDGIV HLQGLIGENE VAVPBVIVPE OKTQAQSGIA		21	OGCTOCATOR  CTTCACTTOC  CACCTOCATOR  CACCTOC	OTCCCTOAAO CACCCTTOTC TCCCAAGACA CTCTCAAGAAG	CACTUTCTAT GGAGTACCOS GGCTCTGGCT AGTTCGCATT CTGA		S1   	VYDGREHTVY VVRVHARVRI		51. 	TAAGACTCA GAATGAGAT AAATCACTGG TGTGGAAGTC GAACGTCAC
THITAMMA GRACCETAC AGGCACTTOC THITATACAG CONTECCTO THITATACAG CONTECCTO ANTAGAG ANTAGA	1	Garivavptp Oslakylslan Leyipogado Valqelaloo Laxelsloipo Telarelslat Lenlploipo Ogsliiinva		ĺ	ANGGOGTON AGGACAGA TGCCTGCTGC CTACCATCA AGGOCCAAG TGGATGAGTT	AAGCTCCSA GCAACACCTA ATCAGATCTT GCGACAGCGC	OCHOGOAGCA ANACTACCT OCOCTCCAAG TCAATGCAAG AAGAGGGAGT		41 	BINBELGYNO BISYVKYLEH		41 	ATTAMAGT TATTCCACC TATTCCAC TOTATACA
AGANCEACTA GONTECTCTO TOGGSTACAG GANTSGAM GANTSGAM ACCATATAGA ANTAGATEC GETTTTAGC GETTTTAGC GOSTOGCTO ANGGSTAGT GOSTOGCTO TOGGSTAGA ANGGAGAGT TECHTTAGC TECHTTAGC GOSTOGCTO TOGGSTAGA ANGGAGAGAT TECHTAGC TECHTAGC TECHTAGC	ATOTAT 31	CSRASQVECT RITPGARNUL LKELOLAGNH DIPMCTPGGL LNRLTLFGNB PIBPGARNGL LMAIGLGNNQ PVCFSPANVR	VLAQNIXAPNE 52	15 -	CCTACTACTA CTGGAGGAAG GCCTTACCCA CAAGAAGG	ATCTTC3OCA GACCCC3CCA CTGGGTAATA GCAATGGAAG	OTOTATOATO TGGGTGCAO GAGTTCCTOT GTGGTCAOO TTAGAOGAOO		31   PTTEEQEAAV QEEEQPETSP TOTAL OPERTY	AMEDDSASEB	g	31 	ATTGACACA GCACTTCACA ACAGAMACA TGGGACAGCT ACTTTACTGT
AAAGCCAATT ACTOGACGTG CCACTTOTAG TATAATTAA TAAACCAAG CCCACTTOTAG CCCACTTOTAG CTCCCCATA TTCCACAACCT TTCCACAACCT TTCCACAACCT TTCCACAACCT TTCCACAACCT TTCCACAACCT TTCCACACCT TTCCTACTCT TTCCTACTCT TACATCACTCT TACATCACT TACATCACT TACATCACT TACATCACT TACATCACT T	ATAATATAC  A ATAATATAC  IN Bequence:  MP_570843.1	AYHGCPSECT ALRIEDNELS OPAHPSOCEN VLRLVENRLT PPSIPMQLPO VLILSHWQLP PQNIPAWVHG NOPRLGTOTV	CCCCKKBQA uence #: NM_0023	<b>=</b> _	TCCACAGCCT CCCTGGCACC GGGAGCCTCT TTCCAGCAGC	CTTTCCTGTG GAAGGAAGTG TGATGGCCTG GGGCACAATT	TOTGATGGG CACCCAAGAT TGCGGGCTAT CCTGGAGGAT AGCAGCTTTG	n sequence: NP_002353.1	21 	QVPGSNPARY	puence 1 #1 RM_00231 344	21 garcccact rccctatata Tacaaaaa	TOTGTCTATT ATGCACTOTT GGAGGAGAG CCATGGGCT TOTGATGACA
(186443 ABANACACA COCCETTACACA COCCETTACACA COCCETACACACA TATATOTA TATATOTA TATATOTA TATATOTA TATATOTA ONATOTACA COCCACACACA COCCACACACACACACACACACACACACACACACACACA	ATCACATA 286 Proteil sesion I: 1	Voccamgadla BPFLN16AL1 LLSSNGLLGI KVPGHLGRLG YLENNH16QL NVFGNLRQLG SLGNNRLRQLG 1 LPLRNMLLLL	IIVA LACSLAACVG NO: 287 DNA gec : Acid Accession sequence: 19		ACCAGANGA OCCTGGTGGG CTCCTCTGGT AGAGTCCTCA CCAATGAGG CCTTGTTCCG	ACAAGGGTG GCATTGCTA GCCTTCCTA TAATCGTCCT	AGGAGCTGGG GGAAACTGCT GCAGTAATCC ATGTGAAAGT CCCTGCGTGA	NO: 266 Protein Accession B: NI	11   	LGNNQ I PPKT WQENYLEYR LEEBEGV	NO: 289 DNA sequence : Acid Accession #: NM_ sequence: 461344	11 	ATOTOCAGTC ATTTANDED OTOLAMATCT CACCTONATT TCCTCONITA
WO 02/ TOTOTOGNAM TOTOTOGNAM COTACOMANTA TOTOTOGNAM MACTITICA	GOTOTACAGA J GOTOTACAGA J Seq ID NO: 2 Protein Acci		IAAIVIGIVA Beq ID NO: Nucleic Aci Coding sequ	-	ANDICTICA GAGGCCTGG TCCTCCC GACGCAGGA TAGAGGCAAC	ATCAMAATT ATGATCTTTG ACCTGCCTGG	GANATCHEES GEORGECCA CAGGTACCCG GANCCAGCT GCCTACCCAT	8eg ID NO: Protein Acc	MBSZQXSQHC GPPQSPQGAB	TCLGLBYDGL GEPRKLLTQD AYPGLREAAL	Seq ID MO: Mucleic Aci Coding sequ	1 COGCOCOCO GOCCACCTOA CATCACOCO	TTGACCGGA CAGCCCATCG GGCCCCAGCA GTTCTACCTG AMATCCCATC
5 10 15		30	35	6	45	. 05	55	9	\$9	2	75	08	85

ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  ANGORATION  Beg ID NO  PROBANDING  I I I I I I I I I I I I I I I I I I I
AGANCETOR AGANCE

œ
r
ヹ
=
es.
~
ര
_
_
-
C
ã,

Seq ID NO: 292 Protein sequence: Protein Accession 8:NP\_002649.1 WO 02/086443 ATCANIAMA TOTOMITTE CTOA

			••			90				•			0 0		0	0 0		•	• •		0 0		0 (			• •		0								
	GGG 60 KHN 120 KI1 180	_	TOUL 360 WIR 420			_	340		34 CT	A00 480	_		A00 057 087			7770			MGC 1200	_				MUC 1680		MAC 1800			CGA 2040		2220			2520		
: :-	CYCPKKPGQQ ALQLGLGKKY KTLRPRFKII		YGGEVTTRAL RVBHFLPWIR		<b>15</b> –	AGCCCGGAGG			GONACCATC		GGAGGAGCTT	-	GUTTURAGO	_	_	COAGGCTATG		_	ATACACCING	-	CGACCCATGG	-	-	AAGGACGGAGG	_	TOTOGRADAG	_		ANTONTAGA			TTGCATTCCA	_	TOOOTITETA		
s _	GNEYFENTHW QOTYHAHRED PERLEFQCOO	BATHCF IDYP IRSKEGRCAQ	анкеооорну Алкокрауут		₽_	GACCGCCOTC	GCGGCACGGG	AAAAGTCCOO	AGGACAACA	CATGODAAAA	CCCAGTGGA	OCCIDENTIC	CAATOTACCA	TOGAATOGGC	ATACCTITAT	TOCCTITIAC	CATCAGTAAA	TANTOACATC	TGAAGAGAAA	CACAAATTGG	AGTAGAATTT	CICAMOOT	OFFITATIFIC	CATCAATTEG	MACATODAA	GAAGAGAGCA	GAAGTGTAAC	TAGGAAAGTA	ATTRACTOR	CCCTTCTTT	TTTGATTAC	TOTACATAC	СТАССТОВВА	ACCOUNTACE	ACTTOGECAC	MANAGONANA
<b>=</b> -	CLPWISATVL CLPWISATVL CADGICKPBSP	GSL18PCW1 AHRND1ALLK	QLIONTVVKLI TO LVBNGRGC		<b>=</b> -	GGAAGCGGGC	ACCACOTGCG	ATGAMATA	ACATGATTGA	TTGAGGCCAA	TCAACCCAA	TAMCAGCA	AGGTTGTCAT	CCATGOGATT	CTGAGGCCAG	GTGCTGCATC	ATAACTATAG	<b>OTCAGAALTA</b>	MOGNAGICAT	ATATTCAGTC	TTGGATGGAG	TCATTCCACT	TOCAGODAAT	TACACACATA	CTTACCTTGA	AGCTAATTAA	OCCITATITI	GATCAGCATT	TCTACAGANA	AATTAATTAA	GTAAAGTATT	TACTOGIAAT	CTTTTAMAGA	AAGRICETCA	TOGRATAATC	CICIONANA
<b>.</b>	ENELHOVPEN KASTDTHGRP PLVORCHVID	-	ENSTDYLYPS VC8LOGRMTL	#: NM_0014:	<b>=</b> _	Terededece	COCCATOCCO	CTTTTOATC	TATGGGAGT	TTCAATACAG	CTGCCCGAGG	GATGAAGCAA	AGAGGAGAAA	TACATOGATO	TOCAUTATAT	ATGGCTTTGA	TTGAAGAACA	TCTAAOTOTO	CAGCTOTTGC	CATTITIONGA	AACTCAGACA	TOGATTIC	DATOCTOTOT	CTCATCACCA	ATTCTOAACT	AACTACCTAA	ATCAATTATA	GAGTTACTTG	AACTAGACAT	OTCAGCCACA	CATGTACATA	THETAATO	AATTTTTOTT	ACATTTTCTC	CTTTTOCAT	ACCCALIGNA
<b>=</b> _	CVLVVSDSKG YEGNGHPYRG PHCYVQVGLK			193 DNA Beq 1 Accembion ance: 932	=-	TOAOTOTCO		CATOTTOOTA	AGTICITIONA	AATGTCCGAG	TOGOTTCACA	CHICHICCA	CCGACATAGG	DOATCATATT	ATTECANGE	TCCAATTOTT	ACTOGAGCCA	CAGCTATTTA	CATCTACGAA	TCAGTCTGAC	CCCTCCTCCA	TTCCTACAAA	ACAGAAAAGA	TOCCANTOCA	ACTGATCCCA	TAGENTACEO	ACTOATON	TGAATGCCCA	TCACTCA TCC	TCTGGGCCA	ATACAGTGTA	CTAMOTOAT		AAATCACTTO	TATOATOTTE	CIUMATAMA
-	MRALLARLLL HCBIDKBYTC 1 YCRNPDRRRR 1			8eq ID NO: 293 DNA sequence Mucleic Acid Accession 9: NM_001498 Coding sequence: 932006		OGCACGAGGC 1			CTACCCTTTO		TAGGCTOTCC		CAAGAAATAT			CTACTATCTO	_	_	ATTENDED OF THE PERSON OF THE	-	DATTTANGE	-:	-	TOTOTAGE		ACACCAGATG		ATGAATTATG	CANCITACA		TCTAGAGTTT	CASCIACIO		TOTAL		W.T.F.CCC.
	10	:	15	50		25	ì		30			36	ત			40	}			45			Ş	ર			22			5	3			65	<b>;</b>	

5

## Seq ID NO: 294 Protein acquence: Protein Accession #: NP\_001489

2

	ê	120	180	240	300	360	420	9	5	600	
 	VBYMLVSPDH	<b>GOTHSEPNTY</b>	KSLPPPDRAI	BKPDHIYMDA	SDIDCRNGVI	DKELYBOLLO	PRPPPPNBD1	KVAQKRDAVL	PPOLIPILAS	SVITDEMNYB	
<b>=</b> _	HVRRHGILOF LHIYRAVKOR HKOVLKMODE VBYMLVSFDH	MIROTPGOPY GGTMSEPNTV	KPNPVEGGAS KSLPPFDBAI	PTEDOEASRA SKPDHIYMDA	MOTCHQUECL GVIPOACBIB EARTLYDQLA TICPIVMALB AASPIYROVV SDIDCRWGVI	ASVODRIRE ERGLEPLANN NYRISKSRYD SIDSYLSKOG BAYNDIDLII DKEIYBQLLO	soidhllagh vahlfirdpl tlfebkihld daneschpen iosthmothr Prppppnsdi	MRVEPRPME VQLTDFENSA YVVPVVLLTR VILSYKLDFL IPLBKVDEMM KVAQKRDAVL	DOMPYFRKDI CKOGNAVVDG CGKAQNSTEL AAEBYTLMBI DYIINGKEGV PPGLIPILAS	PLENMSVOVD TRCBILNYLK LIKKRAGGEL MTVARMMREP IAMHPDYKQD SVITDEMNYB	
<b>=</b> _	LHIYRAVKDR	TLWRPBYGGY	GCPOPTLPEV	KNTPSPPIET	TICPIWALS	SIDSYLSKCO	DANESOHPEN	VILSYKLOPL	AAEEYTUMBI	HTVARMAREP	N8SCLX8
<b>#</b> _	HVRRHG1LOF	KGERTHPNHP	ATSILEENQA LCTITSPPRL GCPOFTLPEV	WINVPIPED	EARYLYDQLA	NYRIBKBRYD	TLPEBKIHLD	YVVPVVLLTR	CCKAONSTEL	LIKKRASGEL	BAPRKVKYSG
<b>=</b> _	GLLEGGSPL ENEETKRHAD I	NKKVRLVLS GEKVLETLØB KGERTNPNHP TLWRPBYGSY I	ATSILEGNOA	WKHPAPETLT RNIGHARGEK VVINVPIPND KNTPSPPIET	OVTFOACBIB	ERGLEPLKYN	VAHLFIRDPL	VQLTDFENSA	CKGGNAVVDG	TRCBILMYLK	LILKCNOJAN ELCECPELLO BAPRKVKYSO BKTDSSM
	TASDOSTTOM	ENKKYRLVLB	EANWAKERE J	NKHPRPBTLT	MOTOMONICELL	BASVDDRTRE	BOIDHLLAQH	CWRVEPRPME	OCHPYPRKD1	YLENMSVDVD	LILKCHOIAN
75					2					£	

	HOLENTA	PDBAI	TYMOA	RNGVI	DKELYBOLLO	PNEDI	GDAVL	I PI LAIS	DEPONYS
<b>s</b> –	V BY	KSLP	BKDD	2009	DKEI	PRPP	KVAQ	PPOL	ENE
₹_	HIDVLKMODE VEYMLVSPDH HIBOTPGOPY GGTMSEPNTV	KPNPVEDGAG	PTEDOEASRA SKPOHIYMDA	AASPFYROYV	EXYMDIDLT!	DISTANCTING	1 PLBKVDEN	DTINCKEGO	TANHODYKOT
<b>n</b> _	LHIYHAVKOR	GCPOPTLPEV	KNTPSPPIET	TICPIWALS	SIDSYLSKCO	DANESOHPEN	VILBYKLOFL	AAEEYTLMBI	MENAPHOREP
<b>1</b> 1-	spl. Gweetrhad hvrrhoilof lhiyravkor hkovlamob veynivspdh 1.8 genletlor koennpanp Tlarpbrosy migotogopy gotasepntv	RKE ATSILEENOA LCTITEPPRI GCPOPTLPEV KPNPVEGGAS KSLPPPDEAI	ILT RNIRHRRGEK UVINVPIPND KNTPSPPIET	CCL QVIPOACBIB EARTLYDQLA TICPIVAALB AASPFYROYV SDIDCRNGVI	TRE ERGLEPLYNN NYRIBKBYD SIDSYLSKCO EXYNDIDLTI	ach vahlfirdpl tlfebrihld daneschpen igstamotmr prpppnsdi	PHE VGLIDFENSA YVVPVVLLTR VILSYKLDFL IPLBRVDENM KVAQKIDAVL	KDI CKOCHAVVDG CGKAQNSTEL AAEEYTLMSI DTIINGKEGV PPGLIPILAS	NY TREGITATIN' (INKRAGORI, MTVARMAREV IANHODYKOD SVITDENNYS
<b>11</b> -	GNEETKRHAD GEKVLET LOS	ATSILEGNOA	RNIRHRRGEK	OVTPOACBIB	ERGLEPLKIN	VAHLFIRDPL	VQLTDFENSA	CKDGNAVVDG	TOCOTTANTA
	23	2	5	ď	8	픙	돭	ë	Ę

	WO 02/086443 Beg ID NO. 335 DNA sequence Nuclair Acid Accession #: Eos sequence Coding sequence: 147-816
~	11 - 11
01	MOTITIODE TRANSCISCO ACCEPTANT TRACEMENT CATTECTICE AFFOCACETY 00CONAGO GANCACOTO TRACANA COCEPCEUS PROMEDICA ENCUANTE 00CONAGO CATATECCA CALCECCO ACCERCAT ESTABANA COCEPCEUS 00CONAGO CALCENTENCE TOCCATETTO TRACATOCO CONTENTE TRACANA CONTENTE TRACATOCO TOCACANA 00CONAGO CATATECCA TOCCATETTO TRACATOCO CONTENTE TOTALANOS 00CONAGO CATATECCA TOCATATA ANACORDA CATATECCE TECACONAC
15	CAGDAGCAG CCTTATTGCA GGCTCTGCCA ATGCTATTCC ACCCAGCDA TTGGATTCTC ATGCATTGT GCAGAAACT GGTAGCATT TCTCTGGAGA TGACGAGAA TGCAGAGAAA TTTATTGATGT TATAAACT AAATATGT
70	AMAMITET COMMITGET OMGINGTOC MOGNOTIC TITOMITGET CATELANDAM GOGGANGET GENERALIO AGNORANC OMMOTIVA ATTICADAM ACTORICA ATTOGETICA TOTATICADAM TANGORALIO AMMOTIVO GOGGANIA TITOTEDAM CITCADADA ATTICADA
25	CTAGANAT CTGTRATA AMGNOTIC TITITCCCA MCTIOIGTI TIGGTRATI TENTICCCA CCTGTGT00 GOTAMIACT ATLACAGICG TGGTTTCTGC A
30	Seq ID Not 256 Protein sequence Protein Accession 8: 50s sequence 1 11 21 31 41 51
35	HIDTERNYN DERYFRER ECDBRYOR ORMLLARIG OADDELLAG MYKEKKLTT GIAIPPROLD SQIDDFTOFR KORMOGNYG RAPVGRYTS SPECIDLEGE ETASSFAGR EINAJIOSIL VEELRCYGGK YEKIPEMEN VOOTAVRIK FFESIIKEA. ROARIDFYH LKYELKENI
04	Sec 1D NO: 197 DAA sequence Buclaic Acid Accession I: Sos sequence Coding sequence: 147-815

922

	-	. :	ä	11	5	ı	
'n	AGTGTTCGGC GGCCAAGGG CCTAGGGGGC	TOGGGCAGGC GATCGGTGCT ACATTTCCCA	ACCETOTOCC TCTOOTGAGA CAACTCCCAG	TGGCTACTTC CGCCTCCCCA AGGGCAGGTT	CCTTCCTCCC TCTACATCAC TCTACAAAAT	ATCCCCTTO TCCCAGGTGC GCCACCAGTG	9 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
0	GAAACAATGA CCCAGGGAAT AAACAAGGAG ATGACAAGGAC		TECTATEOR  CCTATTECA  ACCCAGCCAA  ACCAGAAACCT	AAAAGGAAA GGCTCTGCCA TTGGATTCTC	CTGAAACTOT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG	OTTTANCOT OTTOSCAGO ANGANOCTT CTTCACTOST	2555
55	ACCAGCAGTT CAACAAGAAA CAAAAATATG AAACGATTTT		TOACCTAGAA TATAAAACOT CGAAATGCTT CATCAAGGAA	AMATTAGTGA GAAGGAGTGC GCAGCAAGAT	CAGCCTCCTC AGGACTCCG AAGGACCTAC GTATGAGACG	ATGCGTTGGA ATGCGTTGGA TGCAGTCAGG	1166
8	TTCTACATO CTTCCACAGO TTCCACAGO TTCAAAGGAT		TCATTAATA TTGCTGAAGT TCTGTTAGTA TTGGTTATTT	TTGAGGAGA CTCCTGGCAT AAAGATGTTC TGTATTCCCA	ANAGGATCA ATGTTACCGA TTTTTCCCAA CCTGTGCTGG	ATCACTOTT ATCACTOGC ACCOTTTAT TAGATATTAT	1020
. 59	Seq 1D NO: Protein Acc	298	Protein sequence				
٥	1 HIDKTEKVAV GHAIPPSGLD BINADIKRKL LKKGLAGMI	11     DPETVFKR PR SQIDDFTGFS VKELRCVGQK	21   ECDSPSYOKR XDR.PHOKROS YEKIFEMLEG	.11     GRMALLARKQ   NAPVOGNVTB   VQGPTAVRKR	41   . GAGDSLIAGS SPSGDDLECR PPESTIKEAA	51   AHSKEDOUAT BTABBPKBQQ RCARRDIVSH	120
5	Seq ID ND: Nucleic Act	Seq ID NO: 299 DNA sequence Mucleic Acid Accession 8: 1 Coding sequence: 247-815	8	eedneuce			
8	ACTOTTCOOC GOCCAAACOO CCTAGGGGGC	TGGGGCAGGC GATCGGTGCT ACATTTCCCA	21 ACCCTGTGGC TCTGGTGAGA CNACTCCCAG	10GCTACTTC COCCTCCCA AGGCCAGTT	cerrectese reckentese reckentese	ATCCCCTTO ATCCCCTTO ACCCCATO	1700
\$\$	GAMACAATAA CCCAGGGAAT AAACAAGGAG TGACAGGAG		AGAMAGTIG TTCGTATCAG CCTTATTGCA	GCTGTAGATC ANAGGCAGA GGCTCTGCCA TGGATTCTCA	CTGAAACTOT GGATGGCCT TGTCCAAGC GATTGATGAC	OTTAMOST GTTSGCAAGG AAAGAGCTTA TTCACTGGTT	

WO 02/086443

2
7
2
=
3
300
9
2
$\simeq$
ε
ã,

340	9 .9 •	5 E	9 6	1020	0801
GGAAACGTTA	TOCOTTOGAC	GCAGTCAGGA	ATTOCTOTT	TCACTOOC	AGATATTATT
CAGNANCCTO GTADCAATOC ACCTGTGGGA (	AGCCTCCTCT GCAACTCCGA	AGGACCTACT GCAGTCAGG TATGAGACGA GACTTTGTT	AMGGATCAG A		
OTABCAATOC	ITCTGGAGAT GACCTAGAAT GCAGAGAAAC / PATGCTGAT ATAAAAGGTA AATTAGTGAA (	AMMATATO AMMATETTE GAMATOCTTO ANGOADTON I ACCATTITI TOMATECATE ATCHAGGANG CHOCHAGATO	TTTGAGAGA	TOCTORAGE TECTOGEATA	OTATTCCCAC OUTTTCTGCA
CAGANACCTO		ACCUTATES AMMIETTE GAMIGETTO ACCUTATION (	DOMINATOR ANACOTATOR 1		
186443 FADOATGATO	TANTOCTOAT	MANATOTTO	DAADAACTO	AGCAGGATAT	ACTIONOTITE OTAMATACTA
WO 02/08644	ACAGCAGTTT A	AACCATTTT :	ACACCCCAUA 1	TCCAGAGGC	
		٠,			2

Seq 1D NO: 300 Protein sequence: Protein Accession #: Eos sequence 15

	9	120	180	
ß	AMSKAKKLAIT	<b>ETASSPKBOO</b>	RCMRRDPVKH	
₹_	TOXTERVAY DPETVPRAPA ECOSPSYCKA GRMALLARKO GAGOSLIAGS AMSKAKKLAT	SPRODDLECR 1	INADIKRK VKKLRCVOQK YEKIPEMLEG VQGPTAVRK PPEBIIKEAA RCMRDPVK	
<b>1</b> – 31	GRMALLARKO	NAPVOGNYTS !	VOGPTAVRICE	
<b>1</b> -21	BCDSPSYORR	1 SDANOWNEDS	YEKIPEMLEG	
<b>-</b>	DPETVPKRPR	HAIPPSQLD SQIDDFTGFS P	VKELRCYOOK	
	MTDKTERVAV	CHAIPPSQLD	EINADIKRKL	LEKEL TRAIL
		5	2	

Beq ID NO: 101 DNA sequence Nucleic Acid Accession 8: Bos sequence Coding sequence: 247-812 22

	9	120	180	240			TA 420									TC 960	7		
15	ATCCCCCT	TCCCAGGI	OCCACCAGTG	TCCAGCAAGG	DITTAMACO	OTTGGCAAGG	AAAGAGCTTA	11000100	MANATOTTA	CCCAMAGCC	TOCCTTOCAC	GTCAGGAAAC	THUTHAG		GCTGTTTTC	ACTOGGGGTTC	ADTITATION	TATTATTAC	
₹_	correctee Areceerra	TOCACATCAC TCCCAGGTGK	TCTAGAMAGT	COSTCTCTCC	CTOAAACTGT	GGATGGCCCT	TOTCCAAAGA	CATTCATGAC TTCACTGGT	ACCTGTGGGA	AGCCTCCTCT	OGNALICOGA	ACCTACTGCA	GAGACGAGAC	OTCCCTGGAG	GGATCAGATT	TACCOLATICA	TCCCAAAGCG	TOCTOGIAGA	
ä	TOCCTACTIC	COCCTCCCCA	AGGGCAGGTT	TOAGCTOCCO	<b>ACTOTAGATO</b>	MANGOCAGA	<b>ADDUCTOTODO</b>	TOGATTCTCA	GTAGCAATGC	GCAGAGGAAT	ANGTAUTUNA GUNANTCCON	GAOTOCAAOG	CANDATOTAT	GAGAATACTT	DOMONDADA	TGGCATATGT	ATOTTCTTT	TTCCCACCTG	TICTOCA
<del>-</del>	ACCTUTGGC	TCTGGTGAGA	CAACTCCCAG	TOCCATTITIO	AGAGAAGGTG	TTCOTATCAG	CCTTATTGCA	CCCAGCCAAT	CAGAMACCTG	GACCTAGAAT	ATAMATOTC	ATGCTTGAAG	AAGGAAGCAG	COTATOATTT	TAATGATTGA	TOMOTOTOC	TTAGTAAAAG	TATTTTOTA	CASTCCTOST
=	TOCOGCAGGC	GATCOGTCCT	ACATTTCCCA	ACACTTCAC	CCCATAAAAC	STOACAGTCC .	CAGGAGACAG	DOCTATTOCA	TOGGATGATG	CTCTGGAGAT	TANTOCTOAT	MICTICGM	ATCCATCATC	GAAACTGAAA	ATAATCTCAT	AGGATATTGC	GAMPTECTO	1010111100	AATACTATTA
	AGTETTOCCC 1	30CCAACOO C	CCTAGGGGGC A	ADDRAGOCC 1	JANACAATGA (	CCAGGGAAT o	NACNADBAG C	TCACACGACA 1	TCMGCAAAGA 1	CONSCINE	ACAGAAAT 1	NATATOMAN I	L ADITITITION .	ACCITAMBAA (	CCCCAAATOC J	ACANTOGACC J	CHCHOOCTAN	NAGATAACT	CCATTAGGTA 2
	•	3	•		,	,	٠ ج	-	•	•	•	₽ •	,	_	•	_	45	_	•

Seg ID NO: 302 Protein sequence: Protein Accession #: Eos sequence S

55

Seq ID NO: 103 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 247-815

8

ADTOTTCODE TOGALANCE ACCITOTOSE (
GOCCHACIA GATCOGTOCT TCTGGTGAA (
CCTAGGGGG ACATTTCCCA CACTCCCA) GGAAGGCGC ACAACTTCAC TGCCATTTTG ( 65 2 22 8

Seq 1D NO: 104 Protein sequence: Protein Accession 3: Eos sequence 83

	70 OM	080413	;	;	,			
8	HTDKTEKVAV GHAIPPSOLD BINADIKRL LKKKLKRMI	11   	21   ECDSPSTOKR KORMOKPGS YEKI FEMLEO	AA GRIGILARKO BAPVOGRVTS VQOPTAVRKR	41 	SI AMSKAKKLAT BYASSPKGOO ROARRDEVICH	9 2 2 2	
10	Beq.ID ND: Nucleic Act Coding sequ	8eq.ID ND: 305 DNA sequence Nucleic Acid Accession #: Bos Coding sequence: 87-689		epuendes				
		==	<b>1</b> –		<b>=</b> _	15 —	;	
15	CCAGACTAGC	GCTAGGGGGA GAACUATACA TTATGGTTTC	GOCTOGGGAG GTCAGGATGG	CTAMAGGGA	CCCCAAGAAA	CCTACACTUC	2 2 2	
		TOTCAATTT	<b>AAATTTAATO</b>	CCANDANGTO	CTCTGAGAGG		28	
20	ATCOCAAAA	GAAGGATAT	GOATTCTTCC	AGCOAGCAA TOTTCTGTTC	GAAGAAGAAG AGAATTCCGC	CCCMANTO	200	
	ATANTTTAAA AGTATGAGAA	TGACAGTGAA	AAGCAGCCTT GACTATAAGT	ACATCACTAA	OCCUBACAAG OTTTOATGOT	CTOAAGGAAA	200	
25	CTGCTAAAGT AGGAGGAGGA TTAGAGTAGG	GGAGGAGGAA GGAGGAGGAA GGAGGGCCGT	ALCOTOCANO CATCANTANA AATTCACACA	DANACTOTTT TCTCTTATTT	ATCTOTCTCC GAGAAGTOTC	TTOTOMATAC TOTTOCCTC	7 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
	ATTAGGTTTA	ATTACAAAT GGTTTACATG	TTGATCACGA AAGTGGCCAT	TCATATTGTA GGGTGTCTGG	ADCACCCTOA ACCACCCTOA	ANCTIONATES ANCTIONATES	9 6 6	
ဓ္က	CTGTGCACTT	TOCTOTTOOT	GTGACAAGGC	ATTTAAAGAT	OTTICHOGGA	CAACTOTATA	1020	
	TATCTATAGE	TTGTAAAAG	AACAAAACAA		CCCTTGATGC	TOCTTOCTCO	17.00	
35	GAGGCTGGAC	CTOTTOACTC	TOCADODGOC CTOCTGCCAT	ATCCATTING	CTTCAOOTTO		1260	
	CATGAGAATA TATAGAACTC	TTTTTTTTT	TANGTGGGGT		CTOTTTOTTT		1100	
•	CTCCTOTACT	TANACACAT	TCGCAACGIT	CHOTTATTIT	AACTCTTCT	TTAGAATGCT	1500	
5	CTCCCTATAA	TOACTCACAG	CAGTGAACAA	ACTCAGTGGC	CATTOTATTT	GCACACTOGC	1620	
	TGAAGGAGAG		AGCTACTOTO	TANGCARGGE	TOTOTCTGAG TCAGCAGCCT	TOCCATTICAD	1740	
45	CCTATTTTOT		CTGAGGCTAT	ACAGCTTTA	CAGAGTOTCCC	ACCTCCACCC	1920	
	ACATTATTTO ACTTATTTO	TOGTOCCOA	CATTHOOOT	CTTGAGCCTG	CTOCTOTES	CCTOGATOCC	200	
20	TTGGAAACAC	-	ACCATTACTO	ATAGGCTCCA	TCTTGGGCCA	CCTGAGCTAT	2160	
	GCCTGCTCAT GAAGGAGCTT	AAGTTTAGCT GGTTTGTGTG GGGGAGATGG	CATTCACTGG TCACTGGTTA	AAATOTAGAT TATTAGTGGG	TASTSTANCA TASTSTANCA ACTAMATACC	TTTTATCOAG TTTTATCCAG	222	
55	CTGATGTGTA		TACTOTCCOT	ACCANTGAMO	GATACAGTAC	CTATOMACA	320	
	OTTOMORAC TACGAOTTAT		OGAGGCGGTG ACAGCCTGAT	TCTCTCTCCCC	CCTGTCGGGT	CCTOGATGAG	2200	
9	AAAACTCGGT	TOTANOTTE TOTANOTTE	AATOTOTICC GCCCAGAGGC CATTCTAAGC	ACTIONICA TARAGETERA	GAMTTECCC	ACTANTITAN TCCTGCTTCA	2820	
	CTAGGCCNO		TOTTOCCAGO	CHCOTCAAAT	ATOGANGAGA TCATAACTAO	AACAACCTGC	3940	
65	CAOOGAAGOO	· -	AAAGGGGTAA	CTTTTOTOCT	TCCANAGTAG ACATTGAGTT	CTAAGCAGAA	3120	
	CACACTOTO		CTTCTAGTGG	TOOOGCAGCA	AGATTECTET	TCAACCTTTT	3240	
ć	MAGTGGCATG			TTAGCTTCAT	TTCTGGGCCC CCCATTTAAA		3360	
2	CTACTCCCTC	TAACCACCTC		CICCIOTOR	TOTOTOTTO	<b>GGAAAGAACA</b> TOTCACAAAT	250	
	OTATT 3000	ACCITOGATO	CATTCATTIT	CIGINATAN	o			

MAKODEKEN GDRANAFY OCCRENKK HEVDVIPAB PSKKESKIN THOUSEKEN DDRAKADAN TORRÄNDED ANGEKKED HAPRDPSEP FLÆGERFR I HETIPOLISI GDVAKLODN MONINDERG SEDDERRE SEREKENDE Seq ID NO: 306 Protein sequence: Protein Accession #: NP 005333.1 73 8

9 2 9

Seq ID NO: 307 DNA sequence Nucleic Acid Accession #: IM\_022342 Coding sequence: 1..2278 85

2

23

8

35

WO 02/086443

2

15

82

S

73

86443	TATAATTO TO TAVATCOOD ORTOLOGAT TATTOATO TO TATAAATO TO TATTOATO TO TATAAATO TO TATTOATO TO TATAAATO TO TATTOATO TO TATAAATO TO TATTOATO TO TATAAATO TO TATTOATO TO TATTOATOATO TATTOATOATO TATTOATOATO TATTOATOATOATOATOATOATOATOATOATOATOATOAT	Beq ID NO. 111 Protein sequence: Protein Accession 8 NP_061092.2  1	Coding sequence: 195. 1856  1	CHECCOACIO CETUTIDADI ACCIDIADA DIFICEDA AVETETICATO MACCIONA CONCECCATO CONCECCATO CONCECCAMO CONCENTAR ACAMORICA CONCECCAMO CONCECCAMO CONCECCAMO CONCENTAR ACAMORICA CONCECCAMO CONCENTAR	TRUBALIAN GROCTERAM ALCOLOMOR DEGENERACE TRUBANDAR CRECETURES 1160 TRUBALON CHTTGOTHER TROCHOMOR DEGENERACE TRUBALON CRECETURES 1160 TRUBALON CHTTGOTHER TROCHOMOR TROCHOMOR TRANSCORE RECORDERS 1180 TRUBALON INTERCENCE ALCONOMINE TROCHOMOR TROCHOMOR TRANSCORE TROCHOMOR 1180 TRUBALON INTERCENCE ALCONOMINE TROCHOMOR T
PCT/US02/12476	5 10	15 20 20 25 30 30		50 50 55	65 65 65 65 65 65 65 65 65 65 65 65 65 6
W U UZ/086443	ADMINISTRATION OF THE PROPERTY	S CACHEACH MEDICACCA INCURRAGE ANAMERS CANARIOGN CONTINUAL TO SECURIAL SECU	accordia acciona exactavara certacado dabatrata accerta a tricolada escrizodo Abachado Colancia. A contra contraca canterior canteriora actoanan facecido Gustracio encertacio escrizodas tradaretos atromos recitardes encertacios escrizodas tradaretos trimpos eccinadas Astecidas escrizodas escrizodas atromos cectuadas Astecidas escrizodas escrizodas anterios desendera estimatera tradacidade anterios desendera estimatera tradacidade montras desendera MITATETER TRADACIDA Antigo escandera MITATETER ANACOSTIGA ESCRIPTAS MANTAG.		1 Accession 1: CAT cluster  1 11 11 11 11 11 11 11 11 11 11 11 11

45

6

S

65

2

જ

WO 02/08/6443
TATACCHE TERRECOL TECETAMI TEGETERI ELECTOTA 2400
NATIOCHE TERRECOL MINISTEE MANICHE INSPIRATE NACOCHE 2400
MATERIA GENERALM ELAMAGAT EMPAGAT EMPAGAT 2410

	3180	3240	3300	3360	3420	3480	3540	3600	3660	1720	3780	3840	
	TOCCACCIAC	prominocon	GCCCAGAAGG	AAGGTCTATG	CACAGGGGG	CACACCCTTOA	TATTICITIC	CCTTACCAGG	CTCTGAGGGC	TCTGCATTAT	CAMPICTIAL	AGCACCCTGG	
	TODOSCOCTT COGGNOTITIC TODOSCOAC	CATGACCTTG	<b>OCTOGROATO</b>	TOGGMAGGG	COMPTRETE CACAMGGAGE	OCIACOTOOCC (	<b>GOTCOAGGAC TATTICITIC</b>	TOCTOTATET	GATOTCAGCO	TOGRACCAGC	CCCCCAGCCT	CCTANCANGT	
		OCCUPACION C	AGGAGGAGAT	CCCCCCTGCC	OCGAGGTGCT	<b>GCATGGCCCG</b>	CTGAAATTOA ATGAGGAGCA	ATATCTITIOG	STOCHOCCE SCADOCTOGA	AACTTAAOGA	AAAGTGATAT	TACTTOACCT	
	COCHCHOOCH	AAGGGAGTGC	NGATGAGGAC CACATCTACC	ACAGCCTATT	TCAGGACAT CCTGCGGCAG CAGCTGGCCA (	GOCCATGTGC		TATCACGNAG		OCCOOCACAG	DAGATGGAGG	TCMACCCTT	
086443	TTOCATION CATGOOGCT	CTCCCAGCAC		TOCOGTOCAC	CCTGCGGCAG	CTATGTTTGC	GCAGCTGGT GGCTGCCAAG	CCAGAAGCGC	CAGGGTGGCG	OCTTANACCT	AGGGCCTOGG	TTOCTCCCCA	2000
WO 02/086443	CTTGCATCCT	OCCICCATCA	accaccacca	<b>ADDITIONAL</b>	TTCAGGACAT	CAGGCCACCT	AGCAGCTGGT	AGCTCAAGAG	CONTONION	CTACAGGAGG	CTGAGOTCAC	TTCCTCMC0	ATTGATCOGA

Seq ID NO: 313 Protein sequence: Protein Accession #: NP\_000616

2

2

=

=

20	_	_	_	_	_	_	
,	MACDAR91.PK	TEPHOYAMAG	PKGINNAVER	APCATRRDUT	ODDIOYMUS	KOONESPOPL	9
	MACTARACTER		CALINATION		2007		2
	VETCKKSPES	LVKLDATPLS	<b>SPRHVRIKN</b>	GSOMTFODIL	HHKAKGILTC	ROKBCLOSIM	120
	TPKBLTRGPR	DXPTPPDELL	POAIEPUNOY	TGSUKBAKIB	EHLARVEAVT	KEIETTVTYO	180
,	LTGDELIFAT	KOAWRNAPRC	IGRIOWSNIA	VFDARSCSTA	REMPEHICRE	VRYBTHNGNI	50
2	RSAITVPPOR	<b>SDGKHDPRVW</b>	NACLIRYAGY	OMPDGSIRGD	PANVEPTOLC	IDLGWRPRYG	300
	RPDVVPLVLO	ANGROPELPE	IPPOLVLEVA	MEHPKYENPR	BLELKWYALP	AVANMLLEVG	360
	GLEPPGCPFN	CHYMOTBICV	RDPCDVQR YN	ILEEVORRAG	LETHKLASLW	KDQAVVBINI	420
	AVLHSPOKON	VTIMORHBAA	PSPMKYMONE	YRSRGGCPAD	NINLVPPMSG	BITPVPHQEM	480
9	LAYVLBPBYY	YOVEAMKTHV	WODEKRRPKR	REIPLKVLVK	AVLFACHLHR	KTHABRVRVT	940
<b>⊋</b>	1LFATETOKS	BALAMDLGAL	FECAFINDRAV	CHEKYRLSCL	EBERGLUNT	STFONGOCPG	909
	NOEKLACKBLP	MLKELMNKPR	YAVPOLGESM	YPRICAPAND	TDOXLEHLAN	SQLTPMGEGD	9
	STAGGEDAPR	<b>SWAVQTPRAA</b>	CETTDVRGKO	HIOIPKLYTB	NYTHOPHHYR	LVQDSQPLDL	720
	· SKALSSMHAK	NVPTNRLKSR	ONLOSPTBBR	ATILVELECE	DOCCLAYLPG	EHLOVCPONO	780
•	PALVOGILER	VVDGPTPHQA	VRLEALDESO	<b>BYWVBDKRLP</b>	PCSLEGALTY	PLDITTIPPIO	940
ņ	LLLOXIAQVA	TEEPERORLS	ALCOPERY BY	WKPTWSPTPL	EVLERFPSLA	VBAGFLLSQL	900
	PILKPRPYSI	BSPRDHTPTE	IHLTVAVVTY	HTRDGGGPLH	HOVCSTWINS	LKPQDPVPCP	960
	VRNASGPHLD	RDPSHPCILI	GPOTOIAPPR	SPWQQRLHDS	QHKGVRGGRM	TLVFGCRRPD	1020
	KDHIYOZEML	EMACKOVLHA	VHTAYGRLPG	KPKVYVQDIL	ROCLASEVLR	VLAKEPOHLY	1080
	VCCIDVRMARD	VAHTLKOLVA	AKLKLMEEQV	EDYFFCLKED	KRYHEDIPGA	VPPYEAKIOR	1140
>	VAVQPSSLEM	SAL					

Seq ID NO. 314 DNA sequence Nucleic Acid Accession 8: XM\_087254 Coding sequence: 47.,2332

5

4	TOWATCHOM	CATGITAMA	THUMBARTA	AAGAGACATT	TITCATETE	דוטורוטוז	2.5
•	TOTOCCTTOT	CCTTATOGGA	CICCIAATOO	CATTICABLE	TOTTOCTOMO	OCCATTATAT	200
	TTAATATA	ATOTACAAA	ANGREDICANA	TCTTAGTAMA	GAGTATTET	TACTATTACC	2700
	TTGATTATTG	ACTUTACTAT	TTAMATCTGC	TECHOTAMAT	TATOCTOAAA	ormoccma	2760
	AGAACTCTAT		CACTENTATE	TAMOCHET	CATGODAAAA	<b>ADTOTAXTTO</b>	3820
5	ATACTGAGGA	-	CTCAGTGACC	TOTOTTOTTA	ATTCATTANT	acarterana	2680
2	TTCACAGAGC		ATCATTICE	MCCATTATT	TACTGCAGTA	TOGGGAGTA	2940
	ATTTATACCA	-	CTOTACTOTA	ACACACCTG	TAMAGETAGE	CATATAAATG	8
	CANDOGIATA	TCATATATAC	MATCAGGNA	TCAGOTCCUT	TCACCGAACT	TCAATTGAT	3060
	OTTTACTAAT	_	CAGAGTATAA	AGACCCTATA	<b>OTOGOTANAT</b>	TAGATACTAT	3120
,	TAGCATATTA	٠.	OTCTTTATCA	TTOGATCTT	THOUSENE	AATCTOOTTA	=
≏	ACATATTTAA	7	THEFETTA	CCTGAAGGCT	CTOTOTATAD	TATTECATOR	35
	CATCOTTOTA	Ξ.	ATATCAATAA	AAAGTTTOGA	CAGTATITA	ATATTECKA	1300
	TATGTTTAAT	•	AGAATAGTAT	<b>ODGITAATTAA</b>	ATGAATACM	AAAGAAGAGC	ŝ
	CTCTTTCTGC	-	GACATGCTCT	10CCTTTCTA	TANGCTAGAT	MINDVIII	20
8	ADCOTTTCAG	-	TATTITICAGG	TATOTCATC	TAACTTATAG	CAMCTACCA	3480
2	CANTACAGTO	_	OTOTOCCAGT	ACAGGCATA	TETCAGOTOT	DOCTOTODAA	250
	TUTAAAATU	_	ATCAGGTAAT	<b>OTTAGCAATA</b>	AATTAAATGC	TARGALIGAT	9
	TAATCOOGTA	٠.	TATTACTC	ATTOCACTTC	MANCTANC	TICCATOCTO	3660
	MITTATOM	Ξ.	ATTOTOTA	grittmorri	TATTGAAAG	TAATOTTOTC	3720
į	TTANGATTTA	_	TTAGCTTGAG	AACTATTACC	CAGCTCTAAG	CANATANTON	3780
3	TTOTATACAT	-	TOGETANATE	COGTITITACC	MOTITICOC	TTOWARATOT	380
	ATTOCTES		TTOTOCABCC	CTAAGCTTCC	TTCCCATTTC	ATGAATATAA	900
	<b>ODCTTCTABA</b>	ATTGGACTGG	CAGGGGAAAG	AATOGTAGAG	ACAGAMATTA	AGACTITATO	3960
	CTTOTTTOCT	TOTANACTAT	TATTECTED	CTAATOTAAC	ATTROPCTOR	TCCAGTGATG	4020
;	TAAGGATATT	_	GCTANATATT	WITHCAM	AATAGTCCTT	CTTTACTTA	4080
ဓ္က	GATATTTCAT		AGGAAGATCT	GTTATTCTOG	AAGTACTAAA	AAGAATAATA	3
	CAACCTACAA	٠.	CACTAATTCA	TOTTCCAGAA	GAGGAAATAA	TGAAGATATA	4200
	CTCAGTAGAG		CACCATATOO	AAATTTOCTC	ATABAATCTC	TTATABACC	4260
	TOCATATAAC	• -	CCAGTAGGCC	TOCATTACAT	TTACATOACC	OTOTITATE	5
	GCCATCAAAT		CTGACACCAG	ACANAGACTO	CAMOTOATA	AAATAGCCTA	3
35	TOACCEACTO		COAGGECAGE	TOOCCTATAA	TOGTOCTTAA	AGTGTGATTG	444
1	ATGTAATTT		CATTTOAAGT	TAGTTAAGGA	GAACTETATE	ANNATITE .	500
	AAGTAAATGG		TOTOCTCATC	CTGAACTOTT	ACTCCAAATC	CACTCCOTTT	4360
	TTAMOCANA	_	GATTTANGA	MAGAGTTT	CTATTTATT	AAGAAAGTAA	4620
:	CAATGCAGTC		CASTAGITIT	CTAGGGGTAT	ATTCATCCTO	TAMACTOTT	99
9	ACTACGTAAC	_	AAGGAAAGTG	TOCCULTUDG	ATATTTCTT	MANATICATT	4740
•	CTTTCGAMO	٠.	ATAATTAACT	TACCCTTATC	TOCCANANCE	AGAGCAAAT	4800
	GCTANATACO	•	TCAGTGGTCT	CAAATCGATT	TOCCTCCCTT	TOCCTOOTET	4860
	GAGGGCTGTA	_	TAGTOGCAAG	CACCAAGTCA	<b>STITICCANA</b>	TTGCCCCTCA	6
	<b>ACTICITITIAN</b>	-	Accetacenc	ADCITICABCA	GOCOTAGGCT	CACCCTGGGC	4 9 8 0
5	OGAGCAAGT		GAGAACTACA	<b>GCTACGAAGA</b>	CCTCCTCTCC	AGTTGAGAAA	200
	AGGGGGAGAT		AATTECTAA	Crorcerers	1CTT0G01CT	AAAGCTCATA	2100
	ATACACAAAG		CTGAGCCACA	CCAGGCCCT	ATCCTOAACA	GGAGACTAAA	919
	CAGAGGCAAA		GANATACTTO	CATTCTGCCC	TACAGITAGI	ACCAUGANCE OF	277
Ş	AGGGGGGGG		CATIONER	TICACTIAL	CTOMP TO THE	CACACICCIA	
3	AIMOUNDE	-	CIMPARAIL	CACALLI AAL	AUCTOR	VI VIVILLE I	
	TOCTACTOR	MAMATCICS	TOOCCITY	AGUARAGO	AUARICITOL	ATTENDED OF	
	CALACACTER		TO THE PARTY OF TH	T T T T T T T T T T T T T T T T T T T	CACCACACACA	CATTERITY	5520
	440		TATTTCATA	ABACTBABAC	ACTATTABAG	TOCTOTATA	5580
55	TOTOMATAN		GTTCCTATA	AAAATAGATC	ATAACTCATO	ATATOTITOT	5640
	AATCATOGTA	_	TTATGAGGAA	TOAGTATCTO	GAMATATTOT	AGCAATACTT	570
	COTTTAMAT	7	AGACACTOTO	OCTOTICENAT	<b>STANTCCTTT</b>	AAAAATTCTC	5760
	TOCATTOTCA	_	TATATTATE	TACAGCTACT	CATAATTTT	TAMOTTTAT	285
Ş	GAAGTTATAT	TTATCAAATA	ANANCITIC	TATAT			
3		A Description					

Seq ID NO: 315 Protein sequence: Protein Accession #: XP\_087254

9	<b>-1</b> -	я.	<b>:</b>	π.	₽.	15-	
	MOPRECEING	HKYQBINGRL	VPEGPTPDSS		EQNISYLESI SHLANLSHLT TSBSPATEPE	TGBSFRTSPE	
	CHEKTINEN				LAPBOLETYA BSPOZKALVE	BSPDEKALVE	
6	ARSBILPKCI	GOE I BKTRIH	TLOKLERY KL VDBPALKGLR			I PEARTALOO	
	REEKLAAVPO SLGCCHPHRT	PIEKDLILLG		ATAVEDRIQD KVRBTIBALR SDSECAEGLR GLARRITEDH	MAGIKVAVLT GDKHBTAVBV VIQHGLVVDG TBLBLALREH	CDKHETAVBV TBLBLALREH	
;	BXLPMEVCRN GIMGKEGRQA	EKLPMEVCRN CSAVLCCRNA DIMGREGROA ARNEDYALAR		PLOKAKUTEL IKISPEKPIT LAVDDAMDV SMIQEAKVDI FKFLEKLLPV HGHPYITELA TLVQYPPYKN VCPITPQPLY	LAVODDANDV SMIQEANVOI TLVQYPPYRN VCFITPQPLY	SMIQEANVOI	
72	BIKTFLYNTI	LYDBYYLTLY	NICPTSLPIL POSTLLIGKO		IYBLLEQHYD PHYLGNKPTL YRDIBRORLL IBLLGNOOMP GMTPOTLVY TYNVITYTK	YKDISKARLL	
	MALETH FITTH ILMVVICLPL				GINY EVPIQU LASGBANFAI LDBNCCFPEG EARCABYGRA	LESGBANPAI	
80	LERVICECSP	LBRVIGRCBP THIGREMBAB	DPFYTMORBI	LTLSTADSST	U		

Bog ID NO: 316 DNA sequence Nucleic Acid Accession #: NM\_004473 Coding sequence: 661..1791

83

303

WO 02/086443

৩
_
7
ń
_
7
အ
2
5
_
_
_
ن
_
_

WO 02/086443

Theorems consented and analysis of the analysi

2

15

ACCACCACO

ATCACACA

GOCGCATCT

GOCGCACT

GOCGCACCT

CCCGGCCCOT

ACCACCOGC

ACCAC

ACCACCOGC

ACCAC

2

8

35

45

<del>\$</del>

20

55

				-	COTOTOO	CTCTCCMAGC
	AAGTTGGGC	AGACGCTGCT	TOCTOCIONA	TALAMAKACT	ONTO CARONA	CALCIDIATED
•	TCATCCTOTC	CATCOTOTOC	CTCATCATCA	COCHOCTOOC	TOCTTOOL	COACCAGCCT
3	TOTTGGTGAA	ACACCTCTTO	GAGTATACCC	AGGCAACAGA	OPCTANCETO	CASTACAGC
	CTTGGGCATT	GAATTACCGA	ACCOUNTAGE	001100000000000000000000000000000000000	GGCATCTA	ACCATOGRA
	TTANGAAGAT		AAGAACATTA	AAGAGAAATC	CCTOCOTOAC	CTCATCACA
9	TTTGCTCCA		AGAATOTTTO	AGGCAGCAGC	correccioc	
:	OCTTOCT000		TITATOCICI	TTTACCCAGC	AATGATGET	GCATCACOC
	TCACAGCATA		MATGCOTCO	-		
	ATGAMGITCI	TACTTACATT	ANATITATO	AAATOTATGC	CTGGGTCAM.	SCATTICE
13	AGGOTATCAC				T0CC0,000T	CTOACCTTCT
	CTCTTCATAT	-	TTCGATCTGA		OGCTTTCACA	отосталсло
•	AGCCTCAGT		ACATTTANGA	GTTGTTG	AATGGAAGAG	OFTCACTOR AND
ć	TAMBBACAA				3	ACCTTORICAT
₹	GOGACTCCTC			COCCCAAGCT	GACCECCAAA	ATGAMAAA
	AGGGGGGGG		AAAGGCCACC	ADOTTCA COCCA	CAGTGCAGCGC	COCCUCAGIC
	CCGAAGAGGA		CACATCCACC	TOOGCCACCT	GCCCTTACAG	
36	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACTOGTTGG		
3	TTGCAATCAG	TOTAL	TCAGCCATT	TAGGCCAGAT	GACCCTTCTA	GAGGGCAGCA
•	TGAGAGACAA	CATCCTOTT	GOGAAGGAAT		AAGATACAAC	TCTOTOCTOR
	ACADCTOCTO					ACCOUNTED
30	GAGAGCGAGG		AGCOGTGGGC		GATCAGCCTT	deceadace.
3	TOGGCAACCA	CATCHICAT	AGTGCTATCC	CONNECTED		ACAGETECTOR
	TTGTTACCCA		TACCTOGITO		AGTGATCTTC	
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG			GACTATOCTA
35	AACCAGTGG	TTCACAGAAG	AAGTCACAAG	ACARGOGECE	TARABCAGA	TCACATARGO
	ADGAMAAAGC		GAGGAAGGC			
	OTTCAGTGCC		TATEGRATOR		тостоороос	CCCTTGGCAT
	GOTTONITA	CTEGATORAG	CANGGANGCO	ATOTAGGCAG	CHOCOCCTTC	AGCACCTOOT
4	CCTCGGTGAG	, F	MOGNETIC		OTACTATOCC	AGCATCTACG
	COCTCTCCAT		CTGATCCTGA		AGGAGTTGTC	TTTOTOMOG
	CTATCAACTT	AGCITICATO	ACCIDITACATO	ACGAGCITIT	CONNOCATO	CTTCGAAGCC
31	TOGATGAAGT		CTOCCOTTCC		OTTCATCCAG	AACGTTATCC
45	TOGTOTACET	•		·	OTOGITOCIT	OTGGCAOTGG
	99CCCCTTGT	CATCCTCTT	TCAGTCCTGC		CAGGGTCCTG	ATTCOOONGC
	AGGGCCTTGC			ANGESCHOOL	CCACATCACO	TCCACCATAC
ç	AGCTGCTGGA	TOACAACCAA			OTGTGCGATG	COGTGGCTGG
2	CTOTOCOOCT			TCATCACCAC	CACGGGGCTG	ATGATCOTTC
	TACOCOCT	GTICCAGTT	ACCORDINATE	TOTCATCE	CATCHETAT	CONTRACTOR
	COCTOGAGAG	GATCAATCAC		CTCTOTCCTT		GCCAGAATTA
\$\$	AGNACAAGGC	recerecer	GACTOOCCCC	ADGADDDADA		GAGNACGCAO
3	CTABACACTA	CCUMOAAAC	CTCCCTCTTO	TCCTANGAA	AGTATECTTC	ACGATCAMC
	CCCTCTTCCO	TCTOGTGGAG	TTATCTOGAG	GCTGCATCAS	GATTGATGGA	GTGAGAATCA
	GTGATATTOG		CTCCGAAGCA	AACTCTCTAT	CATTCCTCA	<b>GAGCCOGTGC</b>
09	TOTTOGRAPHIC	CACTOTCAGA	TCANATITIO	ACCCCTTCA	CONSTRUCTOR	GANGACCAGA
;	TTGAATCTGA		AATGGGGATA	ACTTCTCAGT		CAGCTCTTOT
	OCATAGCTAG	AGCCCTGCTC	COCCACTOTA	AGATTCTGAT	TITAGATOM	OCCACAGCTO
,	OTACCATGCT	GACCATTGCC	CATCOCCTGC	ACACOGETICE	AGGCTCCGAT	AGGATTATGG
3	TGCTGGCCCA		OTGGAOTTTO	ACACCCCATC	DOTCCTTCTG	TCCACCACA
	recreector	TGACGAAGTC	TOTAL	AGAGGATTGC	CATTOCCTOC	CTGGGGGGGG
	CCCCTCATCO			OCCUTACEO		
2	ATTCCATATT	CATGTAAACA	AAATTAAGTT	AGGGAGAGTC	ATATTTTGAT	AAAAAATTT
	GOGMCCGTT	ATTATATTO		CTATAATGAA	CCTTTATACO	
	TATTANATA	ACCACHORGO	TAGECTATAT	TTACAGTOM	AATGTAAGCT	GITTATITA
ž	TTOCTGTACT		TITIOCIATI	AGACTOTAGG		TTCATTCT
2	STAGGOOD	TOUTTICACO	GTGCCAGGTT	TICTOGOTOT		ACCTCTCCA
			GACCATOCAG	ACCICCITA	OTTCTCAGGG	CTCCTGCCTT
	CTOTOCTOGT		GTTTCTGTCA	OGNOAOCAGC	GOOCCOAAGC	CCAGGCCCCT
8	TTCTGCCT	TCTTCTTTT	COUNTRY	CTAMONAN	ATCAGTCTAT	CCACACAGAG
	TCCCACTCCC	TCAGGTTCCT	ATOGETGGCC	ACTOCACAGA	acretectac	TCCAGACCT
	ATTCCCACAC	CTCCACAGTT	CAGTOGCAGG	GCTCAGGATT	TCGTGGGTCT	חידוכבינים
88	CHOCOCOCO	TOTOGOGO	orcicione.	CTCTCTCCCC	TCAMOTOTO	CARCTITAAG
;	ACCTCAGGTT	CONTROL	grandaring	GIOTOTICCC	DCAAACCCCC	TTTOTOCIOT
	<b>GGGGCTGGTA</b>	астславтав	acorogrene	rocrorcare	AUTTONATOO	TCAGCOTTGC

GETCHTOT GOODDCOTO ITTURGOOD PROCOCOTT GECTGADOC

BANTICAE TIMOLEMA DATENTOS GOCCOSTOCT GONTRADA

GARANCOLE AFRICADADA GATRATCH COCCOSTOCT GONTRADA

GARANCOLE AFRICADADA CATRATCH COCCOSTOCT GONTRADA

GARANCOL GATRATCH CATRADADA COTTOCOMO CONTROL

GEOTECHTO CATECHCH TRADAMANCH GONTROGAD CONTROL

FORTICATOCT GATRATCHCH TRADAMANCH GATRAGAD CHICCADAG

FORTICATOCT GATRATCHCH GATRATCHCH GARACCHG

FORTICATOCT GATRATCHCH GATRATCHCH THOMAGACHG

FORTICATOCT GATRATCHCH THOMAGACH CHICATOCT

FORTICATOCT GATRATCHCH THOMAGACH CHICATOCT

FORTICATOCT

FORTICATOC

CCGGGGCAGGT G
AGGGGCCCAG G
AGAAGTGAA G
GTATCAOCCA G
GAAAACTCG A
GAAAATACCA T
GAAAATACCA T
ACCCAGTGGA C

88

8

19 TIONTACTOR TTRNTAEGD PPROPENLY VEGEGOETAL TA NOCHLITER ARBOGGINM ALDRAEDIN GOTHETTER TA NOCHLITER ARBOGGINM ALDRAEDIN SEGGINERK AN ANAUNAMA ANAITERA VEMERPETO AVENGTREE PER GUVERELES ELGARESOR GGCHARAGA, BATTOTOPA OP GLAVENDAIS ALFAAGILA, OPAGEPAGE SCOVETTUPE GO QUGABRIGAT RAZEMANTO GIDREVISAM

FKHLTHYROI D GAGVPGEATO R PFYRDNPKKW Q RPKREDLETY P LAADPPVYYP A GCTGARPANP S YGRTSPGOPG A

2

65

Seq ID No. 317 Protein sequence. Protein Accession #: NP\_004464

8

Seq ID NO: 318 DNA sequence Mucleic Acid Accession \$: NN\_005688 Coding sequence: 326..4439

75

PCT/US02/12476

3	317-1123	
WO 02/086443	Coding sequence: 317-1123	
×	. Coding	

PCT/US02/12476

5760 5820

АТОТОТОК СМСТАВАСА ТЕСТОГОВСЕ ТЕМОСКОТТ ТЕСТОМОСЕ СПОТОВИМО СОЛИМСТСТ ВАМАКТОТВА ТАМАКТАТТ ТЕВОКТЕТЕ ТАМАМАМ АМАМАМА МАМАМАМ

WO 02/086443

Seq ID NO: 319 Protein sequence.

2

15

20

25

30

35

COCC ACCETORARY CACTITIONAL INITIETET ATTOCTTOC COMOCINCE
COTTORANAMA CITERANA ACCIDENT
COMMANA CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA CITERANA ACCIDENT
CITERANA CITERANA ACCIDENT
CITERANA CITERANA ACCIDENT
CITERANA CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA ACCIDENT
CITERANA
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANAMA CONTRACT
COMPANA ACCIDENT
COMPANA
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCIDENT
COMPANA ACCI

55.

8

8

THE STREETS OF THE ST

Beg ID NO: 320 DNA sequence Nucleic Acid Accession #: AK022089.1 Coding sequence: 181-1488

5

ACCACCCC A ATGCCACCC A ATGCCTCCCT T ATGCCTCCCT T GACATGGATT

45

20

2662665

ANPEGRELIA THENRESTR DIGERERS VIVOGERLA CLITETER DIGILLER
EATPOERST LASSEDIES VERGERAL SELECTER DIGILLER
EMPERATIOS REGISTROS SERVINES SELECTES VERTERLAR SENGENCE TO SECULIAL SERVINES MANAGERIA DE SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DES SECULIAL DE SECUL

80

Beq ID NO: 321 Protein sequence Protein Accession #: NP\_005438.3

75

2

Beq ID NO: 322 DNA ecquence Nucleic Acid Accession #! NM\_030920.:

85

307

\$ 2 2 2 7 2 2 8

	•
è	=
-	•
3	3
÷	₹
2	7
ŭ	ก
5	Š
5	=
ţ	-
5	,
F	٠,

PCTA																		,
					•													
9 6	25000	1200	1380 1440 1500 1500	1680 1740 1860	1920 200 2100 2100		2580 2760 2760	2820 2860 3000			120 340 300	6 5 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	780		60 120 180 240	2223	1286	900 900 1020 1140
ATAAGGCTGT	AAAATGGGAA GAGGCGTCAA AAGATGATAC CAGGTCGACC	ACACTTTCC CCACCTTTCT	CTANTOCAGO ACTTTOGAGO TOCCAGTOGC CTTCTAGCAG	TTTTACAGAG COGAATGTGG AATGCTATGG	CTGTGAACGA ATCTTCATAA AGTGCAAGAC ACAAGTTCTG ATGGAGACCG	TCTACCATCA CGGATGTOGG GGAAGTGCCT AAGTCTGTTC GGGCAGGGAC	AAGGACCCAA TOGTAGCAGC GGTTCGATCC GCACTGTTGG	TANACAMAC TANAGAMAA AAACGGGGGA TCCCTAATGG AAAA		S1   LLLPPLAASS	ITLPSRLIYY GLL88DYVEI IEPLELVHDE 8RGIPESMKY	TRGVGVBBYO KFFKCSILEY KCSLANGANC ACNONOGRECY	GTPCGPSMMC RDPVRNLHPP PI		51 CCACTCTCTA CTGCCTAGGA TACCAGATGC TCTAAGGAGA	CCTCTCCAAT CCTCTCCAAT CCTGCAAT CCTCCAAT CCTCCAAT	AAGCTTTTCA GOTGGAAGTO TCCTCGCCAC GCTCGGATCC	ANGACAGO TACAGCACAG TGAGCAGATT CTGGGGGGAG CTGTGATCCG
CUMARCATA	ATTCACTACO GOANGCATCA GOCATOTTO GAGAMAAGCA	TOTTGAMA TATTGAMA GCACATACCA CAGCTCAACA	MOCAGCATG AGTCTGCAA CAATGGGAAC ATCATGGAAG	TATAGAGACT TTTGAGGCCA TTTCATGTGG TGCAGGGACG	TGCCGCATG TGCCCACCAA TACAATGGCG GCAGGGTCTG TGCCGGAAGG	CCAACTICCT GATGATGATA TOTTAGATC TCCAAGGGTA GATTICACCT	CCCMGGATG GOTGCCATCC AAGAAGAGA ACACCGCCTT	ANGGATCAGT ACCTOTCAGT ACCTOTCAGT TCTTTTTTT GGAATCATTA		41   TPPCRLLLVL	ISYSNAMOKE KPILDLILAN MPEDOTEVYM LKRRKRAVNP	LATRVILVAV LEYPGCVCSR MEBTGVSHSR HVBCYGLCCK PPNLHKQDGY	DOTOVOYVED PTWAGTDCS I KRR FD PTQOG		41 dretected transpara ctanatita transpara	TCATCAAGTT GGACGTTTAA AGGAAAAACG CTCACTTCAT	TCTTTGTGG TCTTTGTGGG	TGAAGGAAT GGCCAACAGA TGACTGGGGG ACCCCTGGGG
AAGACACCAG	TTATOTOGAO TTACTACCAT TGGACTTCAT GGTTCATGAT	TOWATTANA AGAMATGAMA CTCTTCTCAT TTACAMGGAG	GCAGCGCATT TAAGAGAAGC GAATGAGTAT CCTTGGAATC		AGGGTATGAA CTCTGGTCAG GGGCCGCTGC AACAAAGGCT GAAGGGAAAC CTGTGGAAAC	TOTAGETETA TOTAGETETA OTCEATGATO TCCACTCGAT		TACTOGATCT TTOGGGTGAC ACCTTTCACC TOTTCCAGAA ATGCAATAAA		31   GSVPASAPAR	ntloonesen aspoirapes albtenglho onppleelon	NLVD817KEQ RVTFHYKA88 DCTESMGGCI EAGRECDCOP EYCTGDSGQC	DCGGAHVUD CSNEATCICO GTGMGPROVK	#:	TCCTCTGCCA CCCTCCTCCA TGACTTGCTG	AAGCTOCTCCA AAGCTOCTCC OOOGGTCCTC	CAGAAGATCC TTCTGGCAAT GATAAATGCC GAGAAGGCCT	ACTCCAACTS SCCTACACTS SCCTACACTS TCCCTOTGSA
ACACAAAGGC	DACTICION CACCTOCA CACCTAGA CA	TATATTES TOWNSCATES TOWNSCATES			TTCAGCCACG OTACTGAGA ATCAAATCA ACATCTGGGG AAGACTGA	AACTTCAGGG GTGGTGCCCA CATGTGGCCC TGAGCAGCTG ATGAAGCCAC	CAGTTAGGAA TCATAATAGG GCTGGGGATT GAATCAGCTG	GCACCAGTOT GGAGCTAAAG GTCAAAGAAC TXAAAAGAAC CXAAAATTAA	p_oossos	21   ASCGPORGPA	KNLGVLADED KRNYAVHLAQ BIRGVKDSKV MOYLTMBRGD	THUMPAKSOV DHADAVIILIB VEPSERKPKC SPTECONGYV SDAVNECDIT	TBFYHOGRVI KOKVCSGRGV AILVAAIVLG	Seq ID ND: 126 DNA sequence Nucleic Acid Accession 8: AK074418:1 Coding sequence: 244-1315	21 CATGCTCTCC TACCCATCTCC BACCCATGAG TACTOTOCCT	CATAGGCCAG GATCTACCAG	ACAGTACAGO CCOTTTCCGG TGTCCAGGGA CTGCCTCCTG	CTCTTCCCCT AACCTGTGCC GAGTCTCCAT AGAAATTATC GAGTGTGATGGGG
02/086443 PAT CACOTTOTTO	ATGGTTGT TCTAGGGTG GTGGCTCTGT ATGATAGAGC	CCATCACOTO ANACOTATA OTCAACCTTO	CATGACTTCT TCGCGGGTGA CGCACAAGAG TCGCAGAGGCC	CGAAAATTTT GCCTGCCTTT GTGGAAGCTG AAGAAATGTT	TCATGLCTTT ACTGAATATT TATGCATGCA CAGTGTCAGT CTGAATACAG CTGAATACAG	ATTGACTGCA GATGGAACGC GCCCTAAATA GTGTGTAGTA	ATCCGGATC GCCACCAATC GGGGGCACAG GGCCCCATCT	TOGASTACT TOGASTATAT OSCATOCTA ANCACACACA	Seq ID NO: 325 Protein s Protein Accession 5: NP_	11   	Badymnetae Vlotkarhoo Kooshcyyho Ktlagoybko	TYKKHRBHA BPSKYRQRIK OSLAONLOIO CLPNRPTKLP CLPOPROYEC	IQUQEITP LANSSCPLDS THLITGEIAD	126 DNA seq id Accession Tence: 244-1	11 	ATTACCAGGA CCTTGCGGGA CAGATTCTTC AGCGGCCACA	CTCAGAACCC CTGGCATTIT ACCGCCTACC	TCCATCTGCA GCTCCCTGAT ATGGCTGGT GGGGCTGGCA GAGGGCGCTG
WO 02/	CATACTICANC ACCACAGTAC AGACTCCAAG CTTCGTGTAT	GCAAAAAOT AGCAGTGAAT TAATGATCAC AAAGTCCGTG	DCACCTCATC TOTCTOTTCT ACAAGTATTA AAGCCAAAA	OTCCCATTCT AGGAGGTGGA AAATGGATAC ATTATGCTGT	TAACAATACC OTGTGATATT OCAAGACGGA CAGAGACAAC CTATGAAAAG	TCGAGCTCCA AGGCCGGGTG CTATGTAAA ACAATTCAA GGGCCATGGG	AGATTGCAGT GGGTCCTAGT TATTGTCCTT TACTCAGCAA	ATTCTGGGTA CTTTGGGTGG CTGTCTTT GGGGGCAAA ACGAAGGAAC	Seq 1D NO. Protein Acc	1       MKPPGBBBRQ	RPRANDAAAP INQDSESPYH HYENGKPOYS KSTORPHIIO	LELATWORK ITTHPVONLH LENAVAOVLS RDPLQRGGGA SDGPCONTS	LCTNLTRAPR LDRKCLQ1QA KDEGPKGPBA	Seq ID NO: Nucleic Act Coding sequ		GACTTACCA TTCCCCGCAG GTGATATGGA	GGATCCTTGA CACCAGTATO GTGATTGATG CAAAACCAAG	ATCACCACA ACCAGGCAG GCGATGGAGA CCATACCGAA ACCGAATGGA
	ď	10	15	70	25	30	35	6	45	<u> </u>	20	55	9	65	8	75	8	88

~	OGAAACACAC AACACTGCAG AACACTGCAG	AATTCACGAAGG TCCACGAAGG GAGGACCTCG	CATOTTTATA ATOOTCCCAA GAATGATOCT	ATATATATA ATATATATA CANTTCAACT	TTCCATTAC GGAAGCAAGT TCTCTGTGCA	CCTGGACCAT GATTCTAGGA AGAGCCAATG	222
•	GANGATOCAA CCAAAGCTCA GAACTATGTT	AATTTCCACT AATAATAAAT GTGGTTGCAC	CGATTTCCAA TCCGCCGCAA AGACACGGAG	OTTCACCATG CTTCACCATG AAAATCAGGG	CTOOCTCACA ACTTACCATC CACTTCTTOC		1500
01	AAGCCTTCA AAGCCTTCA GTACCTAGCA	GAACATGGCT CCCAGGGGCC	ACMAGCACCE CCCAACAAA TTACOTOGGA	CATTITICAC	MANTATOCTC GOGACCTGAG	ACCACOTATO OCAGOGACAO	1740
15	GOCCCACCC GOATANTATA		TCCAGACTO OGOOGACTTC OTOCATTGCC	CTOTOGCTOC MACTOGNAT CTCTANATCT		AGAGACGTGG GAAAGGGAGG AATTGGCAGT CATCGTTCCT	1920
70	CCCOOCACT TECACACAGO GAATAAAATA AAAAAAAAAA	ATTECTTA ATTECTANA GCTGCCAGG	AGAMAGCACA TGGCTTAATA GCTCTGCACA AAAAAAAAAAA	TACAGCATOC AACTOTTATA ATGAGCCTCT	TTGCTGCCAA AAGAACTCCT TACCGTTAAA	ACCACCTATO TOACTTOTCA AAAAAAAAAA	222
	8eg ID NO: Protein Acc	327 Prote	in sequence: BABS5075.1				
25	1   	11   TSIIKFNDQD	21   FTTLRDHCL8	31   	41   PAADSBIGQK	S1   LLQBKRLGHV	8
30	IMKAPODLPG  QYAGIPRTRF  SDLHYGFLED  MENGLVBLHA  KRQLHKIRED  TAGGPRNDAO	GPPRFILDDI MOCOGNVEVV ALVDLTGGVI YTVTGAEGIQ GBFMMSCQDF FNFSVORPHE	BRFDIOGGGA IDDRLPVGGD TNIHLHSSPV YRRGMERIS QQKFIAMFIC GTNVVVCVTV	ADCHFLAALA KCLFVRPRPKQ DLVKAVKTAT LANDHGNGET 88 IP ITLORG AVTPSNLKAR	BUTCHPOTRO HOEFWPCLLE KAGBLITCAT EWEGRWSDGB MTLHEGMSOI MTLHEGWSOI DAKFPLDFOV	KILMVQSPEH KAYAKLLGSY PSGPTDTAQA QEWEETCDPR MPRKQVILGN ILAGEONSCP	
35	AT.						
40	Seq 1D NO: 328 D Nucleic Acid Acc Coding sequence:	Req ID NO: 328 DNA sequence Mucleic Acid Accession &: E Coding sequence: 74-2788	puenca 1 %: SC017490.1	1.06			
\$ 5	1 drocorcaco rcorcoraca ocorcocica raccorcacc	11 	21 	31 	41 	\$1    -  - 	9 2 8 5
50	CCTAGGCACA CATGGATGAT CATGCGGCAG GTATGACAGG	GAGGGGCCCC GACTACCGCG GAGGACGTAG CGTGACCGGG CGTGACCGGGG GATGAGGGGGGGGGG	TOGROGANGA CCATCCCAGA AGGAGCTGAC AGGACTGGCCG AGGAGGAGCG AGGACGAGGA	AGAGGATGOA GCTCGACGOC GGCCTGOCC CCCTGCCCGC CCTGCCCGC	GAGGAGCTCA TATGAGGCGG ADGGAGGCAG CGCATGCGCC AAGCGCCGCC AAGCGCCGCC	TTGGAGATGG AGGGACTGGC CAGAGGGGC GTGGGCTCCT AGGTGGAGGG ACCTGGAGGA	
55	TCTCANAGGC CCACCGCTTC GGAGCGCATC CTTGGCACCC GCAGATCTTTG	CACTCTOTOC  AAGAACTTCC  AGCGACATOT  AGCGAC	GCGAAGAGA GCAAGAGAA TGCTGGCTA	CONTRACTOR CONTRACTOR	GOCCCCCGGC CACGGCCACA CTGGTGGTGA GAGGCACGG ATGTACCCCA	TECAGATECA ACTETEMAGA ACTATEMAGA COGNOCTUCE AGTACOACCO	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
09	CATCACCAAC GCTGAGGCAG TGGGTCCTG GGGTCCTTCG GTCGGCGGG				CTGGTGGAGG GGGGTGGTGCA AACAAGTGCA GGCTCCTGTC TATCAGAACT		1020
65	CCGAATCCAG CATCTCCCC CATCTATCAC CACCATCATC	GAGAGTCCAG GCAGATCTGG AACAACTATG CTAGCCACC GATGTGAGGA	DCAAAGTGGC TGGACAGCTG ATGGCTCCCT ACGTGGCCAA TGATCACTAG	GOLGOCCOO CAACCAGA CAACACTGC GAAGACTGC GAAGACAAC CCTCTCCAAG	CTGCCCGCT GACGAGATAG AATGGCTTCC AAGGTTGCTG GATCAGCAGA	CCAAGGAGGC AGCTGACTGG CTGTCTTTGC TAGGGGAACT TCGGAGGAACT	1260
70			AGCCCAAAA GAGACCCTGG CCATCTTCAC ACCCTGTCAG TGTGTCTCAT	CCCAGGGAGG CACAGGGAGG CACAGGCAG CAGGGAGTGG CAGGGAGTTGT TGATGAATTT	AAGCACAAG TCGCAGTTC GGGGCGTCGG ACCTTGGAGG		1600
75	CAGAACCAGC COTCACCTCC CTAGGACCCC CTTGGACATC	AFECATGAGG CTGCAGGCTC TCGCTGACTT CTGTGTGTGG GTGGGCAGCC		ACAGAACCATC CATTGCTGCC CGTGGACCTC CGTGGACCTC CGTGGACCCAC CCACCCCAGC			1920 1980 2040 2160
8	GGCCAATGGC CCAGGAGGTC CCAGATGGAC GACAGGCAGC	AGGGCTGCTG CTGAAGAAGT CAGGACAAGG ATCCCATCTGC	ACCECACCAT ACATCATCTA TOCCCAAGAT COGTGCGGCA	GCCAAGAG GGCCAAGAG GTACAGTGAC CATCGAGTCC GATCGAAGAC	TATOGOSTOO AGGGTCCACC CTGAGGAAAG ATGATCCGCA GACGTCAACA	AGCCCTGCC CGAAGCTCAA AATCTATGGC TGGCGAAGGC	
85	COTTATIOCO GACTITIOCO GAGCAGITA CACTATIGAG	GAGAGCTTCA CGCTACCTTT GTGCEAGAGC GTCCCTGAGA	TAGACACACA CATTCCOGCO AGCTGACATA AGGACTTGGT	AMATTCAGC TOACMCAAT TCMGGGCAAC GGATAAGGCT	GAGCTGTTGC GAGCTGTTGC CGCTTTGGGG CGTCAGATCA	GCATGOCAA TCTTCATACT CCCAGCAGGA ACATCCACAA	2520 2580 2540 2700

9
-
콨
_
7
င္က
S
↽
-
Ù
Ξ
_

2760 2820 2820	3000	1120 1180 1240	3360
ACGACCTGAA TECCTTGGGA GAGCACTTGA	CTGGCATGAC CTTGCCAGTG ACTCAGTACC	CTOCTTTTOC CTOCTTTTOC CCTOCAGGTT	
CAGGATGAAC AAGTTCAGCC ) CCCTATGCCA TCCATAAGGA ) GCTTTATGGA CACAAACCA (		TTAGGGGTTA COTATICAGG TTTICAGGG GCAGGGTTCT	GOCACAGITA COGITITAGIT AAAAA
CAGGATGIAC OCCTATGICGA OCTTTATGGA	AGCACCATOT CTCACCTTTC CTCCCAATTC	TOTOTANTO TITOTANTO	TTATCCACTC TTTOTOCATT MAAAAAAAA
AGTICTUAGG AGTICTUAGG		TCCCTCTTO OTTGAAGATO GAGGGCACGA	OTCATOCOGA CACTCTCTTA TAAAATATAA
086443 rtrtaroaca arccrocaca asoroarca		GCTGCTGAGT GGAGAGCTGC CAGAGAGCTG TGTGGTGGAA	TAMOTTONA TAMOTTONA
WO 02/086413 cerescines attrace assesses trenscrace tre	TOTAL TOTAL	ATOCATORCA ATOCATOTCA TGCCTTTOOC TCTUTOCCC	OTCOCAGGO TTOCTCCCTO TAATTTTAA
	S	9	

Seq ID NO: 329 Protein sequence: Protein Accession #: AAH17490.1 15

		11	17	2	=	51	
6	_			_		_	
2	MARSSERPTM	ABSPACERRG	ASSPACARRG NDPLTSSPOR	BSRRTDALTB	SPGROLPPPE	SPORDLAPPE DESECULOTE	8
	<b>GPLEKEEDGE</b>	SLIGDOMERD	YRAIPELDAY	EAEGLALDDB	DVRELTAGOR	ELAERAMROR	22
	DREAGRALOR	MARGLLYDSD	BEDEERPARK	RROVERATED	<b>GERDEENI 89</b>	I ENLEDLINGH	9
	SVREWSHAD	PRICIHHRPX	NPLRTHVDSH	CHONVENERIS	DMCKENRESL	DMCKENRESL VVNYEDLAAR	240
į	<b>EHVLAYPLPB</b>	APAELLQ1 FD	EALEWILM	HAT I ROYN Y	IHVRISHLPL !	VBELRSLROL	ě
3	HLWQL1RTS0		WIRCIGVLP OLSMVKWKN	KONPVLGPPC	QSQNQEVKPG	SCPECQSAGP	360
	PEVNMEETIY	ONYORIRIOS	SPCKVAAGRL	PRSKDAILLA	DLVDSCKPGD	BIELTGIYAN	Ş
	NYDOSENTAN	GPPUPATUIL	ANHVAKKDNK	VAVQELTDED	VIOLITRIEKD	COLDEKIFAS	9
	LAPSTYCHED	IKROLALALP	OCEPHOPOGK	HKVRGDINVL	LCCDPGTAKE	OPLKYIBKVS	340
ć	SRAIPTT000	ABAVGLTAYV	ORHPVSREWT	LENGALVLAD	ROVCLIDETO	KANDODRTBI	9
₹	HEAMEQ0816	ISKAGIVTSL	DARCTVIAM	NPIGGRYDPS	LIFBENVDLT	RPIISRPDIL	860
	CVVRDTVDPV	<b>QDEMLARPVV</b>	<b>USHVAHHPSN</b>	KEREGLANGS	AABPAMPNTY	GVEPLPOEVL	20
	KKYIIYAKER	VHPKLANDADO	DKVAKMYSDL	RKESHATOSI	PITVRHIESM	IRNAEAHARI	5
	HLRDYVIEDD	VMMAIRVMLE	SPIDIOXPSV	HREMONTEAR	YLSPREDNYB	LLLPILKOLV	9
36	AEGVTYORNE	PGAQCDTIEV		PEKOLVDKAR QINIHMLGAP		YDSBLFRYNK FSHDLKRKMI	Š
S	200						

QP	Coding sequence:	Jence: 257-1645	5791				
2		;	;	:	,	;	
		<b>:</b> -	 - 51	<b>=</b>	₹_	<b>5</b> _	
	arccacacar	orccococcc	OCCIOTOCCA	acceceratec	CTTGGCCGTG	CCCCCCAGC	9
,	CGGGTCGCAC	TAACTCCCTC	OGCGCCCACG	<b>OCOCCOCTAA</b>	CCTCTCOOTT	ATTCCAGGAT	120
3	CTTTOGAGAC	CCGAGGAAG	COSTOTTONC	CAMAGGAIG	ACUATOACT	CACAGAGAAA	180
	AAAGATGGCA	GAACCAAGGG	CAACTAAAGC	COTCAGOTTC	TOWACADCTO	<b>GTAGATGGGC</b>	240
	TOCCTTACTO	AAGGACATGA	TTCAGACTOT	CCCGGACCCA	GCAGCTCATA	TCAAGGAAGC	300
	CTANTCAGT	OTGAGTGAGG	ACCAGTCGTT	OTTTCACTGE	GCCTACCCAA	COCCACACCT	90
Ş	<b>GCCTAACACA</b>	GAGATGACCG	concene	CAGCGACTAT	COACACACT	CCAAGATGAG .	5
2	CCCACCCOTC	CCTCAGCAGG	ATTOOCTOTC	TCAACCCCCA	GCCAGOOTCA	CCATCAAAAT	480
	GONATOTAC	CCTAGCCAGG	TOWATCOUTC	MOCMETER	CCTGATGAAT	OCADIOTOGC	340
	CANAGGCGG	AAGATGGTGG	GCAGCCCAGA	CACCOTTODO	ATGAACTACG	GCAGCTACAT	009
	GGACGAGAAG	CACATOCCAC	CCCCAACAT	DACCACGAAC	GAGCGCAGAG	TTATCOTOCC	099
š	AGCAGATCCT	ACCUTATOGA	GTACAGACCA	TOTOCOOCAG	TOGCTOGAGT	COCCOCTOAA	720
3	AGAATATOGC	CTTCCAGACG	TCAACATCTT	DETATICCAD	AACATCGATG	GGAAGGAACT	780
	GICCAGAIG	ACCAMOUACO	ACTTCCAGAG	GCTCACCCC	AGCTACAACO	CCGACATCCT	9
	TOTAL PROPERTY.	CICCALIAC	TOGAGAGA.	TCTCTTC.	CALITICACT	CAUATORIGI	2 5
	TOAINAGE	TIACACACT	CTCCACGGT	AATGCATGCT	AGAMACACAG	ATTACCATA	96
ç	TOWNER CO.	AGGRAGATICAG	CLICACCOL	TCACGGCCAC	CCCACCCCC	AGTEGRANGE	1020
3	10000	ורוכרונט	Series Company	AACTGAAGAC	CAUCHTE	AUTAUATO	
	TIAN CALL	CT TOTAL CAN	CAMETAGECE	CCITICOMAI	CCAGGCAGTG	OCCAGATOCA OCCAGATOCA	
	200000000000000000000000000000000000000	110000000	AGE ICCION	GUNCAUCTO	AACICOMCI	CATCACCTO	1200
	TO COURT	Ances de la constant		CONTROCTO	משתפונים ברב	SOCIETION OF THE PARTY OF THE P	200
3	Transcoon and	AGC ATTACTOR	ACATOMACIA CONTROLLA	TOTAL PROCESS	AGCOGGGG	TOWNTACTA	
,	THOUGHT.			Discount of the second			
	CTCAGACCTC	CCGTACATOO	GCTCCTATCA	COCCOCOCO	CACAACATCA	ACT TO TOO	000
	accccaccc	CCAGCCTCC	COUTGACATO	TTCCAGTTT	Trigorocco	CANACCCATA	1560
í	CTGGAATTCA	CCAACTOGOO	DTATATACCC	CAACACTAGG	CTCCCCACCA	<b>ACCATATECC</b>	1620
2	11010101010	<b>OGCACTTACT</b>	ACTAAAGACC	TOGCOGAGGC	TTTCCCATC	AGCCTGCATT	1680
	CACCAGCCCA	TOCCACAA	CTCTATCODA	GAACATGAAT	CAMAGEGC	TCAAGAGGAA	1740
	TGAAAAAAGC	TTTACT6999	CTGGGGAAGG	AAGCCGGGA	AGAGATCCAA	AGACTCTTGG	1800
	CAGGGAGTTA	CTGAAGTCTT	ACTACAGAMA	TOAGGAGGAT	CCTANANATO	TCACGAATAT	1860
7,5	GGACATATCA	TCTGTGGACT	GACCTTGTAA	AAGACAGTGT	ATOTAGAAGC	ATGAAGTCTT	1920
2	A STOCK OF THE	S. C.	AGIGGICITA	ACACATOTAT	AAACITIAGA	GIAGAGITIG	1980
	AACATACOTT	TTATAATOCC	ATTTAAGGA	AAACTACCTC	TATTTABABA	TAGETTAGE	2040
	TCAAAACAA	GAGAAAGAC	ACCACACACA	CHOTOCCCA	TCAACACACA	THEATATICA	2160
8	ACTGCATOGC	ATOTOCTOTA	<b>AMOTTODET</b>	TCAAATACAT	TCCCTTTGAT	DOACAGCTOT	2220
ဋ္ဌ	CAGCTTTCTC	AAACTOTOAA	DATGACCCAA	AUTTECAAC	TCCTTTACAG	TATTACCOCC	2280
	ACTATGAACT	AAAAGGTGGG	ACTGAGGATG		GAGCGTGTGA	TTGTAGACAG	2340
	AGGGGTGAAG	AAGGADGAGG	AAGAGGCAGA	GAAGGACGAG	ACCAGGCTGG	GAMGAAACT	2400
	TOTOMOGNA	TGAAGACTGG	ACTCAGGACA	TTTGGGGACT	GTGTACAATG	ACTTATGGAG	2460
70	ACTCGAGGGT	TCATGCAGTC	AGTGTTATAC	CAACCCAGT	OTTAGGAGAA	AGGACACAGC	2520
3	GTAATOGAGA	AAGOGAAGTA	GTAGAATICA	CHANCHANA	TOCOCATOTO	TICTIOIT	2580
	TCTCAAATGA	MAKITIMAC	TGGAATTGTC	TCATATTTAA	GAGAACATT	CAGGACCTCA	2640
	TCATTATGE	geecertrer	10100000	STCAGGT MG	AGATGGCCTT	crroacrace	2100

22 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25			\$ 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		120 180 180		5 6 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0000 0000 0000 0000 0000 0000 0000 0000 0000		1500	1920 1920 2040 2040	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	100000000000000000000000000000000000000	3426
TTGAGTGGG TTTTATATA CAMBACACA GCTTATGT MACTTGGC GTGACTANG		S1   TBKNSPRVPO YGSYMERTHN	DGKELCKYTK TOLPYEPPR SGCIQIMOPL ALRYYYDKII MIPVAPHPPA		81 CCCTGGAATA CAGCTGCCC AGCCGGCCT	GOGCTCCCCC TCTGAAGCCG GCCTACCTGC CCAGGAACAT	GTTCGTCAAC GGAGGCCACC GGGCCCGTG CCGACGGAGG CCTGAAAGCA	CACAGGGAGT CTTGGTGGAG TGAGGTGTG TGAGGTCTAT CATGACCTCC	ACCAGCATT OTOTIGOACC CATCAGCAAC	ACCETTOTAL TOTGOATCAG CCTAGCTCAG		TTOCCCCCTO CCTUTICCACC ADADICEACOS GCTTTCTOTC GCCCTACT GCCCTACT GCCCTACT ACCCCGCATO ACCCCCGCATO ACCCCCGCATO ACCCCCCCCT ACCCCCCCCCCCCT ACCCCCCCCCC	TOGCATOATC TOGCATOATC AGACTCCCGA TTAGTAGAAA		
CAUTITICE TITITICECE CTUMECIOE ACTETOTAT ACTITITIAN ACTITITIAN OTTATANTT		41   TASESEDYOQ VGSPDTVOMS	DVNILLPONI NBPRLAGRAN PTBBRLAGR PHYRYDKLGR MGBYHANPOR YY		ogcaganga gccagaccc gccagacccc	CCATGACCTT AGGGAGACCC ATTGCAAGGG	GCCCACCA CCCTOOTOCT CCCTOATOCT TOTOOCATOT CCAOTCTOAT	GOCAGOTTOC GOCAGOTTOC TOTOGCAGO TOCOGOAGAC TOGCTICAGA	TGAGGCTAGC CACAGGGCAA GCAACCTGCA ATTACCTGGA	CCTTTGGCCT ACTATAGACC AGATGGTGTG TCCTCTCAGG	ANGTOATTCA GGGGGGCAGT GATGGGCAGC CTGAAACCTG TCTCTCCCCA AAAGAGGTC	GOCCEGENCY GOCCEGGG TAAGCTCCAG GATGCCTTGG AGAGAGCTGG CAGGATCACA TTAACTGAGA CCCAGGTCTG	TTCTTTTCTT TAGAOTOCAA CTCTTGCCTC TTTTGTATAT		OCAGGGGGG GCTCCAGCTC GTGTGTCTCA GAAATTTTCA
AGGCGGCCTC CAAGTCAATG ACAAGTTUAT CATGAATTTT CAGAATTTTTTTTTTTTTTTTTTTTT	2	31    - 	EWAVKEYGLP TEDOVDKALO PGLOPYGLLG ARRNGERKEK LYKYPEDLPY TEHNPERIGT	. 020	31 Acrosseca Greensaaa Cousacose	CCCAGAGGA TTGOTGACCC GAGAGCCCAC	TOCAGGGGGC CACAACGTGT GGCCAGCTGG GTCCTGGGCC CTGGGAGAGT	ACAGTGGCACA ACAGTGGCAC TOGCGGGGT CAGTCCTGGT CTAGGCTTCA	ATCTTOOTA CTOOTCAAGA CLOOGCAGO	ATCOTOGAG GACATCAGG GACATGAAGA GCAGACCCGG	GAGAAGCETA CTGGGGGGGT GTGTGCTGGG TACAGCTGGG GACGCTGGC ACAGGATGCA	TCAAAGCCG CTOCCAGGT GCCTCTAGCA TCAGCTGCTT CAGCTGCTG TAAGGTGTGA TGAGGTGTGAAAA	TCAGGACCTT TTGTCCAGGC TCAAATCATT GCCTGGCTAA	OCTORACT OCCTAACT ACCTAACT ATCOCOUTT ACTOCOA	CCCAGGACT ATCCAAGAAG GGSCCAGAGA GGGCATTTGG
CATTITICATE ATAMATATA ATAMATATACACT ATAMATATACACT ATAMATATACACT ATAMATATACACACT ATAMATATACACT CTGAANTATACCCAAAGAAAT	sequence AAA5239	21   EDGSLFECAY QVNGSRNSPD	WSTDHVRQWL YLRETPLPHL STVPKTBDQR EPWYTDPDBV ALQPHPPESS GOIYPMTRLP	900	21  - GOAGTGGTGG CCCCATCGCA CCAGCCCGGT	achahacaaa actoataace ctacacatat Agtactaata	CAGGGAGCTC CCTCTGCAAC GGGAACAGAT GGCCCTGGGT GCACAGCGAG	OTTOOOGAC COTOCAANG TOOCAACTO GAGGATGAA COACAACATC	CCCCAATGTG GATCCACTCA	CANGIDGACT CONGIDGACT COTONATIOC CAGCTITICAG CCGCCTTTGAG CCGGCTTTGAG	CACAGTCCA CTGCAGGGG TGAGTGTGT CAGCCAAAAA CAGCTCCCT CACCCGGG	AGTCCCAGAC CCCACCAGAG CCAGGCCTCA GATTTGTATC TGCTGAATGT GAGGTCCTAC CAAGGCCCAG GOTCAGTGGG	CAGGCCTGTC TTCGCTCTTG CCTCCCAGGT ATGCCACCAT		OTCTTCTCTO ATTTOGCTCC CCCTGGGCCA CAGAAAGTTT
(086443 ATCLCCAGO GTTTGTGCAGA AACTAGTGCAT AGTTATTAGT AAACCAGTTT AAAACCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	331 Protei	11   HIKEALSVVB VTIONECAPS	RVIVPADPTL NADILLSHLH PQSKAAQPSP SCITMEGTNG YKFDPHGIAQ APNPYMASPT	NO: 332 DNA mequence 3 Acid Accession #: NN_ sequence: 283-1794	11 	CCGGCCACCC TTCTGATGCT CGCTGGTGAC	GGAACTTGCA GCGACAGCCA COGAGCAGCC TOGCCCTGGT AGCGTGGCCT	TCCCCTTCCT AAGGCGCTA TCTCTCCCCC TGCTCAGACA	AGAGGGACCT TGCCGCACCT ACTTCAAGAG GCCTGGCTGT	TTGAGGCCTA GCCGGACCAT CCAATGACCC CCATGCCTAA	ANANATTAG AGAGGTAGTG CCAGGCCACC CTCAAAGCGG CACCCCTAC		GRACOSANO GRACOSCOS TRACAGOCAC	CCCAMOTOC TCTACATATT GACACTTCAG CCCTGGCAAT CTGGAGCACC	
WO 02 ACATCAGA ANCOCTAGA ANCOCTAGA ANCOCTAGA TACATAGA TACATAGGA TTACATAGGA TACATAGGA TACATAGGA TACATAGGA TACATAGGA	Seq ID NO: Protein Acc	1   MIQTVPDPAA QDMLSQPPAR	PPPNMTTNER DDPQRLTPBY SANTGKGHPT LELLSDSSNS MTKVHGKRYA LPVTSSSPPA	Seq ID NO: Nucleic Act Coding sequ	AGANAGGET AGANAGGET AGANACATTT GAGGGAGCCC	AGGCTAGCGC AGGAAAGGCC TCTCGGGGCC	CACTACTECT CACTACTECT CACCTCCTT CTGGCCTTGC CAGGAGAAAGC	TCTGAGCAGO GGCTCAGOGC TGTGTGGGAA GCCGTCAGA AACACAGTAT	GCCACCOC GCCACCOC GCCACCOC GCCCACCOC	ACCCUADO ACCOACTOCT CACATTOCCC CACACCCCCA	MACACATAC AGCACCTOAT CTATCTOOOT TCTCOOCCC GTCTGGCCTG	CCCTTGATCA CCCTTGATCA CCCTTGAGTA CCCATCAGTA TCCTCAACAA ACTAGGGCAA ACTAGGGCAA GCCAAGGATG	TITICICCAT TITITITITI CCAGCTCACC OTAGCTGGGA	ACCTCAGCCT TIGITICITA CTAGTICICI ATGCTCCAGC CAAGGAGTGT	CTCGGCCTCT GCTGGCTCTA ATGGGCTCTA
٠,	10	15	70	25	30	35	40	45	20	55	9 ;	8 8	75	08	\$\$

<b>.</b>						
					\$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0	
13540 13560 13560 13710 13710 13710 14710	120 120 140 160 160 170 180	600 1120 1120 1120 1200 1200 1200 1200 12	· ·	120 120 160 160 160 160 160		
CONTINUADO CONTINUADO	51   CTVVLVRREG EQPOTDOQLA PERLEGGLAS PSEREGGSWF ROTLEMILAL LAVMHSQGED KTIVNGIVED CYYPNFSARL	1 coactettee cotoscare cotoscare aactanta aactetta aactetta aactetta aactetta aactetta aactetta aactetta aactetta aactetta aactetta aactetta	S1   DPLVKGTPED	51   I   CTTTCACTCT AGTTCCATCC CCTGGAATTT TGAGTCTGGA ACAAATTT CTACCACTAG		er i normani
GONGGIANT GOTTGANG THETANGE THETANGE GOTGANANA GOTTGETTO THE	41 CKOPTCRCAW CKOPTCRCAW HUGCENOVEI SHOSLYOPLO NILOCCIADLO NILOCCI	41 CCONDETTOR GOCOLANTO AGITALAND AGANATANA AGANATANA GANATANA GOSTATTANA GOSTATTANA GOSTATANA GOSTATANA CTITCAGNA	41 ·   Knyleersob		TATOTTATAC GUACTCAAT CCAMAGAT CCAMAGAT CCAMAGAT TOATACTT TAACACCAC GOSATTACTT ANGTOCCAC TOTACTT ANGTOCCAC TOTACTT ANGTOCCAC TOTACTT ANGTOCCAC TOTACTT ANGTOCCAC TOTACTT ANGTOCCAT TOTACTT TOTACTT ANGTOCCAT TOTACCAT TOTACC	
TANGANGO TRAGANGO TRAGACTANT OTRATGACC TRATGACA TATORAGA AGNAT	11   LVTCTCESPH DGHLCNENVS ROLHSELGES ROLHSELGES TOLMLITHTH FKSRNVLWRS BSTRWTLINKS BSTRWTLINKS	116.1 11   Incompaction of the state of th	117.1 31   00VBKCBESI   00VBKCBESI	11 Adadadator TICAGGATCA TICAGGATCA AGCTGGACTG ACCATAGA ACCCATAGA AAACAATTT CTGCAAACTT	ACTICTAGIT CCCTOTATT ADAMTCTTA ADAMTCTTA ACAMACTO ACCAMATTG ACTICTAGE ACCAMATTG TATTAGAL TATTAGAL ATTAGAL ATTA	3
OSTITUTECTO OFF TOTALOGUEST TO COUNTY TOTALOGUEST TO COUNTY TOTALO	1 COPVIEDED PTEPVHIYCC MIVARRORIO QVALVECVOR ABDWTSRNS AGDWTSRNS QOTP AI AHRD LUBQIRIDCT LUBQIRIDCT VICYDQOTPT VICYDQOTPT	TO BE IN MOULT IN MOU	15 Protein sequence 1810n 8: NP_004117. 1 2. 131 1 2. 131 1 CERLINGUE QUAREFYELDE QUI 18 18 DNA sequence Accession 1: NR_005795	21   CTCT SCAGE TCATCCTAAT AMATCTTC TTCCTTAAG GTCAAATATG AMATAATAG AMATATAGA AGCCTATAGA GACAAAGAGA		
WO 02/186443  parrene dranometa o modular dran	11 LMLHALVTQ NLHRELCRGR ALVALOVLGL PPLVQRTVAR LEHIN ILGF I ARLHVS I TOT ARLHVS I TOT RICHS	Michael Acid Accession Bit My 00115.1. Coding sequence: 108-329  11 11 21 11 21 Coding sequence: 108-329  12 11 21 21 Coding sequence: 108-329  13 12 11 21 Coding Acid Accession Bit My 00115.1. Coding sequence: 108-329  14 12 11 21 Coding Acid Acid Acid Acid Acid Acid Acid Acid	115 Protein cession #1 11 EXEKINGUE VIS 116 DNA sequid Accession	11		
WO 02/18644 TATGETTCO GRADO GR	1 MTLGSPRKGI RHPQERRGGG LILOPVLALL DCTTGSGSGL RETEI YNTVL RLAVSAACGL TLDG GNWWW YRPPYWWWW YRPPYWWWW TALAKH YNTVL	See 1D NO.12 See 1	Seq ID No. 135 Protein Accession  1 1 1 1 HPALHIEDLE EKELIN RIPPERAGEC VIS Seq ID NO. 135 DN. Nocieic Acces	1 CACACACAT TICCCACTT TICCACTT TICCACTT TICCCACTT TICCACTT TICCACTT TICCACTT TICCACTT TICCACTT TICCACTT TICCACTT TICCACTT TICC	ACAGGTTOC ATTROSTOT TTACTACATO TTACTACATO ACATGTOCA ACATGTOCA ACATGTOCA ACATGTOCA ACATGTOCA ACATGTOCA ACATGTOCA ACATGTOCA ACATGATOCA	ATTLICTO
5 10 15	25 20	35 . 35 . 45	55 . 60	65	75 80 85	

11800 11800 11800	100000000000000000000000000000000000000	7 7 8 9 9 9 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2460 2580 2580 2580	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		9 2 2 9	360		120	* * * * * *	12881	906 1020 1080 1080	10000	100000	1920	2226 2226 2326 2326
ATTATECATO GRACIOTES ANACEDES CEATOGES ATGACETES ATGACETES ATGACTETES ATGACT	AGTOTTANAC TOCTTCTCCT TACTTCTCCT AATGACTTTG	TAMATACTOC GGAGAAAAGC GAATTCAAAC CSCCCCAAGA	OTCCTTTTO TITCTTTTC CATCAGTAT GCATCTTAC	CCCTTCCATT AGGATTTCTT ACTCCATTAT CCAATATAT TTTTAAATAA		51   KIMODPIQOA WPRHPASNRT CORITLHENL	LCEGIYLHTL LYIIHQPICA LIPWRPEGKI ENSKALRSAS		s1  -  -  - 	CAAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG	AGTCATCTCT CATGTACCAA CACAATAACG GCGAGATGCC AGACATCAAT	AGACCCOT GAACCCOATG GACAAACCC CATCCAGCAA GAGCCTCCC		ACGANACTO TCACGATAAC GGTCCACTTC	TATGACCAC CACCATCACA CACCATCACA CACCACCACACA CACCACCACACA	COGGGCCANG CANGCCACC CANCTRACAG CANCTRACAGC CHCCATCCAGC
TCTCCTCTAC OTTANTATT TCTGTACATG TGTGCTGATT GCACATCCTT	TCAGGTTAT TGAMATGTT CACTGTTTGG TTCAGTTTATTA	OTOTOGRATI CACCATTCAT TACCCTTATT	GAGTGCGTA CCCTGCTGGC TTTGCTGACA TGTATAATAT ACACCTTGTC	ATAMATTTO AMATCAATOA OCTTOTAMAT AMTTTTAMA TOOGCTGATT		41   IMTAQYECYQ VTKICDQDGN GIFFYFKELS	YLMCCYYPM NCW168DTHL LVPLL018PV QYK1QPGN8P N		41   TOCTCCTCGC CAGGTGCTAA AGAGAGATTG	ATCATGTAGG GAGAATATGT AGAGGCTGGA ACACTGGTGA ACACTGGTGA	TOGGACCTC ACCCTCTOT ACCCTCTOT ACCCTCTOT TOGTGAAGC TCACTCTOCA	TCACCATTCA ATARGCCCA TCACCATTCA ATTATCAATA TCCCATACAT	AGAAGCETET GATACECCAT ACATTTACAA AGGCCAAAGA	AAGTGTGTGA ACATAACACC TCACGAATAA AGCATACCAA		TOCKOTOO COCKOTOCK CACCCATOK ACACCCTOCK TOCCCCOA
CTGATACCCA TITITITICIT COMMITCOM CONTIGANT ACTACATCAT	TCATGATOS TCCATGATAT ATGGTTGTCT GCCAGAGGC AAATTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG	TOOTTOTAL ACATCACCA AOTTCCACCA OGCATUATTC	ACTORATTAT GATCTACTCA ATGINGNGA ATGINGAAA	AGCTGTAAT TATATAAGA TGAAAATGA CAACCTATGT ATACTGTATC	786.1	31 	SCKVSQPIHL AIARSLYYND YMKAVRATLI VQAILRREWN RVLLKPESTLY	798	31 	TCACTTCCCC CTGCTCAAAG TTCGCCATTG GTGCACAAGG GACGTGAACG	TCGTCGGCTG GTGGGAGCC GATAATTCTG TATGAGATCG ACCGTGCTGG	TACACATTTG  AAGCCTCTGG  AAGCCTCTGG  ACCATCGACC	GAMACCAA CATAGCATTO AMAMAGGGG CTGACTGTGG	TACCAGCCCA ATAGACAAGG AACTTTACCC	CCANGEGGA GAGTTCACCT GCCATCTTAC CCGCTCCGGA GTCACCTACG	CTCAACTOOG TCCCTCTATO OGGGAAAATOO CCCCCCTACO CTCAGCTCCC
TOOMTOWIT CTOMONICANIC ACACCOMO CCATTOCTIC ACACTICATICATICATICATICATICATICATICATICA	OCTECACIA OCAMANGEA AMTAGNAG FOACTETOTA CCTTEACATG	AAAGAAATCC TACTAACCTG GGTGTAAGCC ATACATGTTG	CATACCAAA CAATACTAAT TOGAAACTOG ATCTTAGTTO	GGGAATTCCT GCAATCATTT AAAGAAATTG CAAATACATA TTAATATCTG	Poquence NP_003	21   TAKLEES PED GTESWQLCPD LPYLTIGHG	NOALVATNPV GPPLIPACIH KVTHQAESNL RTIPCFNGB LNGKSIHDIE	-	21  -  - 	GAMMACACC TOCCMOTAC AGGACACTO TGCTOTCATT CAMATTCAT	COTOCCTOAD COACCCACT TTTTCCCACT GCAGGCCAGG GCAGGCCAGG	CCAGACCAAG TCTGTTTGTT GGGGGACTAC CAAGCCCATG CACAGACCCC	CCAGCTGAAG TGCGGCTAGG CCGAGTCACA CTGGTATAAC	MAATICATT TOCCAGOCC GATCTOGGA TACTGAGAAC GTATGGGCAG		TOTOTCGATG COCCCGCCT COGCGACGCC COGCGACGGC AGCCGACTCC
086443 raccarttac racracrtta orthanagrt ratcrtoore aarracaaa	DATICATION  OTCTTACACA ACACTTAAAT ATATAATTCA CTTGGACCCA TAAAGAAGAG	ATOTOGOAAA GATGTGACGC TTTCTGAGCT AAAACTAAAC	ATTGGGGCAG CTCAAATGGA CAACTGAGTA ATATCCATTG TTAGGAAAAC	AACAGTGGGA AAACAAATTA AATTTTGTAA AGTCTCAAAT TGTGTGTATG	337 protein (	11 VLLPPPHILV OMLCHNDVA THEKVKTALN	TITLTAVAN HLMWYYPLGM NIVRVLITKL ILMHFQGLLV GYGHDCPBEH	118 DNA sequence id Accession #: NM_00 ience: 25-2379	11     TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT	TTGATGAAGA OTCGCAAGAA ATGCAGAGAC ACCACCTCAC GCTTCACCAT	TCAATGCGTC TOGAAGGGTA GGAAGGATA ACCGAGAGAA GGGGGGACTC	CTGTGGGCTC GCATCTTGGG AGGGCATCAT TCGTCGAGGC	TCTACCACTT TOGACCCTGA GCCAGTTCTT	CCCCGGAGTT TGGTCCTGGA TCACCTTGAA TCACCTTGAA	TCATCTCAGA GCAAGTGCAA TGAGCATCCA TGCTCATCTT CGGAGATCCA	CCAGCTACAA CCGCGCTGAA CTGCGGCACA CGGAGCCACAA CCGAGTCCAT
WO 02/N	TTCOTAGES  OTCCTAGES  CAGAMATTT  ACTCAAGGA  OGGAATGTCA	ACCTACCT CACTATGCT ACATCAACT AAATGGCTGT AAATGGCTGT	TCCCATCTTG TAACTACCCT CTATGAAAAG ATCTTGTGGC TTCTATATCA	TOTCTTACCA TCTACTUTAT ATTTTCTTOS TTTATTTTAT AATGCACA	Seq ID NO: Protein Acc	HERKCTLYFL BGVYCHRTWD WTNYTOGAVA	PPSFVCNSVV IVVAVPASKQ ALLVNLFFLL AEEVYDYING YTVSTISDQP	Seq ID MO: Nucleic Act Coding sequ	1   	CAGATGCACA TCAGCCTCA TTCCGGGTCG ATCTCAGAGT	CATCGGTTGT GTGACAGCAG ATCCTGAAGG AAAAGCTTGG CAGGGCCTCC	OACAACTTCC OTOOGCACCT ACCAAOTACA GCCCACAACG TACAGCTTCA	CAGCAGCCTT GTGCTGGCCA AGTGACAGG CTGGACAGAG	ATTGGGATG ATTGGCATG CATGGCCAGC AGTTCAAAT ACGGCCAGA	CTACCCOTOS OTOSCCOTOF CAGOTOCCO OTOATCACCC	ATGACACCA CCCCCGCGGC AGGACGCGC AAGGACGAGG TACGAGGGCT
s,	10	15	70	. 25	30	35	40	45	20	55	09	65	20	75	08	82

	42448444			
WO 02/086413  TOJGOGGIA TOGGIAGOT COGRADOJA ITTOJANOC CCTUGCTT TIGTITUCA GOOGGIAGOT COGGIAGOT CO	Seq 1D NO. 314 Protein sequence Protein Accession 8: NP_003079  11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 DMA sequence In casesian in TRINESH predicted In casesian in TRINESH predicted In carrictor Tricococcta Accountation In carrictor Tricococcta Accountation In carrictor Tricococcta Accountation In carrictor Tricococcta Contractor In carrictor Tricococcta Accountation In carrictor In carrictor Tricococca In carrictor In carrict	OCCORROMO OF CENTRAL ACCOUNTY TOTALIZACIA TRANSCAR GOLOGOROM OF CONTROLLAR ANAMONIA CENTRAL TRANSCARO TRAN	TECHATION CONTROL AND ADMINISTRATION OF A CONTROL OF A CO
5 10 15	20 25 30	35 40 45	55 55 60 60 65	75 75 80 85
PCT/US02/12476				
2400 2400 2400 2500 2500 2500 2700 2000 2000 3120 3120 3120		120 120 120 120 120 120 120 120 120 120		720 960 960 960 1020 1120 1120 1130 1130 1140 1140 1140 1140 1140 114
WO 02/086443  TETALAGNET COTALAGNE TOGGREGER GETTHABLY CONGECTUAL TETTHAGNET CONGECCES GALCHAGNET CITTHAGNE CONGECUAR CANCERCES TOTALAGNET CONGECCES GALCHAGNET CITTHAGNET CONGECUAR ANTICOLIA CANCECCES GALCHAGNET CITTHAGNET CONGECCES GALCHAGNET TETTHAGNET CONGECCES CONGECCES GALCHAGNET CANCERT GALCHAGNET TETTHAGNET CONGECCES TOTALAGNET GALCHAGNET CANCERT GALCHAGNET THAGACHAR GALCHAGNET CONGECCES GALCHAGNET THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR GALCHAGNET CONGECCES AGACTUAR THAGACHAR ANTICTIATA MACTICAN CONGECCES AGACTUAR THAGAGNA ANTICTIATA MACTICANA TECHNICAL ANTICTIATA GALCHAGNA ANTICTIATA MACTICANA CONCENTION TECHNICATOR GALCHAGNA ANTICTIATA MACTICANA CONCENTION TECHNICATOR GALCHAGNA ANTICTIATA MACTICANA CONCENTION TECHNICATOR GALCHAGNA ANTICTIATA AGACTUARA CONCENTION AGACTUARA ANTICAGGNA ANTICTIATA MACTICANA CONCENTION TECHNICATOR GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA GACCHAGNA GACCHAGNA GACCHAGNA ANTICTIATA ANTICTIATA AGACTUARA GACCHAGNA ANTICTIATA AGACTUARA ANTICTIAT	STATISCA, MATCHANG TOCAUGUS ACTURAGA STATISCA, CTICOCTUS CHACATOR GORDANITOR TOCAUGUS COCCUTOS CHACATOR STATISCA TOCAUGUS COCCUTOS CHACATOR STATISCA TOCAUGUS COCCUTOS CHACATOR STATISCA TOCAUGUS COCCUTOS CHACATOR STATISCA THOUGHAS TAGGOOST CHACATOR CHACATOR THOUGHAS TOCAUGUS CHOCATOR THANASAN TOCAUGUS	11 11 21 21 21 21 21 21 21 21 21 21 21 2	1   1   1   1   1   1   1   1   1   1	GOGGOCCO, GOTGOGACA COCACACA COCTUTATO GOGGOAGO GOGGOTOTO COCCONCTO ACCORDAN COCACACA COCACACA COCCONCTO ACCORDAN COCACACA MARCHEGO AGROCCOTA COCACACA MARCHEGO AGROCCOTA COCACACA MARCHEGO AGROCCOTA COCACACA MARCHEGO AGROCCOTA COCACACA MARCHEGO AGROCCOTA COCACACA MARCHEGO COCCACACA MARCHEGO COCACACACA MARCHEGO COCACACACA MARCHEGO COCACACACA MARCHEGO COCACACA MARCHEGO MAR

<del>\$</del>

Ś

Seq ID NO: 344 DMA sequence published Acid Accession F: NM\_012072 Coding sequence: 149-2107

WO 02/086443

TUTOCCIDA CICUTATIT COCCUON DACENTRY ADDARMA MACCINETO 4331
CUNTRICA COCUNTATIT COCCUON PROJECTA ADDARMA MACCINETO 4331
CUNTRICANA COCUNTATIT CONTRICA ADDARMA MACCINETO 4331
CUNTRICA COCCUON CALCITOLIA ANTICOLO TAMBORIA ADDARMA ADDARMA ADDARMA CONTRICA 4331
CUNTRICA COCCUON CALCITOLIA MATURADO COCACACO COCUNTRIA ADDARMA CALCITOLIA MATURADO COCACACO COCUNTRIA ADDARMA CALCITOLIA MATURADO COCACACO COCUNTRIA ADDARMA CALCITOLIA MATURADO COCACACO COCUNTRIA MACCINA COCUNTRIA ADDARMA CALCITOLIA MACCINA COCUNTRIA ADDARMA CALCITOLIA MACCINA COCUNTRIA ADDARMA CALCITOLIA MACCINA COCUNTRIA CALCITOLIA MACCINA COCUNTRIA ADDARMA CALCITOLIA MACCINA COCUNTRIA ADDARMA CALCITOLIA MACCINA COCUNTRIA CALCITOLIA MACCINA CALCITOLIA MATURA MATURA CALCITOLIA MATURA MATURA MATURA CALCITOLIA MATURA MATU COLORGICO GUATATOLA CITANTICA ACAGAGATA ACCOCCOGO COCCOGO A ACCOCCOGO A ACCOCCOCO A ACCOCCOGO A ACCOCCOCO A ACCOCCOGO A ACCOCCOCO A ACCOCCOGO A ACCOCCOGO A ACCOCCOCO A ACCOCO ATVESTEALS ALALATOREA GTOADTEAN CYTACTINE STRUBANEO, BRICHOROGER.
ATVESTEALS BROWGELER BRALATOREA BRYGHOLDER BRICHOREA BRICHOR HEALMYNDRIC TELEVODOO TEGGGGGGG AAAAGGGGGG SPORVARNIG AFWNSGGGG MACAGERRA HERSENGAL AFALLGETE KOPELIDEAK LALLANGERS DYKTRERAT KTLAKENKY LEGGLAPOO NEWASTOVO AGLALONOR ROSTARNOGH SUGUSTEWOO QLOTPONEGI NAGLAAQOO HERASTOVO ATENTESOT WASSTYGGG TEGGGTFGOA GLAGGOVUG TANGLAAQOO HERSENADA CAGLADMISM YLFGAEVPER AFBSCHINGG STOGGOVOOT ALNGLAGAS Seq ID NO: 345 Protein sequence Protein Accession 8: NP 036204 3eq ID No: 347 Protein sequence Protein Accession B: CAA83435 Sed ID NO: 146 DNA sequence Nucleic Acid Accession #: 211560 Coding sequence: <1-966 8 2 8 35 <del>수</del> 45 S 55 .00 65 2 75 8 12 ន 22

MAGNETICA CELEBRATION CHITCHEN CONSTRUCTOR CONTINUES CON

20

55

33

2

2

8

**令** 

45

S

65

8

75

2

CT/US02/12476	
2	

	WO 02/086443
	Beg ID NO: 148 DRA sequence Muclectide Accession f: No 00658
2	Contrag sequence 250.000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
,	сылымает мамыты есстотым тассылым е сесетом 60 остовыеся таманты отытаестт детстуме сыменет естаниеся 120
0	TANGGECKA CAGCTICTIC ATCODATOS TOTICCICAT OSCIOSOACO CICOTICTIA 180 AGOCACTOT CAGGGAGTT CCTOTIANAS GICHAGACAC TOTCANASGE CATÓTICCAT 240
	AGTCAAAGGT
S	TCCGTOGGC CATGITGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420 TCAAGAAGTG CYGTGAAGGC TCTTGCGGGA TGGCCTGTTT COTTCCCCAG TGAAGGGAGC 480
	CONTICTION TOLICATORS CONTICIONA MATARAMSE CONTICTION CATAMATICO: 540 TREGNOCATE CONTICIONA LIGARICAN TESTICATICO ATTUAMATIC CONOMICTIO 600 MAGINICATE TENENTICAN TESTICANIA A

Seq ID NO: 349 Protein sequence: Protein Accession #: NP\_002629 

HAASSPLIVY VPLIAGTLVL I AQEPVKGPVS TKPGSCPIIL 

Seq ID NO: 350 DNA sequence Nucleic Acid Accession #: NM\_007183 Coding sequence: 75-2468 

<del>수</del> 

ଓ

Seg ID NO: 351 Protei Protein Accession #1

Seq ID No: 353 Protein sequence Protein Accession #: AAA36546 

Seq ID NO: 154 DNA sequence Nucleic Acid Accession #: XM\_002820 Coding sequence: 304-811 8.

COGNITIONAL MANAGERA CITCAGAGO GAMATTIC TICTITIAND ADDODRING 6
CCCOTTOMAC CHARCAGO GAMATTIC CITCITIAND ADDODRING 1
TICAGAGOM COCCUTOM TATATAMAC CATTATATA TOCKNOTATY TOCKNOTATY
TICAGAGOM COCCUTOM THATITICAL TITLOCCTATY TOCKNOTATY TOCKNOTATY
TICAGAGOM COCCUTOM THATITICAL TITLOCCTATY TOCKNOTATY TOCKNOTATY
TICAGAGOM COCCUTOM THATITICAL TITLOCCTATY TOCKNOTATY TOCKNOTATY
TICAGACOM COCCUTOM TOWN TOWN TOCKNOTATY TOCKNOTATY TOCKNOTATY
TICAGACOM COCCUTOM TOWN TOWN TOCKNOTATY TOCKNOTATY TOCKNOTATY
TICAGACOM COCCUTOM TOWN TOCKNOTATY TOCKNOTATY TOCKNOTATY
TICAGACOM COCCUTOM TOWN TOCKNOTATY TOCKNOTATY TOCKNOTATY
TICAGACOM TOCKNOTATY TOWN TOWN TOCKNOTATY TOCKNOTATY TOCKNOTATY
TOCKNOTATY TOKNOCATY CONDUCTOM TOWN TOCKNOTATY TO TOCKNOTATY TO TOCKNOTATY TO TOCKNOTATY TO TOCKNOTATY TO TOCKNOTATY TOCKNOTATY TOTACATY TO TOCKNOTATY TOTACATY TO TOCKNOTATY TOTACATY TO TOTACATY TO TOTACATY TO TOTACATY TO TOCKNOTATY TOTACATY TO TOT 

S

PCT/US02/12476

		9 5	3000	2 2 2 2	25.5	1020	1360	1440 1500 1560 1620	1740 1800 1860 1920	200 2160 2220 2280	2140 2460 2520			2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		9	120 240 300	22222
RLDSR		S1   	OCCUTOCATO CCAGGACCAC CTGCATCCAC GTCCCAAGGCC	CAGCCACAAG AGCGGATGAG TGGGGATGGG	CCAOCTCCTO CCAOCTCCTO		CCACAAGCAC TOGTOGCCGCT TGACCCCCTG ATCTGGGCTC CGGAATCACC	ACTGTCCAGC CCTGAGCCAC GAACGAGGCC GAACGTCAAC		ACTACCCTOA ACTACCCTOA ACTCCGGATO OTGTOTOTOT TOAACTOCAA	TTAACTGGTT CACATAACCA ACAGAAGATG TAAGATGATT		51   OPOCRNERCI CPDGSDESEA RCDEFOCCEG CTCPAGFOLL ESPRIJETAR	KASDPKEREV EPRAJAVDPLO VDSKLHQLES EISILABNIN	tksherpdnpu	51   ACTGAAGATT	ACCCACTCA ACCCACTCA OOTATTGACG CAACACTCTT	ATTOCHOCCE COCCTAATCC CCCCAAAATT ATCAGAAGCC
OVTOSGLEOD HLEDTETTEL		41 	GCCGGAACGA ACCACAGGGA ACAACGGCCA ACAACGGCCA	OTOGACCCAC OCCAGOOTOO ACTTCCAGTO	ACMATGGGG CAGCAGGCTT CAGATGCCTG	CCCTAATCTT GCCTCATCCC TCTACTGGTG ACCCGAAAGA	TOGACTGGOT CCACAGTTGA CCATCGCTGT AGATTGAGAA AATGGCCCAA	AGCTACACA CCACTGACTT CAGACCTGGA TCCTGGCTGA CAAGAGCTCC	OCCTTCCTGC CAATOTGGCT TGGGCTCAAC TCCTGTGCAT TGAATTTTGA	ATATAGGGAG AACATGATGG CATGCACTAC GTGAGTGTAT	TATACACTT TAACATGATG AACTATATTT TTTTTGTAAA		11 APAKECEKD BRIKCOGES MCATELGTC CTOLKIGPS	RKITSAYND RTLFERNLS JOLEGORLYN PSANRLNGL	, i nrum krku	41    -  -	AGAAGCCGAG TACGGGGGCT AACTGTTGTG CCAACTTGGA	GCTACATCE GCCACAATAT TCCCACGCC CATACCACC TCTTATTAT
OVTOSGLEGD	22	)   crrcraccac	CAATTCCAOT GACTOCTTAO TTCACCTOTO TOTCCTOATO	AAGCTGAGCT GAGAAGGACT CGTGGGGACG	TOCACOTOCC TOCACOTOCC	AAGTATTCAC ACCATCAC ACCATCAC AAGGCCAGTG	OGCCTGGCAG ATCTCAGTGG GAACCCCGGG GAACCCCGGG GACCAGGCCA	OTAGACTICA CTGATCTCCT OTOTTCTCGA GAATCTCCA CTGAAGCAGC	GAATACCTGT TGTCCTGACA GACAGTAAGA GTGATAGCCC ACCAAAAGCA	DATEMBETCE TTAAGCCTTO AATTCAGTCC AGGGTCTGT	TATMIGITI TACTGCTGAC ATCATTIGI	. 26	31 AAAADPLLGG PTCDNGHCIH BTCDNGHCIH GLHNNGGCSHIL	TIMPOGRATI SUATURCOLS  TIMPOGRATI SUATURCOLS  NOUDROTIUS DAISMENDIT I  PPOLAVFEDK VPMTDLENEA  ELEVORNOCI STLCLPAPOL	VIALCHSOY	11   CTGATCTATT	SCACCATCAC STTTAATCGA STGCCCCCAT CACTCTGGTG	CTCGAGTACA CTCTAAGAT CACTCTAGGT ATTCTCTCTC
RRTREAMLDS	. sequence saion #: NM 017522 1-2100	21    - 	CGAAAGGAC CGAGGACGAT NGACAGTGAC CGAGGAGGAG	TCCTGCAGAG CTGCCACCGGG GGGCACCTGC	ACTUACONO TOCCTTTONA CATTOATON	TGCTGCTGGC TGTGAAGCG GGAAGTTGCC CTACATGGAC	CTCTCCAGAG CAATAAGACC TAACCTCAGT TGACTGGGGG	CTTGTACTOG CACAAAGACG TGAGGACAAG CAATGGCCTG CATCCATGAG	TOGAGGCTOT CACATOTOCC TOCAAATOAA GCCCATAOTO	ACCACATORA ACCACATOCA TGCCTCATGO GTTTCTATAT	TITTICIATO GTOGAATOCC TACCTTACTC TITAGGTTTT AACATAAGT	N sequence NP_059992	21 	NVVALDVEVA I YWTDEGNKT NGVDRQTLVB PFGIAVFEDK ELEVQPNGGC	AVIGITAPIA. IGHVYPARVA [uence 1 8. M27826	21    ATTTCAAT	TCCATCCCT TCCATCCCCT CCTGTTTCCC AAAACTCCCC	CCTTACTOTO CCTTTAGTOTO TAATCTCTCC AACATCTCCCC
WO 02/086443 жикокр оквивовник	NO: 156 DITA ser o Acid Accession sequence:	11 	CCAAGGAGTG GGAGATGCGA AGACCTGTGC AGTGTGAACGG	CCTCOTOGCO CTACCTCACT	OCCTACAGGG ACCTCAAGAT CTTGTGGCGA	ACTGCAAGGC AGGATCGACC CACTAGATGT TCTATAGCGC	CTCACTCGCG CTCACTCGCCG TCTTCAGCCG TCTATTGGTC	TOAGCCAGGG GTGGAGGCAA TAGCTGTGTT CAAATCGGCT ACATTGTCAT	TCCAGCTAA CTCCCAAGTA GCTACCGAGA GGATCATCGT GAAACTGGAA	CAACAGAAGA TCTATCCTGC ACCCCTTCG GGATGAATGG	GATOTGAGA TGAGGAATTC AATGGCACAG GOOGGGCTTT GCTATCCATC	8eq ID NO: 357 Protein Protein Accession #:	11 	NYSRLIPHLI GLAVDWYHO DQAKIEKSGI LISSTDPLSI LKQPRAPDA	DELHIGRTATI DELHIGRTAC 158 DNA ed d Accessic	11   ACATCTCACC	GATCGCCTCG GGAGGGTAAG TTTTCAAGGG	ATCTGCTTCC TCCAAGCCT CCCTTCAGCT AGCCCTGAGA
WO 02 троккистр	Seq ID NO: Nucleic Aci Coding sequ	1   ATGGGCCTCC	CAAGOGCCGG CCCTCTGTGT TGCCCCAAGA	ACTTGCACCA TOTOTACCTG GCCGCCTGTG	ATCTGCACTO GACCAGAGA TOTTGCACTO		ATCTACTODA OGACGCACTC COACGCACTC ACCOTTCA	ATTGACTTCA CCTTTTBGGA ATTTTCAGTO	GAGCTGAGTG TCCAGCCACT ATGAAGAGGT GCTGTTATCG CTGATCTGGA	ATTGGCCATG GGATGGGATC GTGTATGACT		Seq ID NO. Protein Acc	1     MGLPEPGPLR   PSVMRCDEDD   TCTKQVCPAB   TCVLAIXHCN   DOKTCGDIDS	TEARDR PVKR TIDEQUASPE RGPHYMSDMD IDPSOGNRKT NPHDIVIPHE	MKKCYRDANB YRKTTSEEDB Seq ID NO: Nucleic Aci Coding sequ	1   AGCCCAAGAA	CTCTCACAGT CATTCACAGT CATTGCCTTC CCCAAGCTTC	TAACCAATT TICTICCAA CACAAGACCT CACTTGAAGC TICGCCGCTC
	S	2		2	70	25	30	35	40	45	20	Ş		9	20	75	. 08	82

8844488	WO 02 AGGATTECA ACTECCOAT ATGACATTEC ATCTCCCCA TGAGATCCC TGAGATCCCA TGAGATCCCA ACCCCAATCCT AGCCACCGCCA AGCCACCGCCA	086443 agectrana agectranan accutanan certanan certaecea atmacage	CCCAGGCCAG AACTGAAGAT TTTGTTCCTG GGTTCTTTGT CCAGGGCCAA CCCACCCCAA	ACCATORICAT CCACAAAAA CCCCACCCTA AATICTCCCC CCCCCTTTAA	CCCCTUTAACA ACTGATCAAT ACCCTTGAGA TTOTAATTTT CTGACTCTCT	TTGCACGTAT GCCTTAACTG GTACTTTGTA ATGTACTTTG TTATTACCTT TTTCGGACTC	720 720 900 1020
Seq ID NO.	- 0	359 Procein cession #:	1 sequence AAA65999	•			
1     PKKHLTMPKS   LPSPQGPVSL   TKLSASLTIP	Ø J A	11   	21 RCPIASEVPW QABKPLKTPP LDNDKPPLCP	31   TITEAELRYT LMCQLGGHBF LTSPQYQFLP	41  - LIVEGKBIPC MMBPLVIPTC QDLPBA	S1   LIDTGATHST PLPLLGRAIL	120
Seq ID NO: Nucleic Ac: Coding seq	- ü 6+	NO: 360 DNA sequence : Acid Accession #: NN sequence: 16	Tuence 1 #: KM_0018: 162-558;	ž ~			
٦		<b>=</b> _	<b>::</b> _	<b>=</b> _		<b>15</b> _	
AACCATCAA TOTOTAGCAA TTCOTOGOTT GOTGGAAAAC	4 4 H U	TTAGAAGAA ACATCCCTGG GAGTTCACAG GAAACGGTGG	AAAGCCCTTT COATACCTTG TTGTGAGTGC CTCTGGGATT	GACTTTTTCC GAMAGGACGA GGGGCTCGGA TCACCOTAAC	CCCTCTCCT AGTTGGTCTG GATGGAGCG AACCTCGCA	CCCCATOOC CAGTCOCALT TOGTCCTCTA TTGACCTTCC	2 2 2 2 2
TTCACAATIC	) U U E	TCCAGAGGGA	ATATCAAAA	CAACGGGATT	TTGCACAAC	ACCCCAACA	22
CAAAAAAGG	- 17 -	AATTCAGTCT OOTTCGGAGA		CTATATATAA		ACAGTAAAAC ATTCAGCAAA OGAAAACCTG	
TAGGAATGAG CGAAACCACT	< D H I	CTATCCCTC CGTGGAGAAG TGATAGAAGT	AVAACTOTOA		TGACOGGAG TGATTGTAAG CAATGGAATC		25 C C C C C C C C C C C C C C C C C C C
OTGATCCCAA CACCCAAGGC	- KU	GGCAGCATAT TGCTCAAGCT	GACTACTOTO	AGCATTATAG AGCATTATAG AGATAGATGA			200
TCGAATATCA	4 H	CTATGAGTAT	GGGGLAGCAG	AGACGGAGGC			1080
MAGNATACAA GGACAAATGA ATTATGATTC	< < U	CTATGGAACA GCCAAATCCA CCAGAGGAAA	ATGGAMGTT GTTGAAGAAA AATTCTGAGG		AGCTCCTAGG AGAATATCTA TGAAAACAAA	ACCCCACACC	1200
<b>GCAGGGATTC</b> <b>AAGAATATGA</b>	905	TGATCTTCTG		ATTTAGGCGA			223
AGAAACTGA AGAAAGGAGA CAGGACCTGC	5 5 U	TATTACAGAA ACCAGCAGTG AGGTATTATG	ACAAGCATAA GTTGAGCCTG GGTCCTCCAG	ATOCCATOR GTATOCTTOT GTCTACAAGG	TOCATATOCA COAAOGACCA CCCCACTOGA	GROMANGONC CCAGGACCAG CCCCCTGGTG	1200
ACCCTGGCGA GTCCTCCTGG CAACCATCTC	<00	TAGGGGCCCC TACTATGTTG TGCTCAGGGAA	ATOTTACCOT	TCCOTTATOO TCCOTTATOO	TOOTGATGOT	TCCANGOAC	1620
TGAGAGGCCC GTTCATCTGG AGGGTCCCCC		ACCTGGCCCA GGCCAAAGGT TGGTCCAACG		CTGGAAGACC ATCCAGGTCC GAAAAAGGGG	AGDICCTOTO TCAGGGCCT TCGTCCAGGT	OGGGGGGCTG CGAGGCGTCC OCAGATGGAG	
GRAGAGGAAT OTCTGCCAGO CTGGTGATGA		GCCAGGAGAA TGACAAAGGT TGGAATGAGG		AGGGAGATCS AACGAGGTCC GAGAAATTGG	AGGGTTTGAT TCAAGGTCCT ACCAAGAGGT	CCAGOTCCTC CCAGOTCCTC CTTCCAGOTG	1960 2040 2100
AAGCTGGCCC GTATGGCAGG CTGGGCCTCC	UBU	ACGAGGITTG TOTAGATGC AGOTCAACAA	CTGGGTCCAA CCCCCAGGAC GGGAATCCAG	GGGGAACTCC CAAAAGGGAA GACCTCAGGG	AGGAGCTCCA CATGGGTCCC TCTTCCTGGT	GOGCAGCCTG CAAGGGGAGC CCACAAGGTC	225 225 230 230 230 230 230 230 230 230 230 230
CAATTGGTCC GTGCTGATGG TGGGTCCCCC	8888	TCCTGGTGAA GCCTCCTGGT TGGTCCACAA	AAAGGACCAC CATCCTGGGA GGTCCTATTG		AGGACTTGCT OTCTGGAGAA CCCCCCGGGGA	AAGGGGGCTC OTAAAGGGAG	200
GATTCAAAGG GAGGGNAAGA GTTCAGGTCA	H D 4 4	TORCATOOT TOCCCTOAA	ANGGOATCTA CTAAAAGGTG GGACCCAAAG		AGTTGGTCAA CCCAACTGGA	ATTGOCCOA OACCCAGGTC	12.00
AAGGTGCACG		TCCAAAGGT			TCAGCOTGC		2320
OTGCCGATGG TTGGATTCCC	900	CCCTCCTGGC		AAAGAGGTCC	TCAAGGACCT		9 6 6
ACCETGGGCA	« D L	ACCACAGOGAO ACCACAGOGA TORCACAGOGA	CCAACCOOTT		AATAGOGGAA	COTOGOTATC	3120
CAAAGGGTGA		TCCAGGTCCT	CAAGOTATCT	CAGGGAAGA	TCCACCACCA	GGATTACOTO	125
AAGGTGCCCA	4 U	AATTGGTTTA	GOTCCAGTTO		AGAACGTCCO		320
DADADAAAGO AAGGTCCTGT	O 6	TGCTCCTGGA			TECHOOONOA		349
ACAAGOGTGA GCCCTCCCGG	< 0 0	TCCCCCAOOT	CTTCMOOAC	CAGTTGGTGCAA	CCCTGGAATT	OCTOGNACTO	960
ссавлявает отоллалав		CCCTGGACCT	CCTGGTCGA			GACCCACCTO	3780

'n.
•
-3
~
_
_
~
0
Ō
<b>5</b>
_
=
_
C)
~

WO 02 avaccerea cantragraga	WO 02/086443 cccess, agreccour gascendare accessage accessage retertages 1800 access agreccour agrectative accessage accessage seguines accesses 1800 access agrecours retained analogous gascenses accesses 4200 access agrectatives analogous gascenses accesses 4200
CEGARGEAGE CTGGAGCTGC ACCCGGGTCC GTCAAGATGG CTGGCCCATC	TOTACTICES GENERALDO MANAGAMA INAUGAMAN GETENCAL TOTACTICES GENERALDO GENERALDO INTERNAÇÃO ENTRA TOT TOTACTICES GENERALDO GENERALDO ENTRA GENERALDO GENERALDO TOTACTICO GENERALDO ENTRA TOTACTICA CAROLICAS TOTACTICAS GENERALDO ENTRA TOTACTICA COMOTICATO TOTACTICA GENERALDO ENTRA TOTACTICA COMOTICATO TOTACTICA GENERALDO ENTRA TOTACTICA CONCENTRA ENTRA TOTACTICADA
CTOCKOOTOC OTOCTCCTOO AAGOTCTTCO AAGATGGACC OCTCCAAGGG	E KANDENAKA KANDETAKA MADUTETAN GERAKANESA ENCHANAS 1120 BANANGCOS COURTOOTS CIPUDDOAC TICOMONAN CONDITIONA 1120 BANANGCOS COURTOOTS CIPUDDOAC TICOMONAN CONDITIONA 1120 BANANGCOS CANTECTORIT DAAACAANOO TICOTTOONA GOTOACAACA ROO EN TRANANGCOS CANTECTORIT TICOTTOOL TOOTTOONA GOTOACACAC
ATGGGGGAT GTCCTCAGG GTGGTCTCC CATCTTGTC	TECTIONTICS GENERACES MODIFICACE TRATECTICA GENTRACIA COLAMBAR MAJAMAGET ENTERIORE CENTROCAS MAGRITURA MODIFICE GENERACE TRATEGRA CENTROCAS MAGRITURA CHICANAMA, AGRANAMA ENTERIORE ATRACETA TRATEGRA GENERAL SERVICA CONTRACTOR TRATEGRA TRATEGRA TRATEGRA TRATEGRA ATRACETA TRATEGRA GENERAL SERVICA MAJAMART TRATEGRA MAGRITURA TRATEGRA TRAT
AACAAGACT OTAAAGACCT ACCAAGOTTG CTTGCATTA AACCAGGAAG	THE GARGARIAN CANTIFICAN MEGATICAN GACANICAN GEGESALETT 1980 THE GACANICAN FORCES THE GACANICAN STATEMENT OF CHOLOGRAM ATTENDATE THE CONTRACTOR THE CONTRACTOR THE CONTRACTOR THE CONTRACTOR STATEMENT STATEMENT STATEMENT THE THE CONTRACTOR STATEMENT THE CONTRACTOR STATEMENT THE CONTRACTOR STATEMENT THE STATEMEN
GCCAAAATT OTTATACAA ACCTTTAT TCATTGAAAT ACTTTGOTGA	CACTACCAC TOTACTCAGT CACCAGCTO GTATAATOTO TCATCAGGAA AGACTICCE TOTACTGAST CAMACHATA GAAAATOTOC TATAACATA CAMACATCA ANTATAGTI GTACTTCAG AAAAGCTAT GAAAAAATT CAATACACCA AAATTGATC AAGTACCTAT TOTTGATOTOC ATGATCAGTO TCAAAAATACAA AAATTGATCAGA TCAATTGATOTOC CACCAACCAC CAAAAAATTGAATCAA CAAAAAATTG ACCATTGATC
TITTOTOCCA TACCATTAGA ATCATAAGA TICTCAACTC AATATATAT TOTOTITAAT CCAAACTTO	SEC CATOLOGYT TEALSLAGE TRYTAGEA MACHICAGO STRAINCAGO STOO THE GENTROCK TECETITOTO CORRECAMY CACORCAN MACHITAGAN STOO THE TECHTICAT ATTRIANTY TETTOTOTOT CHARANCE MACHITAGE TRAITCCTAN STOO THE CHITTICAT ATTRIANTY TETTOTOTOT CHARANCE MACHINAGEN STOO THE CANADIAN TRATITATION CACACITAN TEATOTATICAT CHARANCE STOO THE ANTIONAL TRATITATION CACACITAN TEATOTATICAT CHARACCETT 600 TO CACACITACC THATTATICAT CHACTAN TRATICACH COCAMITICS 1600 TO CACACITAC THATTATICAT CHACTAN TRATICACH COCAMITICS 1600
20 CT CT CT CT CT CT CT CT CT CT CT CT CT	and the management

TITCTITGOT TANGGATGAA AITCCTITGT ONG
8eg ID NO: 361 Protein sequence
Protein Accession 8: NP\_001845

45		<b>-</b>	<b>17</b> –		₹-		
<u>.</u>	KEPWSBRWKI	KRWLWDFTVT	TLALIFLPOA	REVRGAAPVD	VLKALDPHNB	PEGISKTTGP	9
	CTNRKNBKGS	DTAYRYBKOA	<b>QLSAPTKQLP</b>	PCCTPPEDP8	ILPTVKPKKG	<b>IQSPLLSIYN</b>	120
	EHGIOOIOVE	VORSPVPLPE	DHTOKPAPED	YPLPRIVNIA	DGKWHRVAIB	VERNIVINIV	180
	DCKKKTTKPL	DRSERAIVDT	NOITVPOTRI	LDEEVPEGDI	DOPLITODPK	AAYDYCEHYB	240
S	PDCDSBAPKA	AGAQEPQIDE	YAPEDITBYD	YEYGEABYKE	AEBVTEGPTV	TEETIAOTEA	300
	HIVDDFORTH	YOTHRSYOTE	APRHVSGTNE	PNPVERI FTR	BYLTGEDYDS	ORKNSEDTLY	360
	EVKRIDGRDS	DILLYDGOLGE	YDPYEYKBYE	DKPTSPPNEB	POPOVPAETD	ITETSINGHO	ç
	AYGEKOOKGE	PAVVEPONLV	ECPPOPAGPA	DINGPPGLOG	<b>DEPOSITION</b>	ROPPGRPGLP	9
:	GADGLPGPPG	•	<b>GDCSKGPT18</b>	AGENDADAIL	COARIALROP	POPMOLTGRP	240
S	<b>GPVGGPGSSG</b>	AKGESGOPGP	QQPRGVQGPP	GPTGKPGKRG	RPGADGGROM	PGEPGAKGDR	909
	GPDGLPGLPG	DKGHRGERGP	COPPOPPCO	CHRGEDGETO	PRGLPGEAGP	RGLLdPRGTP	660
	GAPOOPGNAG	VDGPPGPKGN	MCPOGEPGPP	DONDANDOOD	LPGPQGPIGP	PGEXCIPOGKP	720
	GLAGLPGADG	PPGHPGKEGQ	SCENCALCIPP	OPOGPIGXPO	PROVICADOV	RGLEGBEGER	780
;	GEDGPPGPKG	CMOLKGDROE	VOOLOPRGXD	GPEOPICORAG	PTODPGPSOO	AGENCIALOVP	840
9	GLPGYPGROG	PKGSTGFPGF	PGANGERGAR	GVAGKPOPRO	ORGPICPROS	ROARGPTOKP	006
	GPKGTSGGDG	PPOPPOSRGP	QQPQGPVGPP	CPKGPPGPPG	RMCCPGHPGQ	ROBTGFOCKT	960
	DANDOADAAD	POGPTGBTGP	IGEROYPOPP	DATECREDATE	AAGKEGAKGD	POPOG18GIO	1020
	GPAGLRGPPO	BRGLPGAGGA	POLKGGEGPQ	GPPGPVGSPQ	ERGSAGTAGP	IGLRGR PG PQ	1080
;	GPPGPAGEKG	_	AGRDGVQGPV	<b>GLPGPAGPAG</b>	SPGEDGDKGB	IGEPOORGER	1140
S	COXCENGPPG	PPGLQGPVGA	PGIAGGDORP	GPROCOGMFG	OKGDEGARGP	PCPPGP1GLQ	1200
	GLPGPPGEKG	KNODVOPWOP	POPPOPROPO	GPNOADGPOC	PPGSVGSVGG	VGERGEPGEA	1260
	GWPGPPGEAG	VOOPKGERGE	KGEAGPPGAA	GPPGAKGPPG	DDCPKGNPGP	VGFPGDPGPP	1320
	GELGPAGODG	VOCDKGEDGD	POGPOPPOP	GEAGPPGPPG	KRGPPGAAGA	EGROGEKGAK	1360
	GRACIAECIPPO	KTGPVGPQGP	ACKPOPECLR	GIPGPVGEQG	LPGAAGQDGP	POPMCPPGLP	340
2	GLKGDPGSKO	_	ICPPCEQGEK	GDRGLPGTOG	<b>SPGAKGDGGI</b>	POPACPLOPP	1500
	GPPGLPGPQG	PKCNKGSTGP	ACCRODSGLP	CPPGPPGPPG	EVIQPLPILS	<b>BKKTRRHTEG</b>	1560
	MOADADDNII.	DYSDOKEEIP	GSLANGLKODI	<b>EHMKPPMCTO</b>	THPARTCKUL	DOMAGAHSTO	1620
	EYMIDPNOGC	SCDSPRVYCN	PTSGGSTCIY	POKKSEGVRI	BEWPKEKPGS	WFEEFKROX	1680
	LSYLDVEGNS	INNONTPLK	LLTASARONP	TYHCHOSAAM	YDVSSGGYDX	ALRFIGSNDB	1740
7.2	EMSYDNAPPI	KTLYDGCTBR	KUYEKTVIBI	MEDICAL	VDVM18DPGD	ONDKFOPEVO	1800
	3						

Seq ID NO. 362 DNA sequence Nucleic Acid Accession #: NM\_003107 Coding sequence: 351-1775 8

	8	120	91
51  -	CAGCCGAGAG	CTCCAGCCTO	TOCOCACTIT
<b>‡</b> _	TOTOCAGACT	DAGAGAGACT	CCAAATCTTT
a_	TTAGCACGO	<b>GAGAGAGGGA</b>	AACTCCTTCC
<b>#</b> _	TOCTOTOTAC TITAGGACA	GAGAGAGCGA	AGAGGCGGAG
=_	TTCGAGAAAC 1	DCAGCCCCCT	CTCCTCTGCG
	TOCCCAGC	ACAGCAMCT	GONACTATAA
,	2		

	WO 02	WO 02/086443					
	TCTCTCTTTA	CCCACCTCCG	ОСССТОООЛО	OACTTOACO	<b>OCCUPATION</b>	000000000	~
	COTCTTCCCO	Treasener	OCTTOOCCCG	OCCAACCOO	AGGGCCCGGC	OATCOCOCO ATCOCOCOCO	= =
	AAACCAACAA	TOCCHOAC	ACGGAAGCGC	70070000	CCACACTCC	dactcoooco	; ;
^	CCGGCCTCGA	OCTOGGAATC	accrecaece	CCACGCCCCC	CTCCACCOCC	TCCACGGGCG	Ŧ
	OCAAGGCCGA	CONCECCING	TOTTOCAGA	CCCCAAOTOG	GCACATCAAG	CONCCONTOR	
	TOCACAGOC	COACATETEC	MACCACTCA	OCAMODETO	GARGETOCTC	AAAAACAGGG	: 3
2	ACAAGATCCC	TITCATICOA	аладсодиас	gocTGCGCCT	CAAGCACATG	OCTOACTACC	2
2	CCGACTACAA	GTACCOGCCC	AGGALGAAGG	ACCORDED CO.	CACOCCAC	AGTOCOLOGIC	- 2
	GCOGCCATOO	GOCCOCCOC	ADDOCCOO	GCAGCAAGC	GGGGGGAGGA	GGCGGCGGTG	. 2
	CGAGTGGCGG	COOCCOCCAAC	TCCAAACCOG	COCHOMANA	аластасас	TCCAAAGTOG	ă
15	2020000000	OCCUPATOR OCCUPA	OTTAGGAAG	COCACACCAA	OCTCATOCTO	GCAGGGGGG	33
2	COCCOCCC	OCTOCCCTO	000000000000000000000000000000000000000	CONCORCO	CTOCCTOTAC	AAGGCGCGGA	ä
	CTCCCAGCGC	стсовостос	осстосторо	CAGCCTCGGC	CTCCCCAGC	CTCGCGGCCC	3
	CCGGCCAGCA	CCTGGGGAG	AAGAAGGTGA	AGCGCGTCTA	CCTGTTCGGC	GGCCTGGGCA CCTGGGGCA	3
ឧ	TOTACOAGGA	GGAGGGGGG	OCCURICACIO	COGACGCGC	CAGCCTGAGC	GCCCCACCA	iā
	accepeente	orcecedec	gecogeoct	COCCCOCCO	CCACCGCGGC	TACOCCAGCC	Ξ
	CCCACTCCTC	CTCGCCCGCC	TOCHOROGO	CCTCOTCCTC	COCCITCCTCC	TCGAAGAGG	15.0
;	ACCTGCTCCA	CCTGAACCCC	AGCTCAAACT	TTGAGAGCAT	отсестооос	AGCTTCAGTT	3
2	CCTCOTCOCC	OCTOSACO00	DACCTOGATT	TTAACTTODA	accooderec	GGCTCGCACT	3
	TCGAGTTCCC	DOACTACTOC	ACCCCCAAGG	TOAGCOAGAT	GATCTCGGGA	GACTOGCTCG	5
	CEGGGGGGGT	AGGAGAGGAG	AAAAAAAAA	TOARANAGO	AAACTAAAAG	CACAGACGAA	186
	GAGTTTAAAG	AGAAAAGGGA	AAAAAGAAAG	AAAAAGTAAG	CAGGGCTCOT	TCGCCCGCGT	S
2	renegregate	OGATCAAGGA	0000000000	OTTTT00ACC	COCOCTCCCA	TOCOCCACCT	5
	100000000	GOGACCCACT	CTGCCCAGCC	GOADDGACDC	GGAGGAGGAA	GAGGGTAGAC	2
	TTCGAGTTTG	CTCCCCTTTG	CTTGAAGAGA	CCCCTCCCC	CTCCACCA	CTTCCGGAC	1 2
į	THETCHGCAC	CCCCAGCAAG	AAGGCGAGTT	AGTITICAG	AGACTTGAAG	CACTOCCC	2
ટ	CTTCCTGCAT	CACCACCTTO	OTTIGITI	ATTTOCTTC	TTGGTCAAGA	ANDONOGODA	2 3
	COTGACGAAT	Troccoang	GCACATOTT	TGGGGAACO	CCCCCCCCC	GAGACTCCAC	
	OCAGGCGAAT	TCCCOTTTGG	COCCULTATI	TOCTOCOTOR	TTTCCCCTTG	CCCCTCTOC	ž
<del>6</del>	ACCCANGNAC	CCCOTTOGAA	AGGGGGGGGGG	GGGAGCTAGG	GOCGOGGGG	CTAGGACATO	2 2
	COAACTOGAA	GGGGTTCAC	<b>OGTCANACTO</b>	AAATOGATIT	<b>GCACOTTGGG</b>	DAGCTOGCOG	9
	GACCCCGGAG	GCOTOGAGGA	GAGGAGACTG	TTTCATOTCO	TACAGGGGA	GTCAGTGGAG	
45	GCCGAGTGGT	TTCGGAAAAA	AAAAAAGAAA	AAAAGGG			
	Seq ID NO: 363 Pro Protein Accession	363 Protein	sequence NP_003098	9.6			
Ş	-	<b>1</b> -	11.	- F	<b>3</b>	51	
2	MVOOTHINAEN	TEALLAGESS	DSGAGLELGI	ASSPTPOSTA	STOCKADDPS	WCKTPSGHIK	• :
	ADYPDYKYRP	RKKVKGONAN	BESSANABEK	PGEKGDKVGG	БОООПНОВОО	GGGSSNAGGG	: = :
55	GGGAECGGAN	BKPAQKKBCG GAAADHHBLY	RARTPSASAS KARTPSASAS	ASSAASAA	LAAPGKHLAB	KKVKKVYLPO	* 2
	GLGTSSSPVG YASLRAABPA BPSSSSALDR	OVGAGAD PSD PSBAPSHASS DLDFNPEPGS	PLOUYEREDA GABSHESSSS GGHPRPPDYC	GCSPDAPSLB 690888BDDB TPEVSENISG	ORBSAASSPA PEDDLLDLAP DALEBBIENL	AGR SPADHRO BSWPBSMSLG VPTY	2 3
S						ļ	
3							

Seq ID NO: 164 DNA sequence Pucleic Acid Accession \$: U10860 Coding sequence: 123-2204

55		<b>a</b> _	<b>#</b> -	<b>1</b> -	<b>7</b> -	<b>15</b> –	
	TOCCOOCTOC	TCCTCCACCA	GOCCTCCTTC	TCMCCTCMG	CCCCCCCCCCCC	COACCCTTCC	•
	OCCACCCTOC	COCCCOTCT	COTACTOTCO	CCOTCACCGC	000000000	OCCCTOOCCC	2
•	COATGGCTCT	GTGCAACGGA	GACTCCAAGC	TGGAGAATGC	TOGAGGAGAC	CTTANGGATG	=
2	OCCACCACCA	CTATGAAGGA	<b>ACTOTTOTICA</b>	TTCTGGATGC	TOTTOTTOTO	TACCOCANAC	ž
	TCATAGACCO	AAGAGTGAGG	<b>GAACTOTTCO</b>	TOCAGTICTOA	AATTTTOCCC	TTGGAAACAC	=
	CAGCATTTGC	TATAMAGGAA	CANGGATTCC	GTGCTATTAT	CATCTCTGGA	GGACCTAATT	Ä
	CTGTGTATGC	TOMGATOCT	CCCTCGTTTG	ATCCAGCAAT	ATTCACTATT	GGCAAGCCTG	Ç
	TYCTTGGAAT	TECTATORE	ATGCAGATGA	TCAATAGGT	ATTTOGAGGT	ACTOTOCACA	Ŧ
2	AAAAAAAGTOT	CAGAGAAGAT	GGAGTTTTCA	ACATTAGTGT	<b>GOATAATACA</b>	TOTTCATTAT	ň
	TCAGGGGCCT	TCAGAAGGAA	GAAGTTGTTT	TOCTTACKO	TOGROATAOT	GTAGACAAAG	8
	TAGCTGATOO	ATTCMOOTT	OTOOCACOTT	CTOOMNCAT	AGTAGGAGG	ATAGCAMTO	ž
	AATCTAAAA	GITATATEGA	GCACAGTTCC	ACCCTGAAGT	TOGCCTTACA	GALALTOGAL	2
	AAGTAATACT	GAAGMITTC	CTTTATOATA	TACCTCOATO	CAGTGGAACC	TTCACCOTGC	2
2	MANACHONDA	ACTTGACTGT	ATTCOAGAGA	TCAMGAGAG	AGTAGGCACO	TCANANGTTT	2
	TOSTITIACE	CAGTOGTOGA	STAGACTICAL	CAGITIOIAC	AGCTTTGCTA	AATCGTGCTT	2
	TOAACCAAGA	ACANGTCATT	GCTGTGCACA	TTGATAATOG	CTTTATGAGA	AAACGAGAAA	š
	OCCURRENT	TOARGAGGC	CTCAAAAAGC	TODAYTICA	GOTCAAAGTG	ATMATGCTO	ŝ
į	CHOTTOTT	CTACANTOGA	ACAACAACCC	TACCANTATO	ACATCANGAT	ADAMOCCCAC	50
င္သ	OGMANAGANT	TAGCAMACG	TTAAATATOA	CCACAGTCC	TOAAGAGAAA	ADAMMATCA	Ξ
	TTGGGGATAC	TITIOTIM	ATTOCCAATO	ANOTANTTOO	ADAMATGAAC	TTGAMACCAG	2
	AOGAGOTTE		COTACTITAC	CCTTGCCCAA GOTACTITAC GCCCTGATCT AATTGAAAGT	AATTOAAAGT	OCATOCCTTO	ž

. *			· .			
11120 11120 11120 11200 11200 11200 11200 11200 11200 11200	4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 & 0 & 5 4 0 0 5 5 0 0	6 11 12 12 12 12 12 12 12 12 12 12 12 12		9 0 0 1 1 2 0	1 180 1 180 1 180 1 180 1 180 1 180 1 180
CCATTAGAM CONTITION AMONGTIT AMONGTIT AMONGTIT AMONGTIT AMONGTIT AMONGTIT AMONGTIT CONCENTRY OTTAGAM ANTITION CONCENTRY AMONTOTIT AMONGTIT AMONGTIT AMONGTIT AMONGTIT CONCENTRY AMONTOTIT CONCENTRY AMONTOTIT CONCENTRY AMONTOTIT CONCENTRY AMONTOTIT CONCENTRY AMONTOTIT CONCENTRY AMONTOTIT CONCENTRY	S1   0   0   0   0   0   0   0   0   0   0	DPBABVKEH G18SKORPDH ADPEAHNILR ATPGNEIPVE	51 TACTCTGATC TREGCTCAAC TREGCCCCCT TREGCCCCCTAAC GGCTTTGGAT TCTAGACTT TGGAGTTGCT TGGAGTTGCT TTCAGACTT TCAGACTT	TTCTTCACA GAMANAMA  41 51  42 1 81  43 14  44 84  45 68 68 68 68 68 68 68 68 68 68 68 68 68	\$1       GSGCOTIGCA   CGCCAGCATG	accocractor coocasata coocasata coocasata coocasacc coacaccaca acaccaccaca acaccaccaca cortanococa cactanococa cac
TRACACAGA TITTCATANA TECANOGRAT TCAN	41 IDRRVRELPV LOI CYGNGWH ARGERCYRRI NYELECIRRI GOTEVELIR GOTEVELIR GOTEVELIRRI GOTEVELIR GOTEVELIR GOTEVE GO	BETNNILKIVA GDCRSYSTVC ITSDFWTGIP	41 	ALATAGATA TTCTTCACA 41 41 VBTPRPGKTF KB8VPASDDA LGPPSPVIMP	41     CCCGCTCGCA CGCTCGCAC	COCCUCION GOODSCOO GOODSCOO GOTTOGAGO ATCCCCAC ATCCCCAC ATCCCCAC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACC ATCCCACCACC ATCCCACC ATCCCACC ATCCCACC
CCCATCACA AGACTAAT CTCACACAA CACAGAAC CACCAGAC AACTCACCA TACCCACAT TACCCACAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT AACTCACTAAT	1 31 LDAGAQYGKV PALPTIGKEV LTHGGSFDKY AGCSGTFVQ AGCSGTFVQ HHYDTELIRK	EEPYICHOPP LLPPIKTYCHO PPTDVTPTBL CORSVVIRITE EMB	11	ATAMGO ATAMGO ATAMGO RELEKLING	197 13 13 00000000T 000000000	CTGCCGCCGG GGCGGGCCC GGCCTGCCC GTGCGCTGCT GGCCTTGT ATTTGGGG GCCTTGTG GCCCTGTGC GCCTTGGC GCCTTGGC
CTCSTCAMA ONDATTCCAMA ONDATTCCAMA ONDATTCCAMA MAGCETCAMA OCCUPANO	Sequence, AA6031 21 21 HHYFGAVI VYAEDAPP ROLGKSEVL VILKIPLYDI KRIGKILKT ABGKAELIKT	TIGREGIUSE EUGRUSPO POLLIFUTO, ES ISBLIPANCT TERDOSKLO ITSCHEISMA IN ISBLIPANCA PRODOSKLO VITERPANZ PP WIGNORIDA PHOUNTRAIN PULTSKPPATT EN WIGNORIDA KIPOLSHIPH DITSKPPATT EN Beg ID NO. 166 DNA sequence MUCLSKC ACID ACCESSION   NI (1901) COLING SEGUENCE	21 	TATTOTAL  TATTOT	Beq ID   No. 348 DRN sequence	COCCTOCCO COCCCOLAGE COCCCCACO COCCCCCO COCCCCO COCCCCO COCCCCCO COCCCCC COCCCCC COCCCCC COCCCCCC
CAMAGETAA GAGGAACT GAGGAACT OGCAATETA GAGGAACT CATTOCTA TATTOCT TATTOC	115 Protein 11 11 11 11 11 11 11 11 11 11 11 11 11	ELVERHIPPG TTEDOEKLAD PRACHOVRV MPVILTPLHF KIPGISRIMY 365 DNA seq 1d Accession	11   ADDAMATED ANDAMATED ANDAMATED ANCETTCANT CONTCANTOC ANCETACANA ANDCONANA  GAGTTTGTGT  167 Protein  cession 8:  11  INTERPVENTED  PERGIJALIE  VELPPVCCDI	168 DNA 801 Ld Accession Lance: 11 Adda/ada/ada/acceccectos	TOOGETOCCE TOCTOCTACT COCTOCTOCC COCTOCTOCC COCTOCTOCTOC COCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCT	
THOCUMENTS METTERS GANTETTOS TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOCT TOTOTOSCOC	Beq ID NO. 185 Prot.  1	ILGRELGLEE TILLGRUKACT ESLIFLARLI ESCYAGKISC VYLKMYTEIN Seq ID NO: Nucleic Act	1 1ATOTTOATA TATOTTOATA CTOOGOTCH ATTOGGAAA ACTOTTACA COAGOTTACA COAGOTTACA GAGATTTTO GAGATTTTO	ANAMAAA  Beq ID WO: Protein Acc  I  RALLIYWDKE RRALGTWRA RRALGTWRA RRALGTWRA RRALGTWRA RRALGTWRA RRALGTWRA RRALGTWRA RRALGTWRA	Beq ID NO: Nucleic Act Coding seque 1 ATTCOGGGG CCTGCCGCC	CTGCCGAGAA CGGCTGCCG GTGCGGCGC GGCTTACA GTGCCCTACA CTGCCCTACA TTGGAGAACA AAGCCCTACA AAGCCCTACA
\$ 10 15	5 25 20	35	50 45	55 60 65	07 27	80

	12000.00			11120		120		1750		120	•	120	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	6 6 7 7 8 6 0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	900 960 1020 1080		120
CCTGCACATC	OCCUPACE COCO COCO COCO COCO COCO COCO COCO C	AAGAGAAATT		S1 ERLAACGPPP GLRCY PHPGS IMLOGGGSAG OQELDQVLER PHTGKLIGGA		S1 	GAGAGATAC GAGAAGATAC ACCCATAGCC AACTGTTTGA	TTICACTOTT TTITTAACT ACATATOTAA CTTITACAAT		S1   TEEYAQUFAA GDMLLEKIQB		S1 COAGCTATAT AAACGTGCTG TCACCTGGAG					S1     DONYTEPHUS   LDESDABHEL   RFCILGRESP
ACTCTACTC	AGCTGATCCA AGCAGCAGGA GCCTGUGGC OTGOTGGGTG AGCACCGAGC	AOGAAGGAAAA		41   VLPRCPPCTP CGVYTPRCGG LVENHYDSTH LRPPPAHTPC GGRGECWCYN		41 	CATGCTTCTG CATGCTTCTG AAGAAGTGGT CTGAAAAAAG	AGTECTICTAT CATACCATCA ATATAAGGAA TTGGCCAGTA		41   AINDOPANP ATCVEDVVYR		41 AGGACACCG GCATCACTGA TCTATGAATT	CAAAGCAGA AAAGCAAGG ATCTTGTGCA TCTTGGGAAA	OCCAGATOCT TOCTOCCTTC CCATGGAAGA TTGAAATTTT	CTGTCTCAGT TGCCATATCC TGATATTTTT TGAGGGCAGG		11 HPKAQGHQAK LPLAPDPDRW PBW1 PVNLTV
CCTCTGGAGC	TTCTACATO TTCTACATO OCCACCOOT OAGTGCTTOG GAAAGAGCC	OTACAGOTTT ATAAGATTAA	=	11 COCCOARAB SYCALEGEA SYC	3	AGGACGCTGT OTGGTCCTCC ACCCTACAGA	ATCCACCACA ACCCACACA ACCCATOTOG	TATATATAT TETAMAGATA ANTGAMGATA TITTOTTOTA	£.	31   PPASFNNIQT YKLEEEWHEA	=	31 TACTOGGCTC CCTGCCATGA GGAGACAATG	GAGAGACTCA CTGGATGAAT CTCCGACTGG TTTATGTATA	ATOTATTECT ACOTCACCOO ATCTTTOOCA TOOAAGGTGCAA	TTGGGGAAG AGTTTGACAT TATCTTATAA AGACTGAAAA TGA		31 
TOAGOGGGC	TOTORACCCC OTOTOCATCTC OTACACCCCA AGMANICACA TITATATATOC	CCCTTTGC	NP_000588	21	370 DNA mequence d Accession %: NM_004264 ence: 5-440	21 ACCMOCTTC TTGCMCCAAT CAGCCAGGTA GCAAAAGACA	CAGGCTGCTA CATGTTGTTT CATCAGTGA CATCAGTGA	CCTTTTAGC TTGAATCAGC GTAATACATT TATGTCTCCA	1 sequence NP_00429	11 21   AVBELDQPC NAIGVLOQCG VLIDSLPBER STALQASE KTREGTHSQB LPDB	puence   #: AJ271091  3	21 GCCCATOTC COTACAGAAC TCOTGCCAAA	TCAGTGGTGG TGATCGTTGG CCTAAATAAA AGGATACCTG			n sequence CAB69070	21  - LRVELSDVON TVQKKVSOMN TUTNLRKGYL
(1)86443 accrecada acaracarad	AGTOCTOGTO DOGACCCCA MACCATTOCA NANCACCCOCA GACACCCCATA	ACCCTOT	369 Protein	11 PLPPPFLPL AGGARMPCAS BOTCERRES LAVTEKATE GPUEHLYSUL LPYNESOEAC	NO: 370 DNA sec Acid Accession sequence: 5-44	11 daatcocctc cattgaagta taacaaagac taacacaaaca	ACCTGCTTTA ATOTOTOGAO TGCTGATATT AGACTCATAG	TOACACATTA TANATCATGA ATTAAGGCAT TGACATAATT	371 Protein	11   Avnsladoffc Vlidslesee Ktrsgthsos	8eq ID NO: 372 DXA sequence Nucleic Acid Accession #: AJ: Coding sequence: 1-1113	11 	AGAAAGTGAG CTCCTGACTT AAGAAGAGCG ACTTAAGGAA TCTTTGTCAA	ATOCATACTOT ATOCAGCAAT GAAATTTTAT TTTTCTTTOT	CCTTATATCC TCAATGAGAC TTTCCTTTTT GTCACCTTTA	373 Protei	11   YWAGRIRELY YKLTORGVNI LRLESSOSPE
WO 02 TCCACCATOC	CACCATCODO ACCATCODO OTGCACACC GCCCTOTC TTCCAGTICT	AGGAAGGG	Seq 1D NO: 3	1 MLPRVGCPAL VAPPAAVAAV ELPLQALVAG REPLESGER I STHRLPDER PT I RGDPECH	Seq ID NO: Nucleic Acto Coding seque	1 GGAACATGGC TTTGTAATGC AGACAGCAAT CAGCACTGAT			Seg ID NO: 3 Protein Acce	1 	8eq ID NO: Nucleic Aci Coding sequ	ATGGGGTGG CTGCGCTGG CATTTCAAG	ACAGTACAGA CTGTTTTGG ACAGCTACGA ACTCTTACAA TTCTCCTGGA	TATGACACAT GAAACTATCA CTTCTTGGAA AAAGCTGTGG	CTGTGGATTC ATTCCAATAT AAAGTTAGAT ATAAATTTC CATGCCTGTG	Seq ID NO: Protein Aco	1   MENQVLTPHV PLDLVKPEPV RAKEEERLHK
	~	10		15	25	30	35	04	45	20	55	. 09	65	0,	75	80	85

S
~
*
~
_
त्र
_
S
$\Box$
=
-
Ĉ,
$\sim$
-

880		-						_		-		_			.0	0	10
	v)	2	15	20	25	30	35	40	45	5	\$ \$	9	65	2	75	8	85
											•					•	
92																	
PCT/US02/12476																	
/0S0/																	
7																	
•																	
						•					•						
300		00	2000	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		200		1 1 1 6 6 2 4 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	S & .		60 110 240		8				200000
													¥				
LLGRWPILPI IPGTMBEMQH LMIPLYPLGC LAEAVSVIQB INFRHLYRGR PLUGHAGAVA		ACTATA COTOCI	TCACCTGGAG GGTAAACATT AAAGCGACCA AATGGAGCTC	CTCTCCTGAA ATTCTTGGGA AGAGTCCTTT GGCAGTTGTG	AATGCAGAAC CAGGTACTCT TCGTTACACT QATTCAGTCC	TTTAT		S1     CONVYEPHLE   LDESDAENEL   RFCILGICESP   IPOTMEDAGN	AVSVIC		S1 		51   PKVPBPCQPK		AGGCC TGCTG	ACACAGAGA ACACAGAA ACCTCAACA AGCCGTGCT GCAAGAAGC	ACCTGAGGG TCGCCCGCC CCTGCCGCGT CCTCCCGGATG CCTCCGGATG
A LAS		25 E	រ ស ន ន រ ស ន ន	2 4 4 5 F	2012	5		2 - 89 32 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	25 EVE		a_8888		2-2 2-2		#_688	នួក្ខន្ធន្ធន្ធន្ធន្ធន្ធន <u>ុ</u>	88888 845668
ENTIL!		41 AGCGACACCO GCATCACTGA	CCCAGAGGA CCAAGCAGGA CAAAGCAGGA	AMACCIANGO ATCTTOTICA TCTTGGGAAA GCCAGATGCT	AAATT CATGG	TATT		41 HPKAOGHGAK C LPLAEDPORN I PEMIPUNLIV S	PLYPL		CTCAGCTCA TCCCCAAAC CTCAGCCTG CTTCAACGT		41   COPKVPEPCH		41 	OTOTACCTOO GCGGCCCGCG AACGACGAGG CCCCAACATCC CCCCAACATCC CCCCAACATCC	TCATGGAAG TCCCCTCCC TCCCGCACC GGGTTCGGGC CCCGAGCCTG
T INI		5.4 2.4 2.4 2.4 2.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3	ដូខូវូទូ ខេត្ត១	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	8 E P B I	P P P P		1	E E		=_6266 8688				±_886 882	583888 583888	888844 855588
ETINAIGUT TEPULPBLIG FYMLTCIDMO WKVLTWLRYT KVRF8PPLQI YLIMIPLGLY		1599C	AAACH AGACH AGACH AGACH	CTCCGACTOO TTTATGTATA CGATTCTGTA ATGTATTTCT	AGGGAN AGGGAN	CTTATA		PAISITENUL PEUTKOEKRP PHYNLVQFIG I TEPVLPBLIG I	LTWLR		ACCCACCC AACCATGA CCCAAGTGC GAACCATGC		31  - BPCIPKTKEP		11  - CTAGTGTTTG GACTGGCGC CCCAGTGGGC	OCCUADOCO AGOSTICA AGOSTICA OCCUADOCO AGOSTICA OCCUAGOCO	ACCACCAGGC TCCCTTCCCC CCCGCTCCCG
7.0 T.0 Y.V. I.1.Y	6398	#_¥6	5 F 5 E	5222	555E	5	97479	IL TAN TE	7 KF1	5987	25552 27555	sequence NP_005978	£—87 ₩	2105 35	863_== 1\$1	888388 888338	888888 888888
NAAIG LTCID	5 ₹ 5 ₹	21   GCCGCATGTC CGTACAGAGC	3000 3000 3000 3000 3000 3000 3000 300	CCTAAATAAA AGGATACCTG CCTGACTGTG AGCTGACATG	CATOR	TCAGA: TCAGA: ACAGC	sequence NP_057479	elbov Krvbo Wlrkg Warg	LTCID PBPTL	5 E -1	21 GCAGCCTGC TCCACCCAG GCCTGCAC CAGGTGCT GCAGAAGTAA	AVP_0C	PCOPP	N. 14.	21 	TCCTGGAGCT ACCTGCAGCT TCCCCCAGG	TTANGGGC GGCCGGGC CCCCCCGC CCGCCGTCG
7 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	equen	2-86 2-86	មក ក្នុង ក្នុង ក្នុង	8445	EFFE	855E	e ut	1122	SE ES	ie uol	\$5848±	e ut	2 - 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	lon #.	888 888	855555	: 68883 : 68848
WO 02/086443 EDTPHTVADM MYECCHLAVV B KANVPEVPTL MOLESTRYS F SEPTENTYS F	NACDPRALOO  Seq 1D NO: 374 DNA mequence  Nucleic Acid Accession 8: NM_016398  Coding sequence: 1-113	TOTTON TOAGTO	AAGGAC TGAAAC AAGTGA	ACTOTIACIA ACTIVACCO A ACTOTIACIA ACTIVACOA A TICTOCTICA ACTIVATOA CI TATACACAT TOCATACTOT CI	ATTT:	ACCTTT ACCTTT CCAGGG	Protein ion #1	11 21 11 21 11 21 21 21 21 21 21 21 21 2	LEYEV	MO: 376 DNA sequence : Acid Accession #: NN_005987 sequence: 1-270	AGCAGCAGAA AGCAGCAGCC AGGTGCCTGA CCTTGCCAGCC AGAAGACCTAA	Protein	11 21 1 1 EPPOPOCOO VKOPCOPPO EPCPSTVTPA PAQOKIKOK	8eq ID NO: 378 DNA sequenca Nucleic Acid Accession #: NN_002105 Coding sequence: 74-505	CACTGCGGCG AGCATGTCGG TCGCGCGCCG	ACCOCTOACA ACCOCTOACA ATCCCCCGC GCCOTGACGA AAGACCAGCO	CANGGCCT COGGGCAAGC GCCTCGAGTC CCTGCCCTGT GCTCTTCGGG
WO 02/086443 htvada myrcomu- ppvpyl wsaisipy hetgrf sptlyym	30 31 374 31 374 31 314 31 314	7 AGG	2 X 4 2 2 2 2 3 2 3 2 3 2 3 2 3 2 3 3 3 3 3	2	Stab	F = 5 5 F = 5 5 F = 5 5 F = 5 5	Seq ID NO: 375 Pro Protein Accession	** *** ***	TE NSA	o 376 Acid A	1 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Seq ID NO: 377 Pro Protein Accession	11 - 24 12 - 49 12 - 49	5, 378 Acid A aquenc	######################################	**************************************	158888 53888
WO PKTVAL	DPBALK 10 MC 1e1c A ing se	מאמאת	TTAGAC	GCTAAC CTTAC CTTAC TCCTG	CTTGO CCTTGO CCTTGO TACATO	OTTACK OTTACK AATTTT GCCTOT	tein A	QVLTP! LVXPBI ERBRLS PHTVAL	VPPVP	Seq 1D M Nucleic A Coding se	ATGAATTCTC OTGAACACCA TGCCACCCA ATTCCAGAGC	retn J	1     MSQQQXQPC   PRPCQPKVP	to a	ACAGCAGTTA CTACCTCSCT GTCGCGCTCS	GANGOGCAC GANGTACCTC GANGOGAATC GANGCTAGGC GANGCTAGGC GANGCTAGGC	CATCOLOGY CATCOLOGY TOSCOSCO COSCETOSOS COSCETOSOS
10.7 17.7 11.9	Pag Bruco	A P	2536	A CEL	E	1359	996 Pro	TEN NEW YORK	N I Y	2 × 0	E E E E E E E E E E E E E E E E E E	Prof	1 - B	6 2 0 8 2 0	466	368668	56688
	<b>5</b>		^	0		_	80	0	S	_	· · · ·	0	ν.	0	S	0	~

<del>4</del>

1/186443  CONSISTENCE CONCENSION OFFICIALLY CONCONCINC ATTOCCHIA CONCINCATOR 900  THOCOROUGH CONCONCINC FETCH CONAIN THE THOCKTHE CONCINCANT OFFICIAL 910  THOCOROUGH CONCONCINC FETCH CONAIN OFFICIAL 910  THOCOROUGH CONCONCINC CONCONCINC OFFICIAL 910  THOCOROUGH CONTINCAND OLONGOFT TO TOTAL 120  THOCOROUGH CONTINCAND OLONGOFT TO TOTAL 120  THOCOROUGH CONTINCAND CONFORM TO TOTAL 120  THOCOROUGH CONTINCAND CONFORM TO TOTAL 120  THOCOROUGH CONTINCAND CONFORM TO TOTAL 120  THOCOROUGH CONTINCAND CONFORM TO TOTAL 120  CONTINCE CONTINCAND CONFORM TO TOTAL 120  CONTINCE CONTINCAND CONFORM TO TOTAL 120  CONTINCE CONTINCAND CONFORM TO TOTAL 120  CONTINCE CONTINCAND CONFORM TO TOTAL 120  AND TOTAL TOTAL 121  111  21	10 MA sequence	MATERIANG CREGARIA CORACIAS AMACTITIC MATERIAN ACTITICAT CATEGORIA CORACIAS GENEROCA SOCIODAS TATERICA DECONACT TITUCATO COCCUSADO O COCCUSADO TATERICA CALCONACT TITUCATO COCCUSADO O COCCUSADO TATERICA CALCONACT TITUCATO COCCUSADO O COCCUSADO CONTACTO CALCONACT CONTENTA TAGOSTO TITUCATOS CONTACTO CALCONACT SOCIETA TAGOSTO TITUCATOS CONTRACOS CANTONIOS COCCUSTOS ANTICONOCTOS CALONDOS MATERIANOS CALCONACT MATERIAL TAGOSTO COCUMINACIO COCCASIONE CALCONACT MATERIAL TITUCATOS CALONDOS COCANTANOS CALCONACT MATERIAL TAGOSTO COCCUSADO COCANTANOS CALCONACTA TATOCATO TAGOSTO ACCUSADO COCANTANOS CALCONACTA MATERIAL TAGOSTO COCCUSADO COCANTANOS CALCONACTA MATERIAL TAGOSTO ACCUSADO COCANTANOS CALCONACTA MATERIAL TAGOSTO ACCUSADO CONTRACA CALCONACTA ACCUSADO ACCUSADO ACCUSADO CONTRACA CALCONACTA ACCUSADO ACCUSADO ACCUSADO ACCUSADO CONTRACA CALCONACTA ACCUSADO ACCUSADO ACCUSADO ACCUSADO ACCUSADO ACCUSADO ACCUSADO ACCUSADO ACCUSADO	AGONCIATE ATTACTICC CRAGGAME MACTICCC TTOMANTE AMITHAMA CAMANTAM CALAMATH TRAMATE AMITHAMA CAMANTAM CALAMATH TRAMATE THITOGRAPH TRAMATE THITOGRAPH TRAMATE THITOGRAPH TRAMATE THITOGRAPH TRAMATE THITOGRAPH TRAMATH TR	TYTOAND TOCTOTAM TAGTEGITI GCANTEANA CANGITIGE MANAA M	21 SMCACTE TTSCTI SCENCOT BAGAN: POCNACAT TSCCAI TTCTGCTT ACATO MANTGAM MCTCI DGAGGCC GTGTG
1086443 TOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	380 DNA d Access ence: 11 CAGAAGCT	ATTH TATTORDER  TOA TCCTATA  TOA TCCTATA  TOC CATTORT  TOC CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATTORT  TO CATORT  TO CATTORT  TO CATORT  TO CATORT  TO CATORT  TO CATORT  TO CATORT  TO CATTORT  TO CATORT  TO C	MAN ACCIDENT ACCORDERS (MAN ACCIDENT TO ACCORDERS (MAN ACCIDENT ACCORDERS (MAN ACCIDENT ACCID	F2	11 12 13 14 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18
WO 02  GCCGCGCGG  GCCGCGGGG  AMACGCCGG  AMACGCCGG  CCCGCGGGGGGGGGG	25 8eq 1p Not Not sic Act Coding seque addressed address	CONTRACTOR CONTRACTOR	50 addections concerned concentration concentration substances distributes distributes distributes distributes distributes substances noncentration substances substances noncentration substances substances noncentration substances substances noncentration substances substanc	65 CCCATCOM  64 CCCATCOM  64 CD NO.  PTOLASÍA ACO  1 COMPENDA  POLITYPHORUSOD  75 BAG ID NO.  84 ID NO.  NUCLASÍA ACO  COLITYPHORUSOD  75 BAG ID NO.  NUCLASÍA ACO  COLITYPHORUSOD  76 NUCLASÍA ACO  COLITYPHORUSOD  77 NUCLASÍA ACO  COLITYPHORUSOD  76 NUCLASÍA ACO  COLITYPHORUSOD  77 NUCLASÍA ACO  COLITYPHORUSOD  76 NUCLASÍA ACO  COLITYPHORUSOD  77 NUCLASÍA ACO  10 NUCLASÍA ACO  1	80 1 CABTOCCIO COTTGAGTOC POTOCCIO COTTGAGTOC POTOCCIO CABTGAGA CABTGAAAAA TGAAAATGAC AAACTCCTOG

مِ
•
7
~
_
~
2
20
9
$\overline{}$
5
_
نِ
×
ρ,

2						•													
		•																	
5 5	12665	960 1020 1080	1200	1500	1320	2220	2340 2460 2580 2580 2640		. 60	2000	540		9	2 2 2 2 2 2	2888	8282	960 1020 1060	1200 1260 1320 1380 1440	
AGGAAGATGC CTGCTGATGC	GCACCGGCCA GATGCAGANG TOGCACCATO TCATGGANGT ANGATGTGTA	ATCHAATTC TTCATGATCC ATAATACTGG GAACCTTCAG CACCACCACC	TOGAGCTGAG CCACCATCAC TGATGCCGGT GCATTCCCAC	ATGGGTCTGG CGAGCACCCT GTGCCCTGAT ACMANANCA	AGGATCCGCT TEANGCTCAC TTCCTAAAGA TAAATGTCAT	ANDTCTTAGG TATTGATTAG ATOTACCOC TGAATCCCAC GTGGTATGAT	AGENTATION TETTATICON TETTOTATA GACTITICA TETOTATION		51 	WNPIWPHTL WYTDQIPWPW LFWBTMHTWN RIPDGNCQIN	i svpdrdpab Vplnrakavp		51   	CATAGAAATG AGTTTAGCTG GAGTTAGCA CAGTCTTCAG	CATAACTOTT	TTCCAACAA CATGCATGTG AAACTGAGTC GTGGCCCATG	TACTOCAMC AMCCTOMG TITICTTCMG CATCCTCAGC	CAGAATACA CTAGGAGAT CTGGCTCGT TGCCACTCA GGACACTTAT	
AGATGCCAAA	GGGGAAAATG CACCACCCCG TTCCAGAAAT GGGCTTCAAC GCACAAGTGA	CAGAAGAACG GATOTCCTUA AGCTTCGGGG TTGCTCAATG CCGCCACGGC	GACAACCCC CACTTTCAAG ACAGACGTCC TGCCAAGGGA ACCCAGAACA	COMCETTCA CTOSCICTICA ATOSCAACA CTCTTOOTOT	AACCAGGAAA ACCTTOTTTC TAACCTTTTT TTTTATAGGT	TEACTTATA BAGAAGETAC TEAGETTEC CEAAGETAAC GEOCAAGETAAC	ANTOGRISCO CATATATACA TRACTERCAC CATATATACA GGATTTCACC TCTCTCCTTC		41 	PPPHPGMRR VPIAQVICOVY YKWBFCDWTG PACCOMPLELS	DTBLALTSTL GNVVRSKGLØ		41   	CAGAACACTO TOCAGAGATA CACTTACAGA TOGAGATGAA	AGAGGGAAGA TTTCCAAGTT CATGAACAA	AGTTGAATGC GTTAAATCAA AACTGTTACT AGTCCTGGAT	AATAACAGAA AAATGATGAA TTTTAACCAA	OGAGITATIG AGAGGATTA CTTCCAGAAA AGCCCCCAG AGCCACTIGT CATTATIATC	
GATATTOCCT	GGACAGTGAC ACCTTTTCCT TGGTCAGTAT TGTGACACTT TGTTCCCATC	GACTATOTTC CATTATOTTT CTACAGGTAT TCACACGTAT	ACCTGCTGGT CAGATATGGC CATCCAGATG TOTCGTGACC CTCCGGAGATC	GACTOTGAGA TGACACAGC GCCTTTAAGC TGTGATCTCC	CTTCCCOCA TTAAATTTCO GAGTGGCTAT AAGTTGAATT	TTTTTATOT AGACTAGGA COCOATACTT AGATAGAGA ACAATAGAGA	TACTECTOATA GAATGATATT GOCATGATGE TATTTGAAAT TGATCAGTAA	į,	11 IERPBAYMRE SENTTFRANK	HHWVPDGK TVYRHGRAY HFLNYSTIN IPSKPTPSLG	CVNLTLCD YNP I EN BP	*.	31   CUANTANCT	TTACTGAATC ACCAATGTAC TTCAAGAAGC AGAAACCCAC	GCCAAGTGA CGATCCCACT GGGAGACATT	CTGAAAATGC AAAGCAGCTT TCCAAGCCAT	TOTCAMONA TTCATGCAGA GAGATAGAGA TTCATGAATA	AAGGATACCA ATAAAGGAGA GCTGCGGCCT ACACAAGAAA CAGCCACAGC GAGCGGCTGA	
COOTGAACCT	CATGOTCAGA CTGATGGGAA TCCACACACT ACACAGCCAA GACGGGCATA	CTOTOTITIOT MADATCTCCC CTACCATTM ATACTOTIOM CTGCAGCACC	CTTCTTTAGG GCCAGATTAA AGGTTAACAT TAATAGACTT CTGACCCCAC	TOTOTCT CCT CCCTGGGGGA ACCCAGCCTC TATTTGTCAC	AAGCCGTGTT AAGCAGTTTC AGATGTGCTG TGGTTTGGGG	CTTTTCATTA CTGTGTCCCC CAAGAAGAG CCAGTTTCTA TCCTGATGGA	CTCACTGACA TTATATACCA TCCCTGCACA CATOGCAACT OTTAGACATC	sequence NP_002501	21	DEDGENGTOO VTLOPOLATEV IMPOVLINDP GPCPPPPPPP	tvrrtfingeg Viblivykkh	Seq ID NO: 184 DNA sequence Nucleic Acid Accession #: NM 001134 Coding sequence:	21   CTGCCAATAA	TIGGATICIT OCCCAGITICI ACTGCAATIG	ACTECAGEAT GAAGAAGACA TOTATATATATATATATATATATATATATATATATATA	TGCTGCAAAG GAATTAAGAG ACCCGAACTT TTTACTGAAA	CAAGACACTC CAAGACACTC CAATGTATAA AGGTTTTTAG	AGAGTTGCTA GAATGCCAAG GCAAGGGAA CCCGTTGCTT CCGATGCTT AGAAAAATGG	į
/086443 ATANCATITO ATANCATITO	AACTGACAG AACGTCTTCC ATCTACGTCT OTTTCTGTGA AGAAGACATG	DATCADATTC ACCTTCCTCA CTCAATTATT TCCACCAATC ACTGTGAAAG	AAACCCACCC GATGAAAACT GGAATCTTAG GAAAGCTCCC ACCATCATTT	GTGCATGAGA GTGAACCTCA CCTGACAGAG TGCTTGGCCA	ACCOTOCAA CAAGAATTTA CATTOATOTO ATAGATATTO	AGCAGACTT GATAGAACA AGGTTAACTG CCAATGTAGT ACTCATGAAC	GCTAGACTCA CTTTGCTTOO TTAGTGCTTT TTTTOTATAG CCTGGTTTTT	AMMUNITARA 383 Protest ession W:	11    - 	YVYNNTAMSE BVRVBVNTAN EDETFLKOLP LNLTVKAAAP I VEGILEVNI	PVDVDENCLL SVGCLA I PVT LKNQEPKGVB	184 DNA secid Accession	11    -  -	Adentecata Canantinina Adangcaning	COCACATTCA CAAAAGCCC TCAAGCATAT	AATTCCATCT AGTTACAAAA AAATTTTGGG CAAAGTTAAT	ATOTICCASA GOAACOTOOT AAATCTAAAC	ADACCETETT CCAAGCATTG CCAAGCATTG AAATGCGTTG GGCCATCACC	
WO 0%	ATATOTITAC AAGCCATCAT ATGGAATTTC TTCAGTGAGA GACTGTCTAC	COTOGTACA ATCCBACBA TAGCCACTTC CCTOTTTGTT CCTTAACCTC	CAGACCTTCA TAGGATTCCT AATTGTAGAG GCCATGGCCT GGAGGTCTGT	GACGTACTOT GACGTACTOT GATTTCTOTT CTCCOTTGGC	TOTCHTCTC ACTCAAAAC TTTTCAOTOC TTATTOTTAA	ANGCACTT TNACTAGTAG AGCCTANCC ATGCATANG TTCAATACC	TGCACACTT TGACATTTAG ATTTCCAATT AGATGAGGTC ACTAAAACCA	Seq ID NO: Protein Acc	1   	RWEAGLEADP GOYPOKLGHC TMPQKNDRNE HTYVLMOTPE RYGHFQATIT	Ceitontycs Purmansali Ppgnoskopl	Seq ID MO: Nucleic Act Coding sequ	1   TCCATATTOT	AATCAATTT AATATGGAAT ACCTGGCTAC AAATGGTGAA	TOGAGAAGTA TTCTTGCACA TCACAAGCTG	ATGACAAAT AGGCAGCAC CAGTAATGAA AGAAGTTTAC	TOTCCTACAT TOTCCTACAT TOACCACCCT OTCTATCTCC	TTGCTGTCTC TCCAGACTGA TCCAGGAGAG ATTACTTACA CGCAGCTGAT GTGAGGACAA	
	8	10	15	02	25	30	35	9	45	20	55	Ç	3	65	70	75	80	85	

1680 1740 1860 1920 AVIODODADCE GIOCOCIOLO DI CONTETTO CIUCLOSTOTO GIOCOCCODO CICCONTICO DE CONTICO DE CONTI ORICIDADA TOMATRAC CONTINUE CONTINUE CONTICUE ACTUTATA TOCANO ORIGINAL DE CONTICUE ACTUTATA TOCANO ACTUTATA ACTUTATA ATTICATA ACTUTATA ATTICATA ACTUTATA ATTICATA ACTUTATA ATTICATA ACTUTATA ATTICATA ATT Beg ID NO: 186 DNA sequence Nucleic Acid Accession #: NW 002205.1 Coding sequence: 1..3149 Seq ID NO: 385 Protein sequence Protein Accession #: NP\_001125 ဓ္က 

WO 02	WO 02/086443						PCT/US
Protein Accession #	Section #1 N	1 NP_002196.1	<b>-</b>	<b>7</b> .	31		
MCSRTPESPL GPSVEFYRPG LESSLSSSS DNFTRILEYA GYVTILMGED	HAVQLRMOPR TDOVSVLVGA BEPVEYKSLO PCRSDPGWAA INLVQGQLQT INLVQGQLQT	RAPPLIPLILE PKANTSQPOV WPGATVRAIG GOGYCGGGPB GGASSIYDDS GRGSYFGYAV	LLLPPPPRVG LQGGAVTLCP 681LACAPLY AEFTRTGRVV TLGYBVAVGB AATDVNGDGL	GPYLDARAPA WGASPTQCTP SWRTEKEPLS LGGPGSYPWO PSGDDTEDPY PSGDDTEDPY DPLUVQAPLI	VLEGPPOSPP IEPDSIGGAL DPVGTCYLET QQ1L8ATQEQ AGVPKGALTY	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
	OPOGLGSKPS OPOGLGSKPS PIVSASASLT OKOKGGVRRA SLDPQAPVDS	UTUTOHUBYO QVLQPLMAAS IPPAMPNPEE LPLAGRQATU HGLRPALHYQ	HTPDPPGBAL HTPDPPGBAL ROCELEGNIV TQTLLIGNGA SKER LEDKAQ	ROGROLDONG ACINLÉFCLA REDCREMITY ILLDCGEDNI	YEDLIVGSFO AEGIGIVADSI LANBSEFRDK CVPDLQLEVP	00 00 00 00 00 00 00 00 00 00 00 00 00	
GEOWHYYLGD PAVNGSRLLV BFRLGVRAGA EOGYLELSCP BASSGPOILK YKALKHPYRI	KNALNITPHA CDIGNPMKAG QVTLNGVSKP QALEGOQLLY CPEAECFRLR LPRQL POKER	ONVGEGGAYE ASLMGGLRFT BAVLPPVSDW VTRVTGLNCT CELGPLHCCT	Aelrutappe Vphledorokeb Thup inpkol Sobioliffku Aegbygvelm	AEYBGLVRHP 1QPDPQ1LGK DLQPAVHVY BLDPBGBLHH MAKTFLQRBH IIILAILFGL	GWFBBLBCDY MLANSOSDAV KLINOOPSBI QOKREAPSB OPFBLGCEAV	720 780 900 960	
Seq. ID NO: Nucleic Aci	indofinate Floranskay uke Beg'ID NO: 188 DNA sequen Nucleic Acid Accession 8: Coding sequence: 26.,1453	acquence sequence sion #: NM_00242 s1453	428				
	<b>11</b> _		E-	<b>=</b> _	<b>s</b> —		
AAAGAAGGTA AGTCTGCTCT TGCCCAGCAA AAAGACAGT GGTGACAGG TCCTGAGGTT	AGGGCAGTGA GCCTATCCTC TACCTAGAMA AMTCTCATTG MAGCTAGACA GOTCACTTCA	GAATGATGCA TGAGTAGGGC AGTACTACAA TTAAAAAAAT CTGACCTCT GCCCTTTCC	TCTTGCATTC AGCAAAGAG CCTCGAAAAG CCTCGAAAAG CCTAGGAATG CCAAGGAATG CGAGGAATG CGAGGAATG TGGCATGCCG TGGCATGCCG	CTTOTOCTOT GAGGACTCCA GATGTGAAAC CAGAAGTTCC CGCAAGCCCA AAGTGGAAGA	TOTOTICHOC ACAGGATCT ACTITICANG TICGOTICGA GOTOTICGACT AAACCCACCT	200 00 00 00 00 00 00 00 00 00 00 00 00	•
TACATACAGO TOAGAAAGCT AGGAGAAGCT TOATGGCCCA TATTCACTTT	ATTOTOWATT CTCANAOTCT GATATAATGA GGACACAOTT GATCATCATT	NTACACCAGA GGGAAGAGGT TCTCTTTGGC TGGCTCATGC	TTTGCCAGA GACTCCACTC AGTTAMGAA CTACCCACCT AGAAGATGCA	GATGCTGTTG ACATTCTCCA CATGCAGACT GGACCTGGGC TCAGCCACCA	ATTCTGCCAT GGCTGTATGA TTTACTCTTT TTTATGGAGA	. 4 4 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
	CCACTCTACA GGCATTCAGT AMATCTGTTC GCCATCAGCA	ACTCATTCAC CTCTCTACOO CTCTCTACOO CTCTCACOO	GGGGCTCTTT AGAGGTGGCC ACCTCCCCCT TGAGATGCCA AGAATATCTG	CACTCAGCCA CAGTTCCGCC GCCTCTACTG GCCAAGTGTG TTCTTTAAAG	ACACTGMAGC TTTCGCMAA AGGMACCCCT ATCCTGCTTT ACACATATTT	60 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
CTCTCTTCCA TTTTAMGGA AGGCNTCCAT CAAGGNAAAG	TCATATTION AATGAGTICT ACCTGGGTT AGAAAACAT	ACCCTUANCE ATGCTGCATA GGGCCATCAG TTCCTCCAAC ACTTCTTTGC	TGAAGTTTCAT TGAAGTTAAC AGGAAATGAG CATAAGGAAA AGCGGACAAA	TTGATTTCTG AGCAGGGACA GTACAAGCAG ATTGATGCAG TACTGGAGAT	CATTITUSCE CCGTTTTAT GTTATCCAG CTGTTTCTGA	1020 1140 1200 1260	
	ATGGAGCAG GATGCTGTAT TTTGACCCCA TAGGCGAGAT TAATGTATTA GACTTGCAG GAGCTTGCAG ATAGATGTGT	ATCCCOAL TACAGGCAT ATCCCAGA AGCCGAAA TAGCCCAAA TATCTCCT TATTCTCCT TATTACTCC	ACTATAGE TGGATTTEC GGTGACACAC CAGATATEG TGGTAATET AGTGATGAA AGAATACT TCGATAANAA	ATACTICTICA ATATTAAAA ATATTAAAT TOCTOCATO GANTOTTICT CATGTOCAAT	CAGGAGTTGA GTAACAGCTG AAATCTAATA TTCTGTGACT GGAATTCTTC AGGTGAGAGA	1320 1380 1500 1500 1620 1680	
8eq ID NO: Protein Acc	8eq ID NO: 189 Protein sequence Protein Accession #: NP_002416	. 8equence P_002416					
HILATLVLLC KIQGMQKFLG PDLPRDAVDS HAYPPGPGLY HAYPPGPGLY RELAQPRLS RGEYLEVENS IRGNEVQAGY PRLIADDFPG	11 	11 	11 DIAQQTLEKY TYPENGHESS TYPENGHESS TYPANELGH PLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS TPLVPTKSVPS	HERDORGE PPGMPKMRKT PANKEHGDPY GGENGARCTO ATENMBEDTW PAADKYMRED RMVTHILKSN	S1   RRKDSNLIVK   HLYRIVNY   SFDQPOHSLA   RALFFLINY   RALFFLINS   RALFFLINS   RALFFLINS   RASSHOOF   RASSHOOF   RASSHOOF	60 1120 1120 240 360 413	
Seq ID NO: Nucleic Act Coding sequ	Seq ID NO: 190 DNA sequence Mucleic Acid Accession #: P Coding sequence: 11409	uence #: NM_002421. 09	21.2				
ATGCACAGCT CCAGGGACTC TACTACAACC GTTGAAAAAT GCTGAAACCC	11 TTCCTCCACT TAGNACACA TGAGGAATGA TGAGGCAAAT	11 	31 CTOTTCTOGG GTGGACTTAG GTTGAAAAGC TTTGGGCTGA AGATGTGGAG	41 	S1   ACACAGCTTC CCTGGAAAAA TGGCCCAGTG GAAACCAGTT GGCTCAGTTT	1120 1180 -	

:							
٠,	WO 02  orchologo  racacceso  racacceso  racacceso  crecreso  ounacceso  ounac	(086443 Addranace ATTTCCAG TOAGGAG TOAGGAG CTTTCAG CCACAATT	TOCTOORIA AACASTTONO AACASTTONO TOTTORAGA AACASTOTTONO CAANANATONO CONTICTNO	CAACACATC GAACACATC AAGTCTCT AAGTCTCTT AAGTCTCTT AATTGAAGGG	TOACCTACAG TOACCTACAG MOODICAAGC TTAATOGACC ATGCTCATTT GTGTTGCOGC CTTTGATGA	CTTCCAACTC AGACATCATG TOGAGGAAT TOGAGGAAT TOATGAAGATC CCCTAGCTAC	000000000000000000000000000000000000000
10	ACCTTCAGES GRACGTTCCC AAGCTAACCT TTCTACATGC TGGCCACACGC	OTGATOTTCA AAAATCCTOT TTOATGCTAT GCACAAATCC TGCCAAATGG	OCTAGETCAG CCAGCCCATC AACTAGGATT CTTCTACCGG GCTTGAAGGT	GATGACATTO GOCCCACAA COOCGAGAAG GAAGTTGAGC GCTTACGAAT	ATGGCATCCA CCCCAAAAGC TGATTTCTT TCAATTTCAT TTGCCAACAG		280 840 960 1020
15	CCCAGGACA CCCAAGGACA CTTTCTGAGG GATGAATATA GGAATTGGCC	AAGGAATAA TCTACAGCTC AAAACACTOG AAGGATCTAT ACAAAGTTGA	GTACTOGGCT CTTTOGCTTC AAAAGCTAC GGATCCAGGT TGCAGTTTTC	GTTCAGGGAC CCTAGAACTG TTCTTTGTTG TATCCCAAA	AGAATGTGCT TGAAGCATAT CTAACAAATA TGATAGCACA GATTTTTCTA	ACACOGATAC CCATGCTGCT CTGGAGGTAT TGACTTTCCT TTTCTTTCCT	12000
20	AATAGCTGGT Seq ID NO: Protein Ac	TCAACTGCAG		ACGAAGAGAA 112.1	TITIONCICI		987
25	1 MHSPPELLLL VEKLKOMGER YTPDL/SPADY LAMAROPORD TPSGDVQLAQ	11 LPMGVVSHSP PGLKYTGKPD DHAISKAPQL IGGDAHPDED	21 	11 	41 YYNLKKIDGRQ VLTEGNPRWE ISPYRGDHRD GRSLGLGHST KLTFDALTTI	S1   VEKRRNGGPV OTHLITRIEN MEPPOGPGGN DIGALMYPBY RGEWRFRGR	25 65 65 65 65 65 65 65 65 65 65 65 65 65
35	PYMRINPPYP PMDIYSSPOP GIGHKVDAVP Seq ID NO: Nucleic Aci Coding seque	EVELMPISUP PRTUKHIDAA MKDGFPYFFH 392 DMA sei id Accessioi	WPOLPNGLEA LSEENTGKTY GTRQYKPDPK GTRQYKPDPK Uence 8: NM_0024	AYBPADRDEV FEVANKYHRY TKRILTLOKA 21.2	RPKGNKYWA Deykarhodo Nbwencrky	уосолуциор Тркитанорр	420
40	ATACACACT CCAGGACTC	11 	21   	11   CTOTTCTGG GTOGACTTAG	41 	S1 ACACAGCTTC CCTGGAAAAA	9 8 8
45	OTTOAAAAT GCTGAAACC OTCCTCACTO	TOMOCAAT TOMOCTOAT AGGGAACCC ATTTGCCAAG	OCAGGAATTC GAAGCAGCCC TCGCTGGGAG AGCAGATGTG	TTTGGGCTGA AGATGTGGAG CAACACATC	ANGTOACTOO TOCCTOATOT TOCCTACAO TOACCTACAO	GANCCIONT GACTCAOTT GATTGANAT CTTCCAACTC	
. 20	ATATCTTTTO CTTOCTCATO GAAGGTGAA	TCACACCTCT TCAGGGGAGA CTTTTCAACC CCAACAATTT TTGGACTCTC	GACATTCACC TCATCGGGAC AGGCCCAGGT CAGAGAGTAC CCATTCTACT	AAGTCTCTT AACTCTCCTT ATTGGAGGG AACTTACATC	AGGGTCAAGC TTGATGGACC ATGCTCATTT GTGTTGGGGC CTTTGATGTA	AGACATCATO TGGAGGAAAT TGATGAGGAT TCATGCCCTC CCCTAGCTAC	25655
55	ACCTTCAGTO GGACGTTCCC AAGCTAACCT TTCTACATOC TOGCCACAAC	GTGATGTTCA AAAATCCTGT TTGATGCTAT GCACAAATCC TGCCAAATGG	OCTAGCTCAG CCAGCCCATC AACTACCATT CTTCTACCCO GCTTGNAGCT OTACTGGGCT	OATGACATTO GGCCCACAAA CGGGGAGAAG GAAGTTGAGC GCTTACGAAT GTTCAGGGAC	ATGGCATCCA CCCCAAAGC TGATTTCTT TCAATTTCAT TTGCCAAGA	AOCCATATAT ATGTGACAGT TAMGGAGA TTCTGTTTC AGATGAAGTC ACACGGATAC	9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
. 09	CCCAAGACA CTTTCTGAGG GATGATATA GGAATTGGCC GGAACAAGAC	AAACAACTC AACAACTCAT ACAAAGTTCA ACAAAGTTCA	AMAGETTC GGATCCAGT TGCAGTTTC TGATCCTAAA	CCTAGAACTO TTCTTTGTTG TATCCCAAAA ATGAAAGATG ACGAAGGAA	TOAGGATAT CTACOAATA TOATAGGACA GATTTTTGTA	CUATGCTUCT CTGCAGGTAT TCACTTTCCT TTTCTTTCAT CCAGAAAGCT	
65	AATAGCTGGT	TCAACTGCAG 393 Prote	8 9				
2	2	cession 11	NP_002412.	-	5		
. 22	MISPPLILL VEXLXCHORF YTPDL-PRADV LAHAFORDPG TTESDWQLAQ TYSSTOP PYMRINPFYP PXD1YSSTOP	LPMCVSHBP PGLKVTGKPD DHAIBKAPGL IGGDAHPDED DDIDGIGAIY EVELHPIBVP	PATLETQEQD AETLKVAKQP WENVIELTET ERWINNFREY GREGNPVOPE WPOLPHOLEA	VOLVORTLER RCZVPDVAGF RVSBOGADIA RVHRVAGAL GPOTFRACOS AYEFADRUEV	TYNLKNDGRQ VLTEGNPRE ISPVRGDRD GHSLGLEBST KLTFSLGLEBST RFXGGRXTHA DEXXESSOPE	VEKRONSOPV OTHLTYRIEN NSPPODOGN DIGALAYPEY RGENNFYDR YRDM KANDYP	200000000000000000000000000000000000000
80	GIGHKVDAVP	HIGGELLER	<b>ОТ</b> ЯQҮКРОРК	TKRILTLØKA	HEWFINCARN		
88	Seg ID NO: 19- Nucleic Acid a Coding sequen	No. 194 DNA sequenc Acid Accession N: sequence: 11506	nence 1 #: M_014331 106	331.2		•	
	<b></b>	<b>=</b> -	<b>1</b> 2-	- -	<b>;</b> _		

WO 02/086443 AGRICAN GOLANGETT TOLANAGA MAGMALTO COMMOTTE OFFTECKA AGRICANT TRANSMERT TRANSMERT TRANSMERT TRANSMERT TRANSMERT

WO 02/086443

MANAGOLATE ATTECTED GOOGNACT MOUNTED CONTENTED GOOGNACT MOUNTED CONTENTED GOOGNACT TITALANGA CONTENTED GOOGNACT TITALANGA CONTENTED GOOGNACT TITALANGA CONTENTED GOOGNACT TITALANGA CONTENTED GOOGNACT TITALANGA CONTENTED ANAGOLATE MATERIATA ANACOLATE TITALANGA CONTENTED ANAGOLATE ITALANGA CONTENTED ANAGOLAT TITALANGA CONTENTED ANAGOLAT TITALANGA CONTENTED ANAGOLAT TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANGA TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA CONTENTED TITALANA TITALANA CONTENTED TITALANA T	second and and and and and and and and and a	
TOGGETHER TOGGET	BAGGGAGTC TCCATTATCA TTGGCACCA 00000TTGCTC CADALOGOS GCACTTGGCT 0000CTGCTC CTATTTGGAG TGGGGTGGATTAT TTTTGGAG TGGGTGGAA CTCCTCATA TAGGCCTGG	
ANDOLINE ANDOLINE CECTICACO CONTACTOR CECTICACO CONTACTOR CECTICACO CETICACO CECTICACO CETICACO C	истистите изтаком потименто изтамите соссоване системи столисто отсетии соссоване системите имеетто смаетска соссоване изобаеты тимого месоми массия изтатаме сотпессы сестития	
ATTITITION AND ATTITITION AND ATTITITION AND ATTITITION AND ATTITITION AND ATTITITION AND ATTITITION AND ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION ATTITITION AND ATTITITITION AND ATTITITION AND ATTITITITION AND ATTITITION AND ATTITION AND ATTITITION AND ATTITITION AND ATTITION AND ATTITI	TOGETOGETT INCCPOACT TEGENACIA AGAGEMAN CCTECANIN TOTANTICA TOGECATEG CACCUTTOG CTACTITAGA ACCUTANTO CTOGEGAGG COTOCTITCA TETRAGES CATAGAGAM ATTACATA RESOURCE TETRAGES CATAGAGAM ATTACATA RESOURCE TETRAGES CATAGAGAM ATTACATA RESOURCE TETRAGES ATTACATA CONTICOLO TETRAGES ATTACATA ATTACATA	
ATTATTATA ATTATTATATA ATTATTATA ATTATTAT	WANGSTER, CITCURAN INTELLEGY BATCHTON GETTTAM TECTPORT TRECAGAN BATANTOT CETTTAM TECTPORT TRECAGAN BATANTOT ANTINCTI CRANGAM GOCCURAN GENESTRAT MATTANT TRECAGAN COCCURAN GENESTRAT CRASCAGATTE ANGESTRAT FITECTRACA ANGESTRAT BATCHTOTOT KITANTAN GROATREAT PROPERTY	
NATIONARY NATION	NTTATATO GROUGANG CROSTOST TRONTANT TRYSOLATA NATIONAND TRYSCOLAN RANGTANG ATCTIONA ATCTIONAL OGGODACIC MANTAGON GECTAGNA ATTIONAL TOSTOSTANA CANAGOAN	
TOLANDAMA TOLANDAMA TOLANDAMA TOLANDAMA MODITICATION MOTITICATION MOTITICATION MACTORION MACTORION MACTORION MACTORION MACTORION MACTORION MACTORION MACCORION MACCORI	TITAGOAN ATTOALGATA OTGOTIAGO CONTINICA ATGOSTICOS CANTESTOS COGOLAGOA CANAGACTA GACATTACT ATGOSTICA COGOLAGOA ACCITOLAN TOALGACTAS CATTOTOTOS INGOTITAGO ACCITOLAN TOALGACTAS CATTOTOTOS INGOTITAGO ACCITOLAN TOALGACTAS CATANAMA	
MACCACAN MACCACAN MACCACAN MACCACAN MACCACAN MACCCAN MACCCAN MACCCAN MACCACAN MACCACAN MACCACAN MACCACAN MACCACAN MACCACAN MACCAN MACCAN MACCAN MACCACAN MACAN MACCAN MA	ARKOTECH GATRATOGE ABAGGAGA POETTECET TAGATACEA TITAGATAG SAGACTITA AKOLAGAT ARTOGGATT POTACTOTT ATGAGACAC TECAGGAGT PATRATOGA TITATAGA	
CHAITTICTCOM CHICKTONIAN CHICKOTTAN CHICKOTT	PARTCCTCA TRGALCAC CACCTOTTC ACTAITACT MACATATO ATTENDACE TRANSPACE	
MACCOCTAGO TOLOGICATION TOLOGIC	ITTECTATION ANAMENTA ATTECTED TAMANTATE TITAATTAO ANAMENATA TATTAGAN ANAMENTAGAN ANAMENTAGAN ANAMENTAGAN ANAMENTAGAN ANAMENTAGAN TAMACHTAGA ANAMENATAGAN TEMACHTAGA ANAMENATAGAN TEMACHTAGA ANAMENATAGAN TEMACHTAGA ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ANAMENATAGAN ATTECTAGAN ATT	·
111 111 111 111 111 111 111 111 111 11	INCORPORATE CONCESSION STATEMENT STA	
HINDER CONTROLL OF THE CONTROL OF TH	sequence p_055146.1	
196 DWA se ance: 57 11 11 12 12 13 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16	131   131	
11 CCCCTGGG CCCCCTGGG CCCCCTGGGGCCC CCCCCTGGGGCCCC TTGCTGGGGGGGG	Pance	
SCTTICTOGO CCCCCTGGGGCCTA TCAGGGCCCTA TTACTGGGGGC TTTTTCGGG TATTCGGGT TATGGGCTCT TTTCACTAT	11 41 41	
NCTOTOCTCT TTTCACCTAT	CHOROLITACE CHARGESCEN CORCINECTOR TRACKELATOR 119 CHOROLANTA CHOROCOGNA CHARCENACION 110 CHECHARITA GENERACIONA GENERALIZACIONI 110 CHECHARITA CATRICANO CHARCENACION 110 CHECHARITA CATRICANO CHARCENACION 110 CHECHARITA CATRICANO CHARCENACIONI 110 ATAMAMAMA TIECCOMAMA TIECCOGNA THOROCOGNI CHARCENACIONI 110 GENERACIONE GRANCENCIA THARAMAMAMA TIECCOMAMA	
	TOCOCACCA AGAMATICE ATCATITIOE TACAGICCA, OCCATITIO COCATITIO AGAINCANA ACTOCACITI OTTACITO AGAINCANA ACTOCACITI OTTACACACA	

120 1020 1020 1020		120		;	70000	29288	200000	20000		1120 120 120 120 120		120	2000	2002	840 840 840 1050
CCMAGCTTC TTANTATORCA MAGTCCTTT GTCTACCATT ATATAMAGC ATA		51 RYYYDRYTQB EXYPPULGSM VTRYYPUPRY RKKQP		<b>16</b> _	CAGTCATGT CCTGATCATC CCTGGACATC CTGGACATC TCCCCTGAC	CIOTCACCCC CITCOTCTOS OTACCCCCTO CCACCACOM GACCOTOTTC	GOCGGGGGG CAGAGGAG GCCCAACCAG CTACTTCCGG	GOTOCTOTOC TOCOCTOTOC GOTOCTOTOC GOTOCCCOA GAACCAGCC		B1 TIRVTQVLQK HTFLPEACBY LPAMJTBYPL YLVVLLEVAP TLAVCWHPWQ PRRVVQVLC GTPQSRAEPQ		51   TTCTCTACTA CTTOGCTCAT	CTGTGGACAG AATGAAAGGC GGGAAGCCACC AAAGGGATCC	TATCCUTAGA CATGATTAAT GTATAACAAT TGCTCGAATC	ATTENCACTE ANGOTTENTO TETECRATOT ANTIGNANTA
AAAGAAGATG TTAAACATTC ATCTGAAGAA TTATTAATAC TCAAATGTGA AATGCATAGG		41 DYGPCRALLL BYDDQCEGST PYDEGLCSAN LRFASRIRKI		<b>4</b> _	TCATTGATCA TCACCCAGOT TCACCCAGOT OTTOGCTTG TCATCTGGAA	ACATCGCCAT TGCTCATTGG TGGTCACTGA CCAGCACCCG CCAGCACCCG	AGGCTCGCT GCAGGACCGC TATGCTGGAT GGACGAGGTC	TOTAL CATACA TOCACOTACA TOCACOTACA ADACCACOC ACTCACOCAC GA		41 		41 	AAAAGTCCAT GAATGGAAGG TGGGCATCGT AGATCGAGGG	TACATAGTCA TTCCTTCAAT CTGTTAATTG TCATTGACCG	ATGACCTTIC GAGACCOTCA GTGTCCTAGA TCTTAAATAC AAGGAAATAC
TGAAAAGAA AGAAGCATT TTATGOTTOT TCACCAGTTT TAGCTGCTAT GAATTCCTGATT		31 	1508.1	<b>8</b> –	ACCATOOOAA ACCATOOOA CACATOOTOA TTCTACACCA	CAGOTIANGCA CAGOTIANGCA CTGTTTGCCA TGCNACCTCT ACCAACCTCT	AAAAGCAAA AGCAACAAA ACATTGGCG AAGCACGACT	CCOTTOCCA CCOTTOCCA CCOTTOCCA CCOTTOCCA CTAGAGCCA CATGAAGTTT		11 ITLILOYLII PYSIIMPLT OVKLLIGFVM FINLSSMYVP GEESKTARQ PLEASERTAH PLEASERTH	006475.1	ATTCCCTTT	AACTOGTATA OCTTATATATA TATOGCACTC CTGAGGGAGG	TOOGACACT CTOANTOCTT GCCATGATTA GCCATGATTA OTTOTCCATG	GAAGGAAAA GCCCTTGGAA CTTCCACGAG AAGTACCACA GAGACGCTGG
GCAAAACTT AAAATTCGA TTATTTGCT GOTUATTTA TATATALAC TTOTGAAAC TTOTGACT	n sequence NP_006819	21  - LGDAAQBPTG ACDDACHIB DEATCHGPCA REDCKACAK	squence 1 #: NM_001 161	12-	GGGCAGTGAC CTGGATCAAA GAACAGCGTC GGTGACAGAC GCCCATGGAG	GACGETCAGE GOGACCTTGE ACTGECETTG GOGTETCACT GTECATETGT	OCCANCCC OSCCANCCC	CCCCACCAC CCCCACCAC TOTICCACCAC GATTITCTIA TCTCGAGTCA	in sequence NP_001499.1	21   PEFEVATMIK LVFLIGMPHE PRYKAVEGPC QPETSHMSIC AYMILLEPSE TTDBARFYGR NSAARMORD		ACTCAAGATG TATAAACGCC	CACTTOTANG MIGTIGGGT TOACCATOTT COCCTCAAA	TANTGAGGT TOTTGAATTA CTTAAAAAA TTATCCTAAA	MANCHICATT CATATTEGAG TITTGAGAAA AGCICTTATG AGCACTCTT
()86443 ACOTOCATOT TAGANTECOS TETTATOGE ACMATENT TOGATTATT OUTCACTO CACTOMATENT	NO: 197 Protein n Accession #: NP	11 	NO: 398 DNA sequence Acid Accession #: NM_001508 sequence: 11361	<b>=</b> _	CCAGCCTCCC AGOTOGCCAC OCCTTCTGOO TGCAGAAGGA TCATCGOCAT ACACCCTGTC	TOCACOTOCT AGGCTOTOCC CCCTGOTOGC CCAGCCACO CCTCCAATAT	ACATGATGCA COCAGCTGAG TCCTGAGGCT TCATGGCTGC	ACCOGECACY ACCOGECACY CCCCCCCTT GAACTGAGA ACTCATTGAG CAGAGAATGAG	Beq ID NO: 199 Protei Protein Accession #: 1	11   CSOIIDHSHV HAVSLACSDI PERYIAICHP CARSSTRHEE KKSOKGSLAGG KHDWTR SYFR EKRLRVHAHS	No. 400 DNA sequence c Acid Accession #: NN sequence: 28.,2338	11 	AATACTTCAG TTTTATATOA TTTTGCCCAT GCTATTCTGA	TTGCACCGAG GCAACGTGAA TGACCAAGGA TCATTAACCA ACCAGATTGC	CCTCMATTCA TCACATCAGA CCAATGAGGC TGGCTTCCGA TTATGGGAGG
WO 02/086413 AGATTACCA AGATCATAT ATTACTATATATATATATATATATATATATAT	CC Seq ID NO: Protein Acc	1 MODARPIGLE CROFLYGGE TCEKFFGGC RTCDAFTYTG	Seq ID NO: Nucleic Aci Coding sequ	<b>-</b>	ATGGCTTCAC CCCGAGTTTG TTCGTGATGG AAAGGATACT TTGGTGTTCC	GCTACGCTGC TCAGCTGCGG GTGAACGTGC CAGCCCGAGA	ATOTOCTODA ACCOROCTC ACCATCATCT ATTCOGAGGA		Beg ID NO: Protein Acc	1   MAGPBLPGSD   KGYLGKEVTD ATLLHVLTUS VNVPSHRGJT NCWNWQVLM TRR HUAANZ CREBLGHANH GREBIGHANH GREBIGHANH GREBIGHANH	Seq ID NO: Nucleic Aci	AACAGAACTG TTGCTGCTTA	ACCAMANGA AAANCGACTO TGCCCAGCAG ACAACGCAGC		CAAATTGCTA OCAGCTGCCA TTTGCTCCCA GGAQACAAAG TCTGAGTCTA
8	0	51 5	3	22	30	35	40	. 54	કે	55	9	92	75	80	82

333

9
2
ń
=
3
ŏ
1
⋍
Ù
حَم

	1							
	WO 02/086443	<b>m</b>						
	GOATOTOACO GTOACAGTAT	-	AACAGTAAAT	GGAATCAAA	TOTTOMOCIA	AAAQQATATT	1080	
	STOACAATA ATGOTOTGAT	_	CCATTTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCAAA	1140	
	CANDITIATED AGCTGGCTGG	_	ANACAGCIA	ACCACCTTCA	COGATCITOT	GOCCCAATTA	1200	
	OCCUTOCCAT CTGCTCTGAG	_	DECADATODA	GAATACACTT	TOCTOOCACC	TOTGAATAAT	1260	
^	GCATTITCTO ATGATACTCT		CAGCATGOTT	CAGCGCCTCC	TTAAATTAAAT	TCTGCAGAAT	1320	
	CACATATTOA AAGTAAAAGT		TOGCCTTAAT	CAGCTTTACA	ACCCOCCAAT	ACTGGAAACC	1380	
	ATCGGAGGCA AACAGCTCAG		AGTOTTCOTA	TATCGTACAG	CTOTCTCCAT	TOMMATTCA	1440	
	TOCATGOAGA AAGGGAGTAA	_	CCAAGGGAGA	AACCOTGCGA	TTCCCATATT	CCGCGAGATC	1500	
,	ATCMACCAG CAGAGAAATC	_	CCTCCATGAA	ANDTTANAC	ANGATAAGCG	CTTTAGGACC	1560	
2	TTCCTCAGCC TACTTGAAGC	-	TOCACACTTO	AAAGAGCTCC	TGACACAACC	TOGAGACTOG	1620	
	ACATTATTTO TOCCACCAA	•	DATOCTET	AAGGGAATGA	CTAGTGAAGA	AAAAGAAATT	1680	
	CTGATACGGG ACAAAATGC	-	TCTTCAMAC	ATCATTCTT	ATCACCTOAC	ACCAGGAGTT	1740	
	TTCATTGGAA AAGGATTTGA	•	ACCTOGATOTT	ACTACATT	TAMBACCAC	ACAAGGAAGC	1800	
	AAAATCTTTC TGAAAGAAGT	-	AAATGATACA	CTTCTGGTGA	ATGAATTGAA	ATCAMAGAA	1860	
2	TCTGACATCA TGACAACAAA	⁻.	TOGGOTANT	CATGITGIA	ATAMACTCCT	CTATCCAGCA	1920	
	GACACACCTO TTOGAAATGA	٠.	TCAACTGCTO	DAMATACTTA	ATAMATTAMT	CANTACATC	1980	
	•	٠.	TAGCACCTTC	AAAGAAATCC	COSTGACTOR	CTATACAACT	2040	
	ANAITATAA CCAMGITOT	_	DOMACCANAN	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100	
	ATTATCAMA CTOMAGGACC	_	CACACTAACA	AAAOTCAAA	TTGAAGOTGA	ACCTGAATTC	2160	
25	AGACTGATTA AAGAAGGTGA	-	AACAATAACT	GAAGTGATCC	ATGGAGAGCC	AATTATTAA	2220	
	MATACACCA AMATICATTICA	-	TOGAGTGCCT	GTGGAAATAA	CTCALABAGA	GACACGAGAA	2280	
	GAACGAATCA TTACAGGTCC	-	TOWATANA	TACACTAGGA	TITCIACTOO	AGGTOGAGAA	2340	
	ACADAAGAAA CTCTGAAGAA	-	ATTOTTACA	GAAGAGGTCA	CCAAGGTCAC	CAMTICATI	2400	
	_	_	ATTTGAAGAT	GAAGAATTA	AAAGACTGCT	TCAGGGAGAC	2460	
25	ACACCCOTGA GGAAGTTGCA	- 7	AGCCAACAA	AAAGTTCAAG	OTTCTAGAAG	ACGATTANOG	2520	
	GAAGGTCGTT CTCAGTGAAA	-	ATCCAAAAC	CAGAAAAAA	TOTTTATACA	ACCCTANGTO	2580	
	ALTACCTOA CCTTAGAMAA	٠.	TTGTGAGAGC	CANGITICACT	TCAGGAACTO	AAACATCAGC	2640	
	ACANAGAAGC AATCATCAAA	٠.	TATTCTGA	CACAAATTTA	ATATTTTTT	TTCTGAATGA	2700	
	GAAACATGAG GGAAATTGTG	_	CAGTTAGCCT	CCTOTOOTAA	ADDATTORA	GAAAATATAA	2760	
2	CACCITACAC CCITITICAL		CTTGACATTA	AAAOTTCTOG	CTAACTTTGG	AATCCATTAG	2820	
	AGAMANATCC TTGTCACCAG		ATTCATTACA	ATTCAAATOD	AAGAGTTGTG	AACTGTTATC	2880	
	CCATTGAMA GACCGAGCCT	•	DTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAACCCAT	2940	
	TATCTCTCCA TOGGAGCTA	-	AGTTATAMA	ATAGGTGCTT	<b>GOTTOTACNA</b>	ACTITITATA	3000	
,	TCAMAGGCT TTGCACATTT	_	TATATONOT	GCOTTTACTO	<b>STANTANTS</b>	ATTITITIVE T	3060	
ટ	CACTAATT TOTACTCTCA	_	SANTOTTTOT	CATATGCTTC	TTOCATOCA	<b>EXTITITIVE</b>	3120	
	TCTCAACGT TTCAATAAAA	Ξ.	CONTENTION	GATATAAAGA	DANTTACTTC	AAATTGAGTA	3180	
	ATTCAGAAAA ACTCAAGATT	0	TANGTTANAA	AGTOOTTEGG	ACTTGGGAA			

Seq ID NO: 401 Protein sequence Protein Accession 4: NP\_006466.1

<b></b>		<b>=</b> _	<b>1</b> –	<b>#</b> _	<b>‡</b> _	- 21	
HIPPLPMPSL		LLLLIVNPIN	ANNHYDKILA	ANNHYDKILA HBRIRGROOG DNVCALQQIL GTKKKYF8TC	PINICALOGIE	<b>GTKKKYF8TC</b>	9
KINWYKK81CO		OXTIVLYECC		POYNRMEGMK GCPAVLPIDH	VYOTLGIVGA	TTTORYSDAB	120
KLREEIEGKG		BPTYPAPBNB	AWDNLDSDIR	RGLESNVNVB	LLWALKSHMI	NKRMLTKOLK	180
MUMI I PENYN		NLGLP ENHYP	NOVITANCAR	IIHGNOIATN	OVVIKVIDRVL	TOIGTSIODE	540
IEAEDDL88F		RAMAITEDIL	EALORDGHPT	LPAPTNEAFB	KLPRGVLERF	MGDKVASBAL	300
MXYH1LM7LQ		CBEBINGGAV	PETLEGNTIE	IGCDCDSITA	NGIIOWNKKD	INTERNETIT	360
IDQVLIPDSA KQVIELAGKQ		KOVIELAGKO	OTTITOUNAG	LGLASALRPD GEYTLLAPVN	GEYTLLAPVN	NAPSDDTLBN	470
VORLLKLILO	-	NHILKVKVGL	NELYNGOILE	NELYNGOILE TIGGKOLRVP	VYRTAVCIEN	SCHIBKGSKQG	9
RNCATHIFRE		LIKPAEKSLH	RKLKGDKRPS	TFLBLLEAM	LKBLLTQPGD	WILPVPINDA	20
PKOMTSEEKB		ILI RDKNALO	NIILYHLTPG	VPICKOPEPO VTNILKTTOG	VINILATION	SKIPLKEVND	9
TLLVNELKSK		ESDIMITING	IHWDKLLYP	ADTPVGNDQL	LEI LNKLIKY	IQIKPVRGST	9
PKE I PVTVYT		TKITTKVVEP	KIKVI EGSLO	PIINTEOPTL	TKVKI EGEPE	PRLIXEGETI	720
TEVINGEPII		KKYTKI IDGV	KKYTKIIDGV PVBITEKETR	EERI I TOPEI	KYTA I STGGG	BTEBTLANGL	9
QEEVTKVTXP			IBOGDGHLFE DESIKRLLQG DTFVRKLQAN	DTPVRKLQAN	KKVQGBRRRL	REGR80	

ļ		=-	<b>=</b> _	<b>=</b> -	<b>=</b> _	15 <u>–</u>	
8	ATCCAATACA	GGAGTGACTT	COMACTCCAT	TCTATCACTA	TOAAGAAAG	TOTION	9
	1100101160	GCATCATCTT	acreamene	ATTOGAGTOC	AAGGAACCCC	AGTAGTGAGA	120
	AAGGGTCGCT	OTTCCTGCAT	CAGCACCAAC	CAAGGGACTA	TOCACCTACA	ATCCTTGAAA	180
	GACCTTAMAC	MITTOCCCC	AGCCCTTCC	TOCCAGAMA	TTGAMATCAT	TOCTACACTO	240
ć	AAGAATGGAG	TTCMACATO	TCTANACCCA	GATTCAGCAG	ATOTGAAGGA	ACTGATTAAA	300
2	AAGTGGGAGA	AACAGGTCAG	CCAAAAGAAA	ANGCALANGA	ATGGGAAAA	ACATCAMAA	360
	AAGAAAGTTC	DOTTOWNOT	ANATOTOM	COTTCTCOTC	AAAAGAAGAC	TACATANGAG	420
	ACCACTTCAC	CATABILAT	TCTGTGTTAA	AAATOTTCTA	TATTAATTAT	ACCOCTATCA .	8
	TTCCAAGGA	GOATGGCATA	TAATACAAAG	<b>OCTIVITAM</b>	TTGACTAGAA	AATTTAAAAC	Š
į	ATTACTCTOA	AATTOTAACT	AAAGTTAGAA	AGTTCATTTT	AAGAATCCAA	ACCITTAAGAA	9
?	TTOTTANGO	CTATGATTOT	CTTTGTTGTT	CTACCACCCA	CCAGTTGAAT	TTCATCATGC	99
	TTANGGCCAT	GATTTTAGCA	ATACCCATGE	CTACACAGAT	STCACCOM	CCACATOCCA	22
	CTCACACAG	CTGCCTGGAA	GAGCAGCCCT	AGGCTTCCAC	GTACTGCAGC	CTCCAGAGAG	780
	TATCTGAGGC	ACATOTCAGO	AAGTCCTAAG	CCTGTTAGCA	TGCTGGTGAG	CCAAGCAGTT	940
ć	TOWATTONG	CTGGACCTCA	CCANGETTACT	STOCCATCA	ACCTICITATA	TTGAATCAGC	900
20	CTACAGGCCT	CACACACAT	<b>GTGTCTGAGA</b>	CATTCATIGCT	GATTOTTATT	OCCUPATCACC	960
	ACTOGAGATC	ACCAGTOTOT	<b>OCCUPATION ON</b>	OCCICCITIC	TOGCTTTOOA	AGCCATGTGA	1020
	TICCATCTIO	CCCGCTCAGG	CTGACCACTT	TATTECTITE	TOTTCCCCTT	TOCTTCATTC	1080
	ANGTCAGCTC	THETOCATOC	TACCACUATO	CAGTOCCTTT	CITICICICA	<b>STREACTER</b>	1140
è	CATATGCTCT	GATTTATCTO	AGTCAACTCC	THEOREM	TOTCCCCAAC	ACCCCACAGA	1200
ŝ	AGTOCTITES	TCTCCCAATT	CATCCTCACT	CASTCCASCT	TAGITCAAGE	ביייייייייייייייייייייייייייייייייייייי	1260
	MATAMACCT	TTTTGGACAC	ACAMATTATC	TTAMAACTCC	TOTAL	OCTTCAGTAC	1320
	CACATGGGTG		AACACTCAAT GGTTAACTAA	TTCTTOOTTO	THEATCOLAI	CTCCAACC	1380

HOCCORODA AGCELLIANA LALVIAGANG SESPTERISES PESERPELAB AVRAQPOLUD COPALCEGES ANTIVICAME NITSENDERIALI INVINITSESSE ANTIVICAME NITSENDERIALI MALVINITSESSE DANTIVICAME NITSENDERIA PROGRAMENTE LOCUPITAN ALIALGIALO GRENILALASI HEYLERADA ANTIVICANI SECRETARIA LOCUPITAN LANDIVICANI SECRETARIA LOCUPITAN LANDIVICANI SECRETARIA LOCUPITAN LANDIVICANI SECRETARIA LOCUPITAN LANDIVICANI SECRETARIA CACHIFORNI LANDIVICANI TENNORIZA TENNORIZA CACHIFORNI AVELUBANI LANDIVICANI TENNORIZA TENNORIZA CACHIFORNI AVELUBANI AVELUBANI LANDIVICANI TENNORIZA TENNORIZA CACHIFORNI AVELUBANI AVELUBANI LANDIVICANI TENNORIZA TENNORIZA CACHIFORNI AVELUBANI AVELUB Seq ID NO: 404 DNA sequence Nucleic Acid Accession #: NM\_006670 Coding sequence: 85..1147 \$ છ 

Seq ID No. 406 DNA sequence Nucleic Acid Accession 8:

WO 02/086443 Coding sequence: 1..927

66 130 130 130 130 130 130 130 130 130	\$40 600 730 740 740 840	60 130 340 300		60 130 130 130 130 130	460 540 660 730 840	960 1000 1110 120 120 120 130 140	1550 1560 1560 1560 1560 1560 1560 1560
1	VOCTORATE COCACATE GOCTOCATE OF GOTTTECT COCTOCACE COCACAGO COCACAGO AGACCACA COCACAGO COCACAGO AGACCACA COCACAGO AGACCACA COCACAGO AGACCACA COCACAGO COCACAGO COCACAGO ACACAGO ACACACACO ACACACACO ACACACO AC	seq in Not 407 Protein sequence  1	8eg 1D NO: 408 DNA eequence Nucleic Acid Accession 1: NM_000055.1 Coding sequence: 26.,2299	111 CITCCCCCCC COCCATOR CCCCCCCC CCCCCATOR CCCCCCCCC CCCCCATOR CCCCCCCCCC CCCCCATOR CCCCCCCCCC CCCCCATOR CCCCCCCCCC CCCCCCCCCCC CCCCCCCCCCCCCC	NOTITICACCC GASTICAGINE MATCHACAC MACCOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	стельствия аставляем тетамист осопковая коворате сымпыми ковотель обрасного сымпыми можение мунествия можением горостами еместам совитама совыется еместам совитама ковыется еместами	MATTOCKOE CRAZNECTY STATOCKOE BARBACTTO MATTOCKOE BARBACTTO MATTOCKOE CARTTOCK STATOCKOE CARTTOCK STATOCKOE STATOCKO

35

30

6

S

55

8

2

65

75

25

2

2

<u>.</u>

													•		
COPCPAGFTG ALANGOVCTD BOSPSECHER WCTVENEGO CREDINGDOX CREDINGDOX POTGREPDOAD TRANSTORTIVE VTDDDYAGFT VXLAFREGOT VXLAFREGOT VXLAFREGOT		51 CTCCAGTOTC TCTAAGTOGC TAGTAATCAA		TATACCTC TATTCCCTC ATCACATTC AATCCTCTTT TOTTCTTT OTTCTT TOTTCTT TOTTCTT TOTTCT T	TOTANGTATT CCTATATTOT AACAGGAAAA TGCTGAATGG		51      PAGOPCPRV		81 	GGGCCAATGG AGGGGGAATG CATGGAGTTC AGATGGGTTC	PERUP			B1   YNGMCLQGPA MGGLAYGIDL	Pieaityldo Ngvøriitee
ACTOTEGOOR PRINGVOLAY CORGANIZATE CORGANIZATE EDINGDACINI PRINGSACINI PRINGSACINI PRINGSACINI PRINGSACINI PRINGSACINI RESTRIVAT RESTRIVAT RESTRIVAT RESTRIVAT		41  -  -  -  - 		ACCCTGGCAC CTGCTTCAAA TTTGGGGTTT CTTTTTAAAG			41     NPRBLEKLEI		41 Adectroosac Crectoosac Georgestee Coorcestee Coorcestee Coorcestee	AAAGGAAAA AAAGGAGAAA AAGCAGTGTT ACATTTACAA		TTTANATAG MOTOTOATT OTTTCANTA ATANTTOGA ATANAMAGC		41   QLRQREVVDL GWTPNYKQCB	РИСАЕСВОРL ҮРКСОАӨТОМ
CARGREPOU CACACPOU CEACPOUT BENUDORDE BENUDORTO PREDOCEDO VANDENCE AVOYTARMOV ARPOLOLKAV QUOYTIKNE PT THOLKADA		11 	AAGGTGAGA GTTAGCAAGG TTGCTTCCAAG ATGTCAAGCC CCAAATCAGC	TANTACTOR TOTTCTCACC ATCTATCTCC			31  - TCIBIBNOPV KEMSKRSP	•101	31 	TOTTCOAGAC GOATGOATTC ACCOACTAC TOCOGAGTGT CTCACTTCOG	AGCTGAATOT TGAAATGAAT AATTGOTGCT AGGAGATGCT ATAAATGCTT	TANATGACAT TTACAGACCA ATCAGAGTG CTCTCAGCT TTTTAGAGTG		) 1   	NACCORMYPT VAIW/OTCSD
GLPBYRPLLH RCINTGROFR RGBROORCO WAGANCET RRADNCPR RRADNCPR ROADSDPA WQANPRAV	quence 1 ft MM_001565.1	21 	AATGAAAAGCA ACTGAAAAGCA ATCGATGCAG CATGGAGTAT	AGCTATTCAG TCTTAGTGGA OTACTAAGGA AAGGTATGCA		in sequence NP_001556.1	21 	Tuends 1 8: XM_057(	21 	CAGGAGTGCC TCCCAGGTCG AGTCCTGGAC TTGGGAAAAT			AAAA n sequence XP_057014	21   LLQLPAPSSA PORDGFKGEK	PBGSLRLKCR CBG1GAGLVD
/086443 Асомовият Симистим Симистим Симистим Асоромо Споріодия Взоровод Споріодия Мучидові	NO: 410 DNA sequence c Acid Accession #: b	11 	TCATTOCTAC TCAMMATTT GOGGAGCAAA CACTTCCCTA AAGGTGACCA	CATCATCCTA GGTGCTATGT TCTTCCAAGG AAATAACTAA		2 =	11   LiflTLGIQ Ekrclapesk	No. 413 DWA sequence Acid Accession #: 1 sequence: 143874	11 	CAAGGGCCAG ACACCTGGGA ACCTTTGAGG GGCATAGATC	TOSTATTICA TATTTOGACC STOSTAGGAC ACTTSTICAG ATTATTGAAG	ANAGCANG ANAGCANG GCATTATTCA ACTTACTTCA TITTTCTCT	AAAAAAAA J 413 Protein session #: XE	11   ORLROLLLL ANGIPOTPGI	mrenbalrvi Ihrtssvegi
WO 02/k FLOATWRECO N MOSEICTOWNE INTERCETORINE INTERCETORINE ENVOINTERINGE ENVOINTERINGE FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER FROATRUPER	Seq ID NO: Nucleic Act	1 GAGACATTCC AGCACCATGA ATTCAAGGAG	CONSTITUTO CONSTITUTO TOSAGOCCA TASAGCAGA COTCICCAT GITACACTAA	GCTCTACTOR OCTCTACTOR ACCTTTCCCA TCAGAATCTC	COTACANTIC CTTATTIANT TITICAGISTA TITICAGANTI	8eq ID NO: 411 Pro Protein Accession	1   HONDTAILICC BIIATHKKKG	Seq ID NO: 41 Nucleic Acid Coding sequer	1 OGGAGGGAA OGGAGGGAA OGCTGCCCG CGCTGCCCG CCCCCAAGGG	AATGTGCTTA CATTCCGGGT ICTGAGGGAA ATTGAATTAT	CTOTCAGCOT AGCTATAATT CACTTCTTCT CTGGGTTGGC TTCTCGCATC	CATCTGAATG TTAAATCTA TGGTTAGAAT GGTCTTTGT	CAACCTTAAA Beq ID NO: Protein Acc	1   MRPQGPAA8P GVPGRDGSPG	GKIAECTPTK GEPEROBTIN LPK
	15	, 20	25	30	35	40	45	20	55	9	65	0/	75	<b>8</b>	\$

2628

I LILAALQASG QQQBPLGSDL GPQMLRELQE TNAALQDVRD MLRQQVRBIT

NVPDTACVLL

85

WO 02/086443

PCT/US02/12476

WO 02/086443
Seq ID NO: 414 DRA sequence
Nucleic Acid Accession 8: XM\_084007
Coding sequence: 138..2405

승

CCCTCTTCCS A
CTTCCTCATC
CCTCCTCATC
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACCT
CACTTCACT
CACTT
CACTTCACT
CACTTCACT
CACTT
S જ <del>수</del> 

Seq ID NO: 416 DNA sequence Nucleic Acid Accession 8: 2: Coding sequence: 1:.3487

NALBAMLAYL C RMCYPPLONA C

င္ဆ

Seq ID NO: 415 Protein sequence Protein Accession #: XP\_084007

ဇ္ဗ

S

MARKLSVILI FYRYGENNSL EXHSDNDHHS I GVBASEVTST NESVSEPRKG I

WO 02/086443 сседеляте тасталост дамсталс метемет тастосма в 100

0
•
٠
٠
•
٠
3
₽
Ġ
•
1
i
•
,
L

		ATABLE AND T	TAC LONG.	ACAR LICALL	TOTAL CALLES	TACICOM	9700
	AGAATTCCTC	ATTATTCCAA	TOGANGACTC	CCTTTCTTTA	CCAACAAAAC	Terrettr	8220
S	GAGAGAAAG		TTCCTACAAC		CCCATAGGAC	CTTCCATCTO	8340
	GACTITOGCC	CTCCCCCCCCC	TCCOTTOTTO	CACACTOCOC		ATCACCCTCA	3400
	TCTTCTOTCC		MOCTTCCAC	CACAGGAGGT		TOCAGGAGGA	5520
5	CCTCCTGCAT	CCAATTCTO		GNANGCEEC		CAAGTCCCCA	5590
<b>.</b>	CCAMOCCTT	TCOTTACTTO	GACAAAGOTT	TCCACAGGAG	CTCTTATOAC	TOCOMATACC	8700
	AGGATACAAC	COTTTOAGOT	TCTCAAGAAC	COTACCTTAG	TOATACOOAA	COTTCAAGTA	8760
;	OTCTTOCTT	COGTCACCOT	GCAGCAACCT	CAATCCTAG	CCTCCCACTA	CCACCACCTC	2000
15	ACTOTOTACC	TOGGAGACAC	CATTOCATTO	CAGTOTCTOG		CCCAGCCCCC	5940
	CANATTICCI	GGATCTTCCC	TOACAGGAGG		Cranaraccc		0000
	COCATCACCC	AGRACIOANA	CAGCACCCTT	TCCATCAGG	ACAGCGTCCTT	CTCAGACAGA	6060
;	CACGTGGCGG	CACTGCCCCC	COTTATOCAC		TOGAGACAT		6180
20	CCGGGGCTCA	GCATTCACAT	TCACTOCACT		саесестаес		6240
	1000100100	COCACOGTAC	CCAGATCCGC	COCTOGCAGT	TOCTOCACOO		6300
	GARTICICCA	ACCOUNTED	CTACATCCGC		CCAMCACACA	CAGGCGCTAT	6360
į	CGTGCAGCAG	CCAACGCGGG	CATCACTEGOC	ACCTCCCCGC	GGAGGACGGA	CCTCAGOTAC	6480
2	OGAGGAACCC	TCAAGCTOGA	CTGCAGGGCC	TCGGGGGACC	CCTOOCCOC	CATCCTCTGG	6840
	Addended	CCAAGAGGAT	GATCGACGCG	CICTICAGIT	TTGATAGCAG	ATCAGOTO	6600
	TOCOTAGCTC	GAATAAGGT	TOTTOATOAC	TACGTOGTGC	TCAAAGTGGA	TOTOGERATO	6720
6	AAACCGGCCA		CAAGGAGGAG	AACGACCACA	AAGTCTTCTA	сододсталс	6780
2	CTGANAGTOG	ACTOTOTOGC		CCCAATCCCG		GAGOCTCCCA	6840
	TATGREGATE	TCARCATCO	GACACTCAR	TOTAL	TOGGGATGAG	GRACIANGUA	0000
	GACTACACCT	ОСТТТОСТОХ		DOGANGOACO		CAGAGTCAAG	7020
36	OTGGTGACAG	COCCCCCCAC	CATCCCGAAC	AAGACTTACT	TOOCOGITICA	OGTOCCCTAT	7080
દ	GGAGACGTGG	TCACTOTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
	TIGHTEET	TEATTCAGAS	AGCCCACC	TECTETGAGA	AGTATCAGAT	TACCAGAT	7200
	AGGNACAGGG	COOCACAGGA	TAGGAAGACG		ACCTICAACCT	CCAGCCACC	7320
ç	AAGATCAACG	<b>GTAACCCCAA</b>	CCCCATCACC		AGATAGCAGC	COGOGGCAGT	7380
5	COGAMCTOA	TTGACTGCAA	AGCTGAAGC		COAGGOTOTT	ATGOOCTET	7440
	CCCGAGGGG	ACATOROGRA	THEFT	IATOMARCE	TOTAL POST	ATGCATGCA	0007
	COCAACGAGG	GAGGGGAGGC	GAGGTTGATC	OTGCAGCTCA	CTOTCCTGGA	GCCCATGGAG	7620
	AAACCCATCT		GATCAGCGAG	AAGATCACOG	CCATOGCOOD	CCACACCATC	7680
3	AGCCTCCACT			ACACCCAGCC			7740
	OCCACCOMTC	TGCAGAGTGG	ACAGCAGCTG	CAGCOCTTCT	ACCACAAGGC	TOACOOCATO	7800
	accac Toacc			CTGAAGGTGG			7920
5	AAGCAGTATC		CAGCATCATC	AATOGTGAGA	CCCTGAAGCT	CCCCTGCACC	7980
2	CCTCCCGGG	CTCHOOCAGGG	ACGITICACC	TOGACOCTCC	CONTRACT	acarctoona acarctoona	
	OCCICOOTO	TTGACAGGG			AGACGGAGTA		
	STCACCAGCA	PCCCCOTGAT			GGATCACCAG		6220
3	CCGGTCATCT	ACACCCGGCC	COGGNACACC		ACTOCATOOC		6280
2	CCCAAAGCTG	ACATCACGTG	GOADTTACCO	GATAAGTCGC	ATCTGAAGGC	AGGGGTTCAG	8340
	ACACAGAGAG	ATOCOMACAG	TACARDER CONTROL	ATTOCABLE	ACT TOTAL	Camparation	0044
	AAAACAACTT		CTTCTOMAT	GTGGATTCCA	GAATGATTGC	TTAGGNACTG	8520
ç	ACAACAAAGC	-	AGGGAAGCCA	OCTTOGGGAA	TAGGAGCTCT	TAMATAATGT	6580
3	greacagrac	ATGGTGGCCT	Crogradata	TCAMOTTGAG	GINGATCING	ATCTACATT	8640
	CTITION	TACATCATOC	CAGGGGGTTC	ATTCAGGGTG	TOTOTOTOT	DACTOCAATT	8700
	TITCITCITI	TOCAMTOCC	ACTCGACTGC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
ý	ACATTCATCA	AAAATAAGCC	ATAGACATGA	ACAACACCTC	ACTACCCCAT	TCAAGACGCA	0888
3	TCACCTAGT	ATTRECTOR	TCACTTCAAA	ACTOCAGOTE	CCCCAATAAG	GATTTAGAAC	9940
	CAGAGTGACT	_	TATATATT	AATTCAGAGT	TACATACATA	CAGCTACCAT	09060
	TITATATGAA		CATTICITICS	TOGANCTCAC	TITITATATA	ATGITITATA	9120
7	TATATATIT	TTCCTTTCAL	ATCAGACGAT	GAGACTAGAA	GOADAAATAC	TITCIOICIT	9180
2	ATATAATTT	AAAAATTTC	TCTCCACCT		CASTCACCAC		9300
	CCTTCTCCAG	GAACCCTCCA			AGATTTCCTT		9360
	AACTITACAG	AATTGAATCT	ACACACACATOC	COMPANAGEC	CACAAACTTC	TCTGCAGTAT	9420
75	creectrate		AAGGTGCCTG	CTTCTTCCCC	AGCCATGAGT	CASTITISTIC	9540
	ATACTOTACA ATACTOTACA	TACACGACCT	<b>MATARTATCS</b>	TRACTOCTTT	ACTOTATETT	TAAGOTCAAT	9600
	Ca CT neg	417 Protestn	a Creamen				
8	Protein Ac		UP_056234.1				

ATTECNOSCE COLAMICTAM CEDALOGO GOCCOGO ACTACOGO GIATTAMA 6
ACCITICUM ANGONOMICA DE AUTOCOCO CONTINUE ACTACOGO GIATTAMA ACTACOCOMO GIATTAMA ACTACOCOMO GIATTAMA ACTACOCOMO GIATTAMA ACTACOCOMO GIATTAMA ACTACOCOMO GIATTAMA ACTACOCOMO GIATTAMA ACCIDIANA ACTACOCOMO GIATTAMA ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA DE ACCIDIANA ACTACOCOMO GIATTAMA ACCIDIANA ACTACOCOMO GIATTAMA CIATTAMA C sequence Seq ID NO: 418 DNA sequence Nucleic Acid Accession 8: Eos Coding sequence: 1..5001 S 

S1 | | Adiarhueri | Synklavitg | PSTPTFLDYP

| | CTPRSLAGVP A DLESLQVPVP B NULHOUMPST P

CACYVPSEVH C IPSIPDGALR D TSLRLLHLEG N NLYLOGNPWT C

PCT/US02/12476

CONCEDENT OF CONCE LKSCKBRYPP D TYGHPAREI Q PNCSIVFNOP H DXDADMLTGD E VLDCANDACI N WGNLRLAFDI M decorractic of corractic of corractic of corractions of corrections of corractions of corrections eq ID: NO: 422 DNA sequence Nucleic Acid Accession #: NM\_003014.2 Coding sequence: 238..648 MEDHINECKC L KKEGLAGLWH T BIBLLNHSCD P SCCCPRCOTO D LPOINITOLK V QLHQOMPDA M TCTUTATION OF CONTROLLING TO CONTROL Seq ID NO: 420 DNA sequence Nucleic Acid Accession 8: 3 Coding sequence: 128..1237 HCCSCCRVAK YCBAKCOKKA WP BEKYTSTPL SERHEKTED KK CHETTICHAR HOBYGOLVP SC LUMILHTBEER RKQLROQYCF SC THEFOREWAY GYGMKYGKL QL ECDANIRAB decodertro deceesand de residente descende de MACTECT DESCENDA MECTECT DESCENDA MANTANCE CITATORNA MANTANCE S <del>4</del> 

WO 0.0/086443

GENCHACCHA GORTHACHT TEACHCEAN TECHACETS ARTHUCH GORDAUAN GO

ဓ္က

<del>\$</del>

11

THE ADMENTIAL TEQUEBLOW DDISHWASS GEVUNSHOP VLETGUCKWA A STREE KEZAMONTOK GIARRALISE MAINGAGE GENESKOWA 6 STREE KEZAMONTOK GIARRALISE HALDSCHEE ANABOGERO GENESKOWA 18 STREE ANABOGERO GENESKOWA 18 STREET STREE

HOTKLITRO

PROGRAFIA

PERSATTAR

PONTENTER

sag 10 NO: 419 Protein sequence Protein Accession #: Eos sequence

ACCOCAGO STORMAN STATEMENT TREATMENS CHARGERY 1440
OSTITUTET STANGERY CANAGEAN STORMANS TREATMENS CHARGERY 1840
OSTITUTET STANGERY CANAGEAN STORMANS TREATMENT STANGERY STORMANS TREATMENT 1840
OSTITUTET STANGERY ACCOUNT TREATMENT TREATMENS TRATEMENT 1850
MANCHARD STORMANS ACCOUNT TREATMENT AMANDERS STANGERY STANGERY 1850
TANGERS TO TREATMENT STORMANS ACCOUNT AMANDERS STANGERY STANGERS ACCOUNTS STANGERS AND STANGERS AND STANGERS STANGERS STANGERS STANGERS AND STANGERS STANGERS STANGERS AND STANGERS AND STANGERS A

S

2

2

ຂ

. 9292000

Beg 1D NO: 426 DNA sequence Nucleic Acid Accession #: NN\_001474.2 Coding sequence: 37..3036

ຂ 23

20

35

92222

Beq ID NO: 423 Protein sequence Protein Accesson #: NP\_003005.1

23

ဓ္က

BC010423

Seq ID NO: 424 DNA sequence Nucleic Acid Accession 8: 9 Coding sequence: 248..1760

6

5

တ္သ

33

<del>4</del>

45

S

55 ဇ္တ

8

8

8 .

ACCECACION OF CONTROLL OF CONT

8

55

2

75

8

85

345

88

8

WO 02/086443

S

Sag ID NO: 427 Protein sequence Protein Accession B: NP\_003465

•	WO 0; ANATCANGO TTTAGCAAT	WO 02/086443 АМТСАКОВ ОАСТОСТВАЯ АМТСТСТВАЮ ТТТАВСКАТА АВВИВАВОВО ТССИМОВОВА ОВВИВАКОВАЯ ВАМАКОМОМ АВМОМЛОМ	TAMO GOACHOOLTE BOSA CHANTAMOO MGA GOCTOTGCC	TTCCAGATCC CAGAGAGAGA	TAATTOGAAA	2 2
<b>S</b>	Seq ID No. 429 Prot Protein Accession #	429 Protein sequence				
01		1 11 21 21 CENTRAL STREET OF STREET	ATAP PEGPGDRSBQ FTIM NAGKEDAGGK	41 Oxorlelont Betxdalkok Hpydlilher	51 	
15	CGEEVICEA IT EACHILPEPE RR	T HBYQYQCEQN WGBLCB: S BRETGRGAKO BYGBKBI	ILBF CTBAIGKPP HPNA KARGRVGGL	apperopovd Aogpeobbew	RTKLSRAHHO EDEQSEYBDI	••••
06		Seq ID NO: 430 DNA sequence Nucleic Acid Accession #: NY Coding sequence: 231489	NY_005940			
	1 	11   	11	41	51   	
25	TCTGCGGCCT TCTGCGGCCG	CCCCCATGC TGCTGCTGCT  I GACOTCCACC ACCTGCCATGC  AGTAGCCCGG CACCTGCCCC	TOCT OCTCCAGCOS ATOC COAAGAGGAGG	CCCCCCCTOC OGOCCACAGC	TOCCCOOCATOC CCTCOCCATOC	
30		AGGTTCOTGC TTCCCATGGC	TOCK COACCCATCT DCOD OCCCTOCIONO TOCA GOAGCAGOTO	AAGACGGACC CGGCAGACGA	TCACCTACAD TCACCTACAD TCACCTACAD	
en en en en en en en en en en en en en e		ATCGACTTCO CTCGCCCATO	ACTO GRACETTACT NCTO GRATGOGGAC NCCC CAAGACTCAC	C GACCTGCCGT C GACCTGCCGT C GAGAAGGGG	TTGATGGGCC ATGTCCACTT	
35	AGCCCATGAA GTCCGCCTTC	TACACCTTIC		ACAGCAGCCA CCAGATGACT	AGGCCTAAT	
		ATAGACACCA TCCTTTGACG TGGGGCCTCC		CCAGACGCCC GAGCTCTTTT GGCTACCCAG	COCCAGATOC	
40		CACCCACTCC	CTOT GOACHCOOC	TTCCAGGATG	CCCAGGCCA	==:
45	CAGCACCCGG	AAGAACAAGA COTOTAGACA	TOTAL COMMONAGE	GACTACTOOC ACTOACTOOA	OTTTCACC AAGGGGGCC	122
	CCTCTACTGG	MAGTITICACC	NOOT GAAGGCTCTO	THECHERAC	CATGOCTTOD	222
20	ATCITITATES GGTGGGGTAC AGCGACTGTC	CTGTGGGCAC AACCACCATG TCAGACTGGG	TOGG ACTIGACCCA CCC GAAGGGCCAC CCT TTGGCATGAC	TOTCTCCTGC GCAGGTCGTG TTAAGAGGAA	AGGGGGATGG GTCACCTGCC	1222
	GGGACCCGCT GTAGCACCAT TCCTTCCAGG	ATGCAGGTCC GGCAGGACTG GGCTGGCACT		CTOTATOCCT CTOTATOCCT CCATGGGCTT	OTCCCTCAGG OTTOTGAGGT CAGCCCTGGC	222
CC	ATCTGTCTGC ATCTGTCTGC GTTCACAGTC	CTTCTGGCTG AAATGGGGAG	TOS MATCTOTTC	AGGTCTTOOT TCCAGAATCC ACCCCAGGCC	AGGCCAAAA AGGCCAAAAA CTGGAGGCTG	2222
09	ATCCTCCAAA	GCCATTOTAA	TAC AGREGATATA	MCCTCTC	TICTUTAL	
	Beq ID NO: Protein Ac	40: 431 Protein sequence Accession #: NP_005931				
9	1	11	31	11	151  -  -	
70	PAPATQEAPR LVQEQVRQTM PPPKTHREGD YPLSLEPDDC	PASSLAPPRC GVPDPSDQLB AEALKWBDV TPLIFTSVHB VHPDYDETWT IGDDQCTDLL RGVCHLYGOP WPTVTSRPP		BOGRWEKTDL RYWKGDDLPP LGLCHTTAAK	TYRILRPWO DGPGGILAHA ALMBAPYTER PDACEASFDA	
75	VSTIRGELP QYMYYDGEKP PVPRRATDWR ABPANTFL	Pragpynrlr Vladapltel Gvpseidaap	TYPA LASRHWOGLP MAA LVHOPEKHKI NYFL RORLYWKFDP	epvdaapeda Ypfrgrdywr Vrukalegfp	Qch imppga Phpstrruds Rlvgpdppgc	
08	Beg ID NO: Nucleic Ac Coding seq	Seg ID No: 432 DNA sequence Nucleic Acid Accession #: NM Coding sequence: 202.,1563	NM_024022			
	ACCOCACC GOALAGGET CCATCTACAT AGAGGTCCTG	11 21 00 00 00 00 00 00 00 00 00 00 00 00 00	11 	41 	\$1 drandacca trectoara accodatore Accecette	
	*****	30111100	10AT 11000011	STOCKE	ALCOUNTE	•

Seq ID NO: 428 DNA sequence. Nucleic Acid Accession 8: NM\_003714 Coding sequence: 135..1041

\* 2 2 2 2

•
7
~
_
ñ
8
S
=
5
-
u
ፈ
_

WO 02/086443 спотсмето стоссметам мотятятес мятемене

	ATTROCTOTTO		ATTACCACTO	CTGCCATTGA	TOTOGRAPOCA	MATCATOMIC	750	
	TCAGGGAAGT	ACAGATOTOO	CTCATCCTAT	AAGTGTATCG	AGCTGATAGC	TCGATOTGAC	0 1	
S	AATOCCOTOC	TCCAGGTGTT	CACAGCTGCT	TCOTOGAGA	CONTOTOCTIC	COATGACTOO	000	
	GATACCTCA	GAGTGAGCTC	CTOGAGGG	CAGTICCGG	AGGAGTTTGT	GTCCATCGAT	720	
_	TOTOCCTCTO	GCCACOTGGT GCCACOTGGT	TACCTTOCAG	TOCACAGE	OTGOTCATAG	AAOGGCTAC	780 000	
•	CTTCAGTTCC	AGOGCTACCA	сстотоссоо	COCTCTOTCA	TCACGCCCCT		960	
	CTAGTTCCC	TOTTODACAA	TOCAGOCOCA	TCCCACTTGG	TOGAGAAGAT	TOTCTACCAC	1080	
S	CTCACGTTCA	ATGAAATGAT		TOCCTOCCCA	ACTICTORAGA		1200	
	CCTOTCCTOA	ACCACGCGC	COTCCCTTO	ATTTCCACA	AGATCTOCAA		1320	
•	GACAGCTGCC		CCCCTCCATG	CTCTOCGCGG	ANGAGAGGAG	OCOTIGOCOTO OCTOTOGAAO	1380	
≳	TTAGTOGGAG	COACCAGCTT	TOCCATCGGC	TOCGCAGAGG	TOWACAAGC	TOGGOTOTAC	1500	
	TOAAGAGGAA		AGCCACCTGA	OTTOCTORGO	TCATCAACAC		1620	
	COGCACCAGT	AGCAGGCCCG	AAAGAGGCAC	ACCIACCACAC	ACCETTODAG	CACCTICAA	1680	
Š	OCTOCATATA			ООЛОТСТСОС		AGGCTGGAGT	1800	
	CCTCAGCTTC	CCCAGTAGCT	GGACCACAG	TOCOCTACCO	CCACACCCAA	CTAATTTTTO	1920	
	TATITITAGE		TTTCACCATO		TOCTCTCAAA	CCCCTGACCT	1980	:
0	CCTAGCCTCA	COCTOCTITO	TOATCTTCAC	TAGACAA	AGAAGCAGCA	ACTTGCAAGG	2100	
	GCGGCCTTC		ATCTOGITIT		GTCTTGCAAA	ATTECTOACO	2160	
	CCAGCCCAGA		TOCAGTCACT	GCACGITTIC	ATCTCTAGGG	ACCAGAACCA	1280	
55	AACCCACCCT	GOCCIATITI	CATGATTACT	TTCACATOTO	GOCIAGOTT'NA TOGTOCTTOA	COTATATTO	2400	
	NAMA.			T. CAMMA	-	Nonmonous .		
9	Seq ID NO: Protein Aco	Seq ID NO: 433 Protein sequence Protein Accession #: NP_076927	n sequence TP_076927					
	-	11	ដ	11	<b>\$</b>	21		
	_	_	_	_	_	_	;	
23	MOEMDPPAVE	APPSPRBLFG PDCSGKYRCR	SPRCIELIA	POADAVAAQI RCDOVSDCIO	LELLPLKFFP GEDEYRCVRV	CCONAVLOVE CCONAVLOVE	120	
	TAASHKIMCA	DOWKGHYANV REDCASGHVV	TLOCTACOHR	VESDNLRVES RGYSSRIVGG	LEGGFREEFV	GABLOPOOK	200	
ç	LCGGSVITPL	MITTANHOVY AGPLTPNEMI VERVYGOTTE	OLYLPKSWTI OPVCLPNSBB DEMICACYLF	OVICE VIELEDIA NP PDGKVCNT	PAPSHLVEKI GOMGATEDOG GODI VITARE	DASPVLNHAA	360	
2	OIOCAEVNKP	AKENTANTE BEL	DWINEQUERD	LKT	GGPLACUERR	LAKENGAIBE		
55	Seq ID NO: Nucleic Ac Coding seq	434 DNA id Access uence: 97	sequence ton #: NM_000493	493.2				
		11.	<b>z</b> .	11		81		
5	CACCTTCTGC	ACTOCTCATC	i TGGCCAGAGG	AAGCTTCAGA	ANGCTGCCAA	GOCACCATCT	09	
2	CCAGGAACTC		GAATCCATCT	GAGAATATOC	TECCACAAT	ACCUITITIO	120	
	ACAGGCATAA	AAGGCCCACT	ACCCAACACC	AAGACACAGT	TCTTCATTCC	CTACACCATA	240	
4	GGACCTCGAG	GOCACCCAGO	TCCTTCTGGA	CCACCAGGAA		COGAAOTCCT	360	
3	OGRETECANO	GAGAGCCAGG GACTCCCAGG	AAACCAGGA	CCACCGGGGAC	CATATOGACC	AGGGAAACCA	480	
	CCCCCTCCAC		AGGACCCCGG		GACCCACAGG	ANTCCCTGGA	600	
2	CCCAGGGGCT	TTCCTGGAGA GATATGGTGC	AAAGGGTGCA	CCAGGAGTCC	CHOOTATIGNA	TOGACAGANA	<b>6</b> 60 720	
	GOTCCCACAG		CCCTCCTGGA	GTOGGAAAAA	GAGGTGAAAA	TOCOUTICCA	084	
	CCAGGTCCC	AAGOCCCTCC	TOOODAACOA	GCCCAGAAG	GCATTGGAAA	GCCAGGAGCT	000	
2	ATAGCTGGGC		TOCTOOCTET	GOGALACCIO	GCTTGCCAGG	CCTGAAGGA	1020	
	GATCTTCCTG		TCTGACTGGA	CCCCCTOGGA	ANGGGGACA	CCAAGGACCA	1080	
5	CCTGCAGGAT		TAGGGGGAA	AGGGGTTCCC	OTGAGACAGG CTGGGTCAGA	TOGAMACCA	1260	
2	AAAGTTGATC	CTGGAGTTGG	ACCACCTCCT	CCTAAGGGTA	ACCCAGGGTT	ACCAGGACCA	1320 1380	
	GCAAAGGGAA GCTACTAGAG		CAATGGAGAG	<b>GCTGGCCCAA</b> ATTCCAGGAT	амертоссес тесетрорге	TOGAATACCA	1500	
33	ACCGGGGCAC ACCGGGCCAC	CAGGGCCTCC	TOGCCCAGCT AGGTCCAAGA	OCCATAGOA OCCACTOTO	CTANGGOCCT	CAATGGACCC	1560 1620	
	CCCCTGGGC	CTCCAGGCCC	ACCAGGTCAA TGGGACCCCT	OCAGTCATGC CTTOTTAGTG	CTGAGGGTTT	TATAAAGGCA GGTAACAGGA	1680	

WO 02/186443

AVECTOR TRUTTICE TREATECT TECAMACTH ACCORDAN ADAMCTICE 1800

TITLICATION ANALYTIC GRANACOGO CANGOGOTH ATRACCOLDA GATRACATE 1800

TITLICATION ANALYTIC GRANACOGO CANGOGOTH ATRACCOLD GATRACATE 1800

TATLICATION ACCORDAN GATRACAGO ANTOCATE TO TRATECTOR TO ADAMANIA 2000

CACATAGOTH ACCORDAN GATRACAGO ANTOCATE TO ANALYTICE 1800

CACATAGOTH CONTROLLA CONTROLLA ANTOCATA ANALYTICE 1800

ANALYTICAT TO ANALYTICATA ANTOCATA ANTOCATA ANALYTICE 1800

ANALYTICATA TRANSACT ANALOGOM ANTOCATA ANALYTICA 2000

TATLICATA TRANSACT ANALOGOM ANTOCATA ANALYTICA 2000

ANALYTICATA TRANSACT ANALOGOM ANTOCATA ANALATOCA 2000

TATLICATA TRANSACT ANALOGOM ANTOCATA ANALATOCA 2000

ANALATICATA TRANSACT ANALOGOM ANTOCATA ANALATOCA 2000

TATLICATA TRANSACT ANALOGOM ANTOCATA ANALATOCA 2000

ANALATORY TRANSACT ANALATOCATA ANALATOCA ANALATOCA 2000

ANALATORY TRANSACT ANALATOCATA ANALATOCA ANALATOCA 2000

ANALATORY TRANSACT ANALATOCATA ANALATOCATA ANALATOCA 2000

ANALATORY TRANSACT ANALATOCATA ANALATOCATA ANALATOCA 2000

ANALATORY TRANSACT ANALATOCATA ANALATOC ANTIGOGOGO CICACCOCIC DICECTORE TAXACCOCICA ACCICACIO 6

TOCACTORIO CICACIONE GOOGOGOGO GOOGOGOGO CONTOCOCIO

TOCACOCIO CONTOCOCIO CONTOCOCIO 
TOCACOCIO CONTOCOCIO

TOCACOCIO CONTOCOCIO

TOCACOCIO CONTOCOCIO

TOCACOCIO CONTOCOCIO

TOCACOCIO

ACCAGCATT TOTGGCTGCA GCCAGGCTGCA PROJEKTSENG SENEMACILO, LILANLIANG BASAGETCHO HOLOGOWRI GPOCERITOG GRATICCES LARICCESARA MILDOGGCUP DROGOGGEP BADDIODEDGS AVETVIPEL GRATICCESS MIGGARAPET REGISTICLES GREGOROWAN PREFEURICO GRATIFINES GETSGESSENG GETARANCE CELEBRAZOPO GRATIONACHA PRIFEULICA GRATILIFAGO GETARASSESS MIGGARAPET REGISTICLES GREGOROWAN PRIFEULICA GRATILIFAGO CYLLIPPOGO CYLL ACAMCACTE
TOATCCTOOT
ACACCCTOOT TTTCCCATTA Seg ID No: 418 DNA sequence Nucleic Acid Accession #: NM\_004004.1 Coding sequence: 1..681 Seg ID NO: 436 DNA sequence Nucleic Acid Accession #: XM\_062811 Coding sequence: 1..888 OCTOTACATT OCAGGOGAC Beq ID NO: 415 Protein sequence Protein Accession #: NP\_000484. Seq ID NO: 437 Protein sequence Protein Accession #: XP\_062811 GCACGCTGCA GGCTCACCGT GGCGACATGA ATGAATTGGG GGAAAGATCT AAGGAGGTGT 55 2 75 80 82 10 <del>6</del> 45 S 8 65 30 35 2 8 25

349

923

2555

9	
_	
7	
Ň	
_	
7	
3	
n	
∍	
_	
-	
٠	
~	

MOMOGNOTO GCTACANTOL CHATTECCE ATCTECCACA TECOGCTATO GOCCUTODO GUARATEMA GOMATICAT CAMOGOGNO ATMAMAGNO MATTAMACH ATTEMACH GUARAMACC MANAGOTCO CHTCHANGC TECUTOTOTO GUACTAGIC MACHAGNA ATCHANACC MANAGOTCO CHTCHANGC TECUTOTOTO GUACTAGIC MACHAGNA TECHCONO FORFITCOL AGCONCETTE ATTAMACHT TECHTATIOTO GUACAGONO TECTCANO ROBRICTOR GAMANICAMA GCTORICATO TECCANOLOT TECHNOSIO TETTCANOLOT CACCAGON GAMANICAMA GCTORICATO TOCTAGONO ATTATATATA ATTEMACH GACTAMATH GATTAMATH TETTCATOGA MATTOMANA MACCAGATTA A

WO 02/086443

9 2 2 9 1 1 8 0 1 1 8 0

MOMOTLOTIL O MOVCYDHYPP I IKTOKVRIDS S PVSRPTEKTV F

ಣ

15

Seq ID NO: 439 Protoin sequence Protein Accession 4: NP\_003985.

2

Seq ID NO: 440 DNA sequence Nucleic Acid Accession #: XM\_061091.1 Coding sequence: 1..2481

25

30

5

33

45

	WO 02/086443 тылстварс мождестури овтистское месинствив ивсериство оитыствия мачеровая тревитавац отвичетем услуге	
S	Seq ID NO: 442 DWA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1, 3424	
10	11 11 11 11 11 11 11 11 11 11 11 11 11	
15	мостомых можения компетств оспосноять обместия птетстику и постоямых можения и можения и можения и птетстику и птетстику и птетстику и птетстику и птетстику и птетстику и птетстику и птетстику и птетстику и птетстику и и птетстику и и птетстику и и и и и и и и и и и и и и и и и и	
70	GOGNATION ACCOUNTY ANGINGTON NGDANGOON OF CONTROL ANGINACION OND ANGINETO ANGINETO CONTROL	
25	ANADORICOS CONSINCET TRESCUENTE ENTÓCICAS ENCENTER. DUETDAMA ANADORICE TRACOLOCE TRACOLOCE CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CETACORACIO CATACORACIO CATACORACIO CATACORACIO CATACORATIO CATACORACIO CATACORATIO CATACORACIO CATACORATIO CATACORACIO CATACORATIO CATACORACIO CATACORATIO CATACORATIO CATACORATIO CATACORATIO CATACORACIO CATACORATIO CATACORATIO CATACORATIO CATACORATIO CATACORATICA	
30	TETTOTION GEOGRAPHICS GEOGRAPHICS TO THE STATE OF THE STA	
35	OCCUMENTO UNIVERSITY OF THE STATE OF THE STA	
40	GOTTOACAC CANACCACC COGGTGCON TOCTOGGGGC TAGATGGGGT GOCTOGGCC TOCTOCACA AUGITAGACA TCCAGAGGGT TOCCOGGCT GOTTOCCCA AUGITAGACA TCCAGAGGAT TOCAGGCAT CTCCCCCAGA ACTUAGAGA TCCTTGGGGGT GGGGCCTGTC CTAGATGAGG OTTTGGGGAA	
\$0	CECOMBATH CENTRATION OFFICIALS AND ADMINISTRATION ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING ACCORDING TO CONTROL ACCORDING TO CONTROL ACCORDING ACCORDING TO CONTROL ACCORDING ACCORDING TO CONTROL ACCORDING ACCORDING TO CONTROL ACC	
¥	Seq 1D NO: 443 Protein sequence Protein Accession #: Zos sequence	

TO BOANTITION TECTORANA OCCOCCOSO
OCCOCATO OCCOCATO
OCCOCATO OCCOCATO
OCCOCATO OCCOCATO
OCCOCATO OCCOCATO
OCCOCATO OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOCATO
OCCOC

INTECCAMATA CITCLAGIANE MECLOGIANT DIA
COCCURATO CONTRACTOR DIA
COCCURATO CONTRACTOR DIA
CONTRACTOR CONTRACTOR DIA
CONTRACTOR CONTRACTOR DIA
CONTRACTOR CONTRACTOR DIA
CONTRACTOR CONTRACTOR DIA
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR
CONTRACTOR CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTRACTOR
CONTR

20

55

S

65

55	-	::	11	ı	<b>=</b>	53	
	 NPPPLLLEAV	CVPLPSRVPP	 SLPLQEVHVB	KETICKISM	 BIOPINCBAAV	HINTELDGSN	ø
	SVCKCSPERS	KHPATTVŒ	-	CAFOFSBTPH	LEPPLOSPST		=
9	PAVGVRPPRN	EGLHALASEP EGLHALASEP	GLPGGRNAGV RGORVLLAEG	VEDATNOLPS	KBOCDVALPS TLSSSAICSS	KOLKERGVTV ATPOCRVEAH	2 5
	PCEHRTLEM	REFACHAPON	ROBRRTLAVL	AAHCPFYSHK	RVPLTHPATC	YRTTCPOPCD	2
	RAKVPVKRPV	VPEGLEGOYQC RAVLBEDSRA	RVCVATYSRE	LLVAVPVGEY	RVDLLFLLOS ODVPOLVMSL	DGIPPROGPT	3 3
65	LTGSALROAA	ERGPOSATRT TOSPKHVMVY	SDPODLPNOI	LLTESHSEDE	VAGPARHARA	RELLLLOVGS DLVPMLD78A	9 4
	SVGPENFAOM	OSPVRSCALO	PEVNPDVTQV	GLVVYGBOVQ	TAPGLDTKPT	RAMERAISO	9
	APTLOGVOSA EVLVVGVGPV	GTALLHI YOK LEEGLARLAG	PRESELTHVAA	TADLRYRODY	LIENLOSEAK	PACKLRUNGI OPVNICKPSP	9 7
2	CHANGG CVLQ RTPP GNYREG	NGSYRCKCRD LOTENVPTPW	GWEGDHCENR	EMSBCBVCVB	QONILETPLR	HMAPVQEG88	78
27	Seq ID NO: Nucleic Act Coding sequ	Seq ID NO: 444 DNA sequence Nucleic Acid Accession #: 1 Coding sequence: 892156	25	Eos sequence			
	1    - 	11  -  -  -	21         	1)   TGAGTAGAGC	41    -  -	51    -  -	ŭ
8	OTCGCCGCTC TGTTTTCCTG		ATATCAACAT TGCCCCCATC		CAGGAAGTCC	AAGCCOTCTG	22
	AGAAACCATC	CTCTTAGATG	CAGCTOCCAG	COACOCANA	TOGTOCTCOO DOGAGCTTTO	AAAGOTCCAA	ž Š

HENTEGITHI INLIGEROR HALVALLE VERBERALA ROTRIVANO DETLIMICO E CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA IN CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA CONSTRUCTO E SANCHITA SANCHITA CONSTRUCTO E SANCHITA CONSTRUCT

Seq ID NO: 441 Protein sequence Protein Accession N: XP\_061091.1

2

73

8

8

350

351

COLATTICC, A'CLOUTET ORGANITE COCCADADOR MONTECOR MOCHAGA TOMAGARA GONTITICAM GUAGAGOS KETTECOR MARCHER TOMAGARA GONTITICAM GUAGAGOS KETTECOR DANINETE TOMAGARA GUECTECA GEOMANTO CELARICETE ATRIVITEDA CIDARDORA GUECTICAGO 83

1	2
•	3
•	3
	3
Ę	3
6	•

WO 02/086443

	LC1/030																																				
	99	720	780	640	8	96	1020	1080	1140	1200	1260	1320	1380	140	1500	1560	1620	1680	1740	1800	1860	1920	1980	2040	2100	2160	2220	2280	2340	2400	2460	2520	2580	2640	2100	2760	
	CCAGGTGGGA	CTCAGCAGGT	<b>OCTUDADOCO</b>	AGATOOTCCO	CEGTOCTOCC	CCACCTGCTA	<b>GCACATOTOT</b>	OGGAGGCTAA	TOGACAGCTC	COTTTORCO	OCAGGGAGCT	OGAOCCTOGA	AGGCGGCAGA	TOOTOGITTE	CAAGGGGGGG	AGGAGATCAC	ACCAMATOCC	ANGCCCTOGA	CTCAGATGCA	CACAGOTCOC	AACCCACCCG	OCT CAOCCOO	CCCGGCCTGG	CAGCOOTTCC	<b>COCCIDITION</b>	TOGCAGCTTA	AAGCCAAGCA	TCCTGCAGAA	AGAACCGATT	TACCCCTCCC	TOTCTGTGCC	ACTGAGGGAG	TOTCACCCAC	TACCTGCTGT	COGTCCTGAA	AGAATGTTGT	
	GTCAGGTTTC	OTOCTOTOO	TODOCCATOT		COGACCCTTG	ACCCACCTG	CAGAATOGAG	<b>DECTITIODAD</b>		TECHNOLOGY		CACCTOGICT (		CCACOTAGAG	COCONTCACO	GCAGAGCTGG	GATCTGTTCA	TGCCGGACAC	GAGAATTTTG									odcyccroco		OCAGCAGCCG :	CCTTCTGGAA	CACTATTOTO				AATOCTCGCC	900000000000000000000000000000000000000
	rocrorocog		CCTCAGCAGC			AGTOTTOCTA	OCAGCCCTGC		GOTCGACCTC	GOCCANGING		OGATOTOCCT	GACGGGCAGT	CCAGGACCGG	TOCOGGCCCA	accortacea	DOATCCTCAG	осооссуда			10001110000	CCCCTACCTA				CCGGGATTCC				GTGCAGGAGG	ATGGTGCCTA						CTAGAGGATC
	TCACTOTOTT	CCGAGCCTAG	TCTTCAGCAC	ADDITIONOC	CATGCTOGAG	OCTGONAGAG	CCTGTGACTC	ACCAGTOCCT	TOGANTOCAG	OCTTCCT000	CTCOGGCCCG	COCAGTACCA	OCCCCACCT	CCAGGACAGG	AGGATGAGGT	TAGGCAGTGA	TOOTCTACTC	OCAGCCOGCA	CCTCTGCCTC	CCCTCCAOTT	AGGTGCAGAC	TTAGCCAGGC	ATGACAAAGT	TOCTCACAGO	ATOGCATCTC	THECAGGICC	AGGACGTCCT	ccadccccrd	OTCOCCATOO	CATOGCTCCC	COCCACTGNA	CTCCCCCC	CATOCTOCT	THRATOTOT	TCTGCCACCT	ACOTTCCTTT	CAOCCETT
0,770	GAMOGOTO	<b>GCACTOGCCA</b>	ACCAACOGCC	TOCAGGGTCG	OOCUATGCCC	COCTTCTACA	TOCCCAGGCC	CTOGACGGCT	ANDCTONOCC	ACTICTOGACO	AGCGAGGACT	graceratad	recordora	GOGADCGCCA	TCACACTCCG	CTOCTOCOTO	AAGCATGTGA	GGGAAGCTGT	ATOTTOGACA	AGANGCTOTO	TATOGCACCC	CTGCGGGCCA	CTCCACATCT	<b>GCTGTGGTGG</b>	CTOAGGAACA	CTGCGGAGGC	COUTACCACC	CTCTGCAAAC	COCTOCAAGT	COCTGAGGCA	GAGAAGGCCT	AGANTOTICHG.	CAACTOCAGC.	OTTOMANA OT	OCCTATOTCA	TAGCOOCCTG	ATGCCCAGCA
CTT ZBOTCO OM	GCAGCTGAAG	DOMOCTOCAT	GGAGGATGCC	CACCICCAGAC	OCAN TTCGCT	ないないの	CAGGACCACC	TCCAGAAGGA	CTOTOCCCTO	TOCCCCACC		_			OCTCACTOAG	AGAGCTGCTC	AGGCAGCCCA	TGAGCTGCAG	CCTCOTCTTC	GAGCTTTOTO	cerdendary.	OCCUCCATO			TGCCCAGAAG			<b>OCCUPTCIAC</b>	TGGGAGCTAC		-	CCAGGTCCTT	GAGGATOTCC	MACGATGET			TOCOUTA
				4	n					2					2				6	2				40	Ç				ć	ş				36	ç		

Beq ID NO: 445 Protein sequence Protein Accession 9: Dos sequence 6

		1-	<b>z</b> -	#_	<b>=</b> -	<b>15</b> —	
;	MPPPLLLEAV	CVPLERRVPP		SLPLOEVHVB KETIGKIBAA BROOMCBAAV DIMPLEDGEN	BICHMICBAAV	DIMPLLOGSN	9
3	SVCKOSFERS	KHPAITVCDG		LDISPERVRY GAPQPSSTPH	LEPPLOSPST	<b>QOEVKARIKR</b>	120
	MVPROGRTET	SLALKYLLHR	<b>GLPGGRNABV</b>	POILIIVIDG KSQCDVALPS	KSQCDVALPS	KOLKERGVTV	98
	FAVGVRPPRW	<b>EXLHALASEP</b>	ROCHVLLAED	VEDATINGLIPB	TLESSAICSS	ATPDCRVEAH	5
	PCERRTLEM	REPACINAPOW	RUSRRTLAVL J	AAHCPPYSWK	RVPLTHPATC	TRITICAGECO	300
	SOPCONGGIC		LCPLA POGEA	VPEGLDGYQC LCPLAFGGEA NCALKLBLEC	RVDLLPLLDS	BAGTTLDGFL	960
2	RAKVPVKRPV	RAVLSEDSRA		RVGVATYSRE LLVAVPVGEY	ODVPDLVMSL DGIPPRGGPT	DOIPPROGRE	<b>4</b> 20
	LTGSALROAA	ENGPOSATRT	GODRPRRVVV	LLTESHSEDB	VAGPARITARA	RELLLIGVES	9
	EAVRAELBEI	TGGPKHVMVY	BOPODLPNOI	PRIQUELCER	ORPGCRTQAL	DEVPNEDTBA	940
	BVGPENFAOM	<b>OBPVRSCALQ</b>		PEVNPDVTOV GLVVYGSQVQ	TAPGLDTKPT	RAJMERA I BO	909
	APYLOGVOBA	GTALLHI YDK	VMTVQRGARP	<b>GVPKAVVVLT</b>	<b>OGR</b> QAEDAAV	PACKLRINGI	99
?	BVLVVGVGPV	LSECURALAG	PRESTITIVA	YADLRYHODV	YADLRYHODV LIENLCGEAK OPVNLCKPSP	OPVARCKPSP	720
	CHIEGSCATO	CHARGOCALO NOBYRCKCRD GWEGPRCENR FLRRP	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence Nucleic Acid Accession \$: NM\_031942.1 Coding sequence: 145.:1260

8

		:	=	:	;			
		==	₹_	ī -	<b>:</b>	<b>7</b> –		
CCCGAGCCCC	g	occented	OCCODETED	acacacaca	CCTGCCAGCC	OCCUPACTOC	ş	
TOCTOCTOR	t	CCTGTGGGAC	COCTOACCOC	CCGCCTGCTC	COCTCTCCCC	<b>GCTCCAAGCG</b>	120	
COGATCTGGG	R	CACCCCCCAC	CAGCATOGAC	acreaceaca	TOCCOCAGAA	AGATCTCAGA	180	
<b>GTANGANGA</b>	á	ACTTANAGA	ATTCAGATAT	<b>STGAAGTTGA</b>	TITCCATGGA	AACCTCGTCA	240	
TCCTCTGATO	2	ACAGITICIDA	CAGCTTTGCT	TCTGATAATT	TTGCAACAC	GAGGCTGCAG	90	
TCAGTTCGGG	8	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360	
<b>GCGATGAAGT</b>	b	TTCCAGCGCG	GAOTACCAGG	OGAGCAACCA	ACMANANGC	AGAGTCCCGC	50	
CAGCCTCAG	2	AGAATTCTGT	GACTGATTCC	ACTCCOATT	CAGAAGATGA	AAGTGGAATG	9	
ATTITIO	8	AGANAAGGC	TITANATATA	AGGANAGA	AAGCAATOCT	TOCAMACTO	240	
ATOTCTOAAT	ŧ	TAGAMAGETT	CCCTOCCTCG	TTCCOTOGAA	GACATCCCCT	CCCAGGCTCC	009	
GACTCACUAT	¥	CAAGGAGACC	GCGAAGGCOT	ACATTCCCGG	CTGTTGCTTC	CAGGAGAAAC	999	
CCTGAACGGA	5	GAGCTCOTCC	TCTTACCAGG	TCAAGGTCCC	<b>ODATCCTCOG</b>	OTCCCTTGAC	55	
<b>ACTICITACCCA</b>	ð	TODAGGAGGA	OCACCAAGAG	GATAAGTACA	TOTTGGTGAG	AAAGAGAAG	780	
ACCORDODATO	2	OCTACATORA	TGAAGATGAC	CTGCCCAGAA	OCCURCACIC	CAGATCATCC	9	
OTGACCCTTC	ပ္	CGCATATAAT	TOCCCCAGTO	GAAGAAATTA	CACAGGAGGA	OTTOGAGAAC	8	
OTCTGCAGCA	đ	ATTCTCGAGA	GAAGATATAT	AACCOTTCAC	TOGOCTICTAC	TTGTCATCM	96	
TOCCOTCAGA	5	AGACTATIGA	TACCAMACA	AACTOCAGAA	ACCCAGACTO	CT000000TT	1020	
CCACCCACT	t	TCTOTOGCCC	CTOCCTTCGA	MCCGTTATO	GTGAAGAGGT	CAGGGATGCT	1080	
CTACTODATC	ដ	COAACTOOCA	TTOCCCOCCT	TOTCOAGGAA	TCTGCAACTG	CAGTITICAGE	1140	
COGCAGCAA	2		TOCOACTOOD	OTCCTTOTO	ATTTAGGGAA	ATATCATOCC	1200	
TTTGGGAATG	Ę	TOCATOCCTA	CTTGAMAGG	CTGAAACAGG	MITTOMAT	GCAAGCATAA	1260	
TATCTODAM	3				THEFTETA	ANDITTOCAA	1320	
COLUMN	ţ	GAMACCITGAG	TAMMATCH	TOATGATCAG	CCTOTTTCAT	MONACTCC	1380	
AATCAAGT	4	AATCAAGTTA ATCTTAGCAG ACATGTGTT	ACATOTOTT	CTOGACCATC		ACADAAGGTA TATTGOTAGT	1440	

လ

જ

PCT/US02/12476																		•		•	٠																															•											
	GC 430						AT 960										. ~	AC 1860				٠.	2280	•	Ň.	2460	10 2580	Ā	2700	7 2760	W 2860	~	3000	3120	A 3160	7240	32	~ .	3540	3600	720	: 5	3840	0065 2	4020	4140	1200	70 4260 A 4320	4360	440	4360	C 4620 T 4680	N 4740	0987 +	4920	5040	2 5100	G 5220	T 5280	5 5140 F 5400	5460	A 5580	
Committee of the Commit	TOCH CONCATO	TTOO GOOCCACATC	NTOT AGACGAAA	ATAC ATTICTOR	TITE TOACCACT	ACAG CAAGATOT	ACTO TOCKOCTO	свою осестоския	CETA TAACAACO	CAG COTOLOG	ICAT TOCCTACA	CAG CTGCCGGTTT	COTA TOACGACG	JANG GACCCTCO	CAT CACATECAA	CAT TOOTHTON	מדד כאסכאמכיזם	COT GTCCGAGTAC	THE CHARLES	-	_		TOTAL CARDACGOGG	TO CAGGAGGG	TCA GNACGAGAGA	AND MICHOLOGY	TOWN ANCHARGAC	וככד כדפפואכפו	ATGG CATCCAGGTG	TON CANTICOATA	CAG AGTOCTOGA	COT TESCTTCAM	AGE CAMATETTO	TOO GOATGOCTOO	OCT BATGGGCOM	GCC TOTACCTOOM	GOA GACCTGGG	DAG GTAGTCTO	OCC MCCTCACAG	ככד מכבוכתספכ	MAN TONCTOTON	COC ACACOGGATO	ADD ADDONATOR	ATO CROSCOCACTO	מכב בוככבומככם	TON GCACAGAGGA	CAC AGNAGTGAG	GAA ATATAGAAAA	CAA GATGGGAAAG	TIC TOGANATOO				CCT GGCCCACCTT	TIT ATMARCTIC	CCC MCTGCACCC	AGG GAGGTCTTTC	AGT GOTCATGGAG	AGT TITCACTOTT	DAN AGTTOTOR	TCC TAMCCATTC	TIT ANGGAAAGC	
	CATOO GOODAY	TITUACITOS ATACCITIOS TICOAGOCA COCAGCITORA	ככדסס ככנססדם	CTCCA TCCATC	GOLAC GCACACTTT	CTCGG ACCGTG	CACC TCATCACTO	CCACO TACCAA	ACTOG GAMATI	ATCATCTCTO CCACATACAG	CCCATCATCA GACACTICAT	TOTOT GCCTGGACAG	COAGA CONSCOR	GOACC ATAGCOC	ATATO ATGGCCCAT	CATAACAACO TOACCOS	accre accer	CATGACGTCG ACGCTCCGT	CONTRACTOR CACACACANA	Ų	CATTACCAGE ANTACCAACE	OCCC COCCOAACT	COCCEDENTAL AGGAACGTC		Trectorage Torage	TANKE WORK	TOOT CTCAGCTGAA	OCACT TOTTCO	CNOTT CGGAGGA	SCORA CONTOCTOR	AGGCC CATGGAC	DCAAA TOCCATT		CAGCA GACCAGI	CCOTO TITICAGCCCT	CACT TOTACA	300AC CATATCAGGA	TOACC CAGCTAGGAG	CTOTA ACCAACA	JANGA GOCANGO	SCATT TCACATGGTA	TOOST GCCCCAG	SCAST CCASTAGGGC	CAGAG AGGTAAAATG	CTCAG GGATTICAGC	CTITO CTOCTIATOR	MAGG TRANSTC	JANCT GAGCACAGGG ATTC AGAGCTGGAA	MAGT GAGCCCCM	CCTG AGGTAGCTTC	FACAA TGACAGCTAG	эстта ататтаасаа этасы сыстыастас	маат амадессиас	octo creterecer	CTCTA TCTGTGGTTT	TOCCT COCTOCA	AGCC AACTGTCAGG	ICCAG GOOGATTAGT	ACOUT THOTHS	MATA TOTATTIONA	01	TIGAG TIAGGICITI	
	GAACATC ATAGTGATG	OCCACCACTTC TITE	GATTCAC TTCC	CATCAGO GACCI	ADATOGO CCOON	AACCCTC CTCC	OCCANICC ACA	THOOTETATE TITCO	AGAGCAC ATTCC	GENERALCE ALAUM	CCGGGAGCCG GCCAT	detacaeade aaga			AGGNATT CAGT	GAGCTGCCCC CATAA	AGROTTETTE GGAGA	ATCTOTOTTC CATON	TOWNER TOWNER	AATGAAGATC ATCAA	SAGCACC CATTA	CCACTOGGAC CAGAC	TOTTCACAT COCT	BOACAAA GTOGA	AGGCTOTTO TICCT	TOTAL STATE	GCCCAAGAAG CTCTTTGGTT		GGGAAGAAG TACCCCAGTT	SCITITIONS TATOR	MONTACOTC TECAGAGGCE	AAGTTO AAAGAGCAAA	OCTORACACTO CACACTORGO	GACGGTGACT CTTGGCAGCA	AGCTGCCTGG GAAGG	COOGAA ACATT	TTCAGTGGGG GTTTGGGGAC	IGGCAGO AGCCC	MATCH TACTO	CTOCCTATCC TTOCO	MOTODC AGOTT	TATCCAT GATGC	TTOAGG GGTCT	AGGANGGETT CTTGETTACA	CARCCTCTOS ANTOS	GAGOGGAGCA ATGGGCTTTG	TOCCTCTOAC TCCAAGAGG	CTCGC CTGGGATTC	TTTTAACAGA TOGGGAAAGT	TOCCCA GOCACTCCTO	AATGAC TAGAGTAGAA	GTCAGCCCAG CCTGCGCTTG	CTGCAG CTCTA	AGCTGCTGCT TAATO	AAGAGG GAGAACTCTA	CAAAGAGGC CTCCTGCT	TCCCCA GGTGG		ATGLECTICE TOTCCACGGT	CAGTICATIT AAAA	TACAGGATCT GTACATAMA	CATTITICING UTANCACAAA	
 U2/U86443	DOCTICTORO CCC	TOGGATTIAN OCC	DOGICAGIA CC	ACCCACCCAC ATA	CTTCTTCAC GGA	TOTOMOTO TO	CTTCTOOAT OCC	AMCTEGATT THE	CCCAGGITA TTC	CAAGCGGCC GTT	COCTOAAGCC CCO	0 (			NTTTCCANT TAG	ATGCCTOGCA GAO	TTACTTCCAG AGD	GGGATAAGAC ATC	GOAGAGGGC CAT		BOGCECTCAC CAD	CARCACCAT CCA	TCCTCTCGGA TGT	PRACETTICCA GAD	ACGAGGACTC AGG	CAGOOMICAG TEA		ο.	TTGAAGTGGA TGG	ACCATGGGA GGT	CATCAMGGG ANG	MOACAGGGG TCT	CONTRACTO GOVERNMENT	GOTAGACTAT GAC	CCTGCCAGC AGC	OCTOCAGOCC AAT		MAGATCCA CT	TTGGCCTTA AGG	מספטנאפאא כדפ	AGTICTORGA TIC	GOATATCCAC TOA	ACTANTOCC TAG	ACTUCATOR CAR	GONDATONGO CACK	AGTOTOGOTCA GACK	CAGGCAGCCC TGC	TOTACTICATA CTC	AAGCCTTCA TTT	AACCOGCCC AGAC	TEGANGGAA AGG	TICACTACCT GTO	GOCTCTCCT GTC		UL				AAATGACCTC ATG		TOTTICACAG TAC	TOTTATTET OTT	
O/7II OA	CCGGACOTTO	AMOTTIBOTO	CAGCAGCTOG	GOAGGTTATO	TTOGGCCACT	CTTGGCCTCC	OCTOTOTOCCA	COATCTOAGG	GCANTOTACT		GACGCCGACC	AACCAGGACC			ATAGGCCAGA	COCCIGATA	GACOTTCCGA 1	GACATOGATO			TACCTGGAGG	CTGCAGAAGG	ACATTCTCCA 1	OTCTTCOTOA C	TACTACTOGG	CCAAAGAACA	<b>OCTOTOGRAD A</b>	CATTICTION	T CGCTTACA T	CTGCAAGGCA T	GTOCTTATED C	AAGCTTOGGG	CAAGITICATO	OCCACCTOOT O	OTCCCCCAGC C	CCCCTGGGGC G		OTOCTOACAO	GAGAAAGAGC C	DATTAGGAGE 1	AGGCCCTTT A	AACAGTTCAT G	GAGAGGTGAG A	CONTINUE	TTTGCTGGGG G	ATGATGGAGA A	ATTCAGTCCC C	ADACCCTAGA T		TTGCCTCAC A	GACAAGTCCC	כדוכאכדדום ז	TOGTOCTACC T	GOTCCACCCC A			ATCACACTOG Q				OTTOTACATA T	TTOTOCOTOCT 1	
			_			_	,			_				_			٠.	_			_								_								_							_							_										_		

5640 9700 8760			22222	2 2 2 2 3	55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		8	22522		200000	200000	1200	1740 1860 1920	20000	22,000	240 2760 2760	2940 3000 3120
TTTTCGGGA TGACCANGA AGAATAAAG		15 —	DTMVNSTILM LHIGEEIDOV ANGLEGTELK NGLLIKDVVG YPOYIPKPRO SEHIPLGKPY	REPAIIRHFI SLFVGESCHV VALEGRHTSA SVFHDVDGSV MKIIKNDFPS	DNI RVGLCYP GLLFLKLKAO PKKLFGBOLK GRVVBHTSFR LKLKEOMAFV				ACOSTCTATT CCGATTOTTT AGTOCCTCT GOTATTCAGC		TTTCTAACTO CATCGAGGCT TTCAATOTTT CATGATAAAG	COCCACTOR CACCATOR CA		ACAGTCCATO CACTGCTTCT CTCCTTGTCA ATCACAGAGG	GAGGAACTO TACTCCCAG TCCACTACC AAGGACAAGC	GACCACOGG GAGGCTCAGG GATGAGGCAG CTGGTGACTA	GCAGCCTGC CCTCATTIGC GCTCATAGTC GCTCATAGTC
TAGCTGGTCC GGCATCACCA TCACTGTCAG AMMANAA		<b>#</b> _	PVRPKLTVTI QVKVAGKPMY GHIKPALGPK PGRCVTVHGB XMCKNITGDB XMCKNITGDB	PHQDADPLKP DDGSKQBIKN NIQHCTFRKF NQLDHDGDKT IQAYKTSHLR	AIMLINENKO REHYYDDEDB TERAVUDVPM IQYVVIDGNQ VLEKLGADRG		41   CAGAGOCTOG	ACCTORCANT ACTOTCTCOS GOACTTCCTC GOCCACATCC		CCTTCACCCA TOGACTTATT TGACACCTAT CGATOGCAGG	ATATICATIOA ATATICATIOA TOGGGAATAT OTOGTTICAAT GAAAGCTCAC	TOGAGITANC CTAGGACCOAA GAGGCCCAAA GGATAATGTA CATGTACCAG	ATGCTACCC CATCAOTT GGGACAGCA	TCGCTGCGTC CTCTTGGGC CTGTCTTGGC GTGCAAGATG	TOCAGAITCT CUTOGAATG CCGAGCACAT GGCCTCTGCC	CAAGAACCAG TTTCAGAGGG GCTGGGGGGA CCTGCTGAAG	ATGGAGAGT CAGTCCCCAG TGCCTTAGGG CCCTAGATGT CTAGCCCAAA
OTTGCGAAA ATTTCTTGTA CTTCAAGAAG AMAAAAAAA		<b>n</b> -	BYRVRPLCCK VLPCRBCAPN CNPPDPDTPO YIRDLBIHHT GTLLPSDRDB NP I PHHVPTO	FLBIIBARYB TLABGGTPPY RGIGLYDGPI VPPGEPGPWP ICSGCYAOMY	HWDQTAPAEL MDKVEQSYPG DCTATAYPKF GKKYPSSEDG RYVSRGPWTR VKKKL	สายของเล	31      TGCTATCGGA	ACCAGGGTCT ACCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG	ACCTOONA TOCTOCTCAC TCATTAMON OAOONGNOCT TOTATOGANG	TOAACAAAAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC TGGATGACAT		GOTTIGCTOR GOTTIGCTOT GONAGCCTOT TONACTIGGA CTGATINCTC	OCOTOGOCA TEGOGOGOCA TOGOGOGOCA TOGAGOATAT	ATACATICTC TOGGCTATAA CTTTTGACGA	ACTOTOCCOC COGOCCCTC TCTATAACAA AAACCACCOA	TCATTGCCTA ACAGCTGCCA GGGGCATTT CCTGCCGCTG	CCCACTCATO CAGAGGATT AGTOAGCTCC CTCCAGGAGA TAGAAAATT
TCTTTTTCT OTATOTANC TATATOTOCA AMMANANA	in sequence XP_051860.2	17_	ACYDRGRACR YEMYGAEERG DKCYPYRHII DERGGYDPPT DHCLGLLVKS AAAGSEETOF	TRABAKDKRP CRFADNOIGL TLPIOQNFPI AFEDVPITSR CINVPDWRGA	VYTLQKGYTI KTGVFVRTLQ ALIPKNAVS MNDFAYIKVD NSIVLWASKQ KIPQVVPIPV	. sequence sion #: Eos se [612861	21       		CCTGAGTTGC GCCAGGCAC GCCAGCTGG ATTGACACG ACCATCATT	TODACATTC GAMGGAGCT GTCATCCATT CAGTATTTGA TCTCGAMATC		ATACAGGCCA CAGGATTATA TTCCTCTGTG AGCACCATTC ATTGCCAGTA	GAGATAGACG ATGGGGGAGA TTCGATACCT GOCACGGAGC	TCCATCCATC AAGGACGTTG GAACGCAACA TCGGACCGTG	AACCTCATCA CACGTACCAA CTGGGAAAT AACGGAGTCA		OTENTIALOS CTTATGAGCA AGTOCACAGA CACAGGGGG GCTGGAAATA
086443 Gaatgettg Taggesttt Atteateaaa Aatgeegaaa	451 Proteir	<b>=</b> _	VYKKGODYR P GOTLV LABTD RNI IVMCEMB PINFHLAGOV EDOPBEKNT P ANPNINLINC	CMIIDNGVKT LRGGDVMLDS GPGGLDHSGR 6CPHWNYTGI NDWNLVRHPD	RETHYOOYOP VENELLEGTS HKGCERIKIK EBSKQHFFHL LFMYVATIPD VTLDTEDHKA	A Acces	11    - 	AGCCAGCGGG COGCTTGCC CCGCTGCGGT CACTGCCAGG	TOACCAGAGC TATCGGCCAG CTCAGAGGAA GCACATCCTG GGGCAATTTC	AMACTETE CTATTITIT ATCAGGACA AGOTETOGIC TGATGAAGGT	CAAACACTTC TCCATCATCT CCGGGTATTC TGAGTGGGTT TAAAGGTGGG	COMMANGE CONTETACE CONTETACE CANTETEMAC TACCCTEETC	CATCCGGGAG CATCATAGTG TTTCTTTGAC ACACTTGGAG	CAGGGACTC CTTGTTGATC TGGGCCGGAG CCTCCTCCCC	TOCOMOMO	GCCGGCCATC COGCGGGGAT GCTTACAGGA GGCTCAGGGA	CTTTGCTCAC GGCTTTGCTG AAGAGGTGA GGGAACTGAG GGATTTCAGA
WO 02/086443 ACCITICATE DANSIGERS OTHERSTRY AND ACTIVITY TAINTHET ATTOTATES ANTOTETA ANTOTEMA	Seq ID NO: Protein Acc			NNRAHSNYRA AYKNQDHGAM GTEMMONRIM LAFRIANNANQ SEYPGSYLTK	HPLYLEGALT ROTTPELLSD NEREKPAPCS TKOHFLEVKM NSILGOIPMO GPKGSPRPIM	Seq ID NO: Nucleic Act Coding seque	1   GAGCTAGGGC	COCCOCOGO ACTACCACT ACTCCCOOO ACAGGAACA TGCTAACCAT	CTOGOTOCC ACCATOTOCA CCATCCACAT TOCOMACCCO GCCCTTTCCA	ATOGACAGA CAGAAGAGA TCGACCCCA AAGAGATGA TTGCAGTGAA	AATTGGGAAG TGAAAGGAAA CTGCTGCTGC CTTTGTCCAG TATCTCAGAC	AGOTTOTA AGO	TGTACCTGCA TGACCTGCAA ACATCTGCAA TTAAGGCAGC	CCACATACAT GCTCCAATOO TCACGGAAGA AGTCTGGAAC	ODATOCCAA OATATTOOTT OTTATTOAA OGGCTOOCAT	AGCCCGGGA CCTGGCTICTT CCTCTGGAAT	COCCOCCEO CCTCCACCCA CCTCCACCCA CCTCCACCCA CCTCCACCCAC
'n		10	15	70	25	30	35	04	45	20	55	09	92	70	75	80	82

ø
~
*
~
≂
Ñ
8
ഗ
₽
≥
ς.
Ų
Д,

PCT/US02/12476
1210 1210 1210 1210 1210 1210 1210 1210
ADDRESSION OF THE STATE OF THE
CICKAGETA AOGUAGOGO CATATECCETO GAAGAAAG CATATECCETO GAAGAAAG CATATETOTTO ACTACETOT CHECKACATO COTTOTOTO CHECKACATO TETTOTOTO CHECKACATO TETTOTOTOTO CHECKACATO TETOGETOTO CACACATOT TETOGETOTO CACACATOT TETOGETOTO CACACATOT TETOGETOTO CACACATOT TETOGETOTO CACACATOTOTOTOTOTOTO CATATATATATATATATATATATATATATATATATATAT
GRAMABAC CRECKATA ANTICETECO CRECKENTO CRECKEN
CCCAGAN TOTOGOO TOTOGO
186443 GOMAGNAGE COCCOMBAT ANTACKTUBA COCCOMBAT ANTACKTUBA CACTACTOR COCCUTTORTO TOCOGRACIO TOCOGRACIO TOCOGRACIO TOCOGRACIO TOCOGRACIO TOCOGRACIO TOCOGRACIO TOCOGRACI TOCOGRAC
WO 02/086413  TANGARIA GAMAGINA GAMAGINA GAMAGINA MACKOCCACCT COCUTODO TO

Seq ID NO: 453 Protein sequence Protein Accession #: Sos sequence

∴ જ

		==	12.	ij.	<b>\$</b> .	51	
MCAAGRODFL	200	PKAMLTISML		TLICPPGATS TVAAGCPDQS	PELOPWNPGH	DODRHVHIGO	8
<b>GKTLLLTSSA</b>	TEBA	TWEIRIGED	GKLVIKDHDE	PIVLRTRHIL	IDNOGELHAG	SALCPFOCHE	120
TIILK	TILYGRADE	DIGPOPYYGL	KYIGVOKOGA	LELHCOKKLS	WIFLWITTHP	GGMAEGGYPP	180
BREMG	BREMCHROVI	VHVIDPREGT	VIHSDRFDIY	RSKKESERLV	OYLNAVPDOR	ILBVAVNDEG	<b>3</b> 40
SRNLC	SKNLODMARK	NITKLOSKHP	LHLGPRHPWS	PLTVXGNP88	SVEDH I EYHO	HRUBAAARVP	300
KLP	KLPOTEHOEY	FNVBLBSENV	<b>ODVENTEMPD</b>	TEN SQT KGG	EK1 SDLATKAH		360
IOAT	COATTAGGW	LOTEVATRE	ODYRFACYDR	GRACREYRVR	PLCCKPVRPK	LTVTIDTNVN	<b>4</b> 20
1112	BT I LAILEDNY	OSWKPCDTLV	IASTDYSMYD	AREPOVLPCR	SCAPHOVKVA	GRPMYLHIGH	9
BIDG	IDGVDHRAB	VOLLGRATIV	MORMBDKCYP	YRNHICMPFD	PUTPOGHIKE	ALGPKAAHLB	5
PEL PEL	TELKHICOO	LVOQYPIHPH	LAGDVDEROG	YDPPTYINDL	BIHNTPSRCV	TVHGSNGLLI	909
Š	DWGWBLD	HCP PTEDGPB	<b>ERNTFDHCLO</b>	LLVKSGTLLP	BDRDSKHCKM	ITEDSYPGYI	999
PKPR	PKPRQDCNAV	STEMMANDWN	NLINCAAAGS	RETOPWPIPH	HVPTGPBVGM	YSPOYBERIP	720
1.0KP	<b>GKPYINRAA</b>	SITTRAGMILD	NGVKTTEABA	KOKRPFLS11	SARYBPHODA	DPLKPREPAI	98
IRHP	CRHPIAYION	DIMAMLROOD	VALDSCHPRO	EAGEOFLLTO	MICAGOILLOG	DEAABGHAQG	940
PSPP	PSPPCRCLLX	LVITCSPFAH	VSLAHB				

Seq ID NO: 454 DNA sequence Nucleic Acid Accession #: NM\_013282.2 Coding sequence: 85..2466 

	۰		۰		۰	۰			۰		۰	۰	۰					
	۰	73	18	ž	30	360	420	7	3	8	9	120	18	3	Š	9	1020	
	OTOCTGOTAA AACTGATGGG GGTTTTTGCT	COOGRAGICAG	DOCOAAGATC	CHANCAGATG	CCADCTCCTG	<b>GCTCTCCGAC</b>	CCACGGCGAG	GACCIGNATES	OCCUTGETTE	CTGCAGCTCC	COACTACCC	CACCATCATC	COACAACCCC	CAGGACGGCG	TOGGATCATC	OCTTOACAAC	CONNECTED OCCUTANTE ANGUATION AGRACOACOT GARCAGACTA	
15 —	Ę			3	g	ğ	8	9	g	É		ğ			ğ	5	200	
	ATOGG	GGACCATOOA	AGGAOCTGAG	TCTACAGGGG	ATGACACCAT	TOCOL	TCCAC	TOTOGOATGA	ATGGG	GOCIACGAGCC	TGAAATACGA	COCCOCCCC	ACTACAACCC	GAGAC	TOMOGRACIO	CCCAT	2000	
<b>:</b> _	200				ATGAC	ACCAAGGAGC GGGACTCCGA	GAGTCAGACA AGTCCTCCAC	1930	OCTOGGDACA CONACATOOD	GOCIAC	TGAAA	88		ATCTCCAGGA AGCGCGAGAC	5 OVE	CCGGGTGAAG GGAGCCCCAT	AGGAC	
	<b>SOTA</b>	ATCCAGGTTC	ACCAAGOTOG	CAGAGGCTGT	GTCCGCCTGA	DOAGC	AGACA	CAGGCCAGCC GATGAGGACA	SGACA	DACGEGGAAG GECCETECE	ATTTACCAGO	GACCOTCCCAG	OTCATGCTCA	CAGGA	GATGATTCTC	DANO	ð	
<b>:</b> —		ATCC	ACCOV	CAGAG		ACCA	GAGTC	GATON	907700	9	Ě	600	DTCAT	ATCTO	GATTA	0000	AGG	
	SAGAG	CACCATOTOG		OCCAGGCCTG	CGACTACGAG	CCCCACAGC	CONOT	NOCC	CGAT	DONO	200	8	000	COGNO	0000	9000	ě	
ī-	TOGCTCAGAG	CACCA	STCCADGCTG	OCCING	GACT	8	GGGCCAGAGT	CAGGC	GTACOTCGAT	GACGC	GGAGGACOTC	GAACTCCAGG	GOCCAGOTO	CGACGCGGAG	0675576909	GATTGAGCGG	50000	
		<b>8</b> 000		T00F	Ę	ij							-		į	3	88	
=	<b>GAGCATOGCA</b>	TCAGCGCCGA	TOCACTCOCT	TCCACGTGGA	ATACCCTCTT	accromecr	<b>OCTOCTOCCT</b>	AGACTGACAG	AGGTCAATGA	TOOTCAGGE	COCCCCTOCA	TOSTCCAGAT	ACCTOGAGGT	OCTICIONIA	ACCICAACOT	ANOTETICAA	CONG	
						SA SA	ğ										9	
	COACTCCTTA	TCCCTCCCC	ACCCACACOO	SADDAGGETOT	SAGGACOCC	TCCGCCAGA	ACCCACTCCG	300000000	COCCTOTACA	SAGGCCCAGG	ACCITCCAGGC	CACAACCICC	ACTOCCAGO	NAGGAGCGG	COCONACTO	TCOTOGACG	CCCATGAGAC	
	G	6	ž	J	Ö	ь	ž	6	ď	Ö	ž	3	₹	3	ช	F	ប	
55				5	2				٠	ဥ				ç	₹			
- •					_					_				•				

WO 02/086443

autocorrea Colocolora deculadad autolocia harodolo autocorrea colocolora c ജ .8 

Seq ID NO: 455 Protein sequence Protein Accession 8: NP\_037414.1 

	<b></b> -	=-	12	11.		18
40	MAIQVRINDG YEVRIADTIQ PADEDANDET DVIYHVKYDD			HLINVEELAR KIQELENUED DIQELPYROK OMEDGHTUPD HHTERDEEL EDTDSOCCED QESEDKSETH GENARIDER VONDETNENN PROMOVENT RAMESEREC ESTSHEALEE SEDVENALNI IIMOOLEVO OVVHLENNED SPERSOFHUE	dlarlfyrgk Osesdkesth Rkaperc Ovvalayndd	I GLORLFYRGK OMEDGHTLFD SGEGNESTH GEAARSTGE KRAERDERC GSTERFLEE TVYMERYNED HERERGFHYD
45	AEISRICRETR SCHICKDDVN PECRUDASEV IPGIPVGTWM			I I FVDEVPKI LMCDECDMAP SSSORDNOKG DRSNDGAYSL		
20	SCGRDLSONK OGRNSKYAPA LGLTWQYPEG SPRRTSKKTK TPQCICCQEL	CONSIGNAR PRINCIPATE OF WATCHEROX GOTAMETAL REDDERING CANADOR SERVICES OF SOCIETA OF SOC	LTNTNRALAL VVKYMPEKOK EKENSKREEB SSLIREDKSN HNVCKDCLDR	LINTHRALAL NCPAPINDOB VVKYMPEKOK SOFLVMRYLL EKENSKREEB EOGEOOFAS SELIREDKSN AKLMNEVLAS HNVCKDCLOR SFRAQVECE	CABALDMREG KPVRVVRIVK RRDDOSPOM TKEGKDRIKK RTGGKMKKK SAGGDESRAG LKDRPASGSP PQLFLSKVES ACRYDLGRSY AMGVNGPLGT	CABAKDHRGO KPVAVNANK RRDDOSEDAM TKEGIDAIKK RTCKGKKKK BAGOOPERAG LKDRPASGSP PQLFLSKVES ACHTDLGRSY AMGYNOPLOT

600 600 720 720 720

Seq ID NO: 456 DNA sequence Nucleic Acid Accession #: NM\_001200.1 . Coding sequence: 325..1514

		<b>=</b> -	12-	Ξ.	<b>4</b> .	15.	
,	GOGGACTTCT	TOWACTTOCA	GGGAGAATAA	CTTGCGCACC	CCACTITIBOD	CCCGTGCCTT	
3	TOCCCCADCG	<b>GAGCCTGCTT</b>	COCCATCTCC	GAGCCCCACC	OCCUPACION	TOCTOCOCCT	_
	TOCCCUACAC	TONONOCTO	Treceagest	GALANGAGAG	ACTOCOCOOC	COCCACCCO	_
	GAGAAGGAGG	AGGCAAAGAA	ANGGAACGCA	CATTCOOTCC	TTGCCCAGG	TCCTTTGACC	•
	AGAGITITIC	CATGTGGACG	CICITICAL	<b><i><u>adacatore</u></i></b>	COSCONDENT	CTTAGACGGA	_
٠	CTOCOOLCTC	CTAAAGGTCG	ACCATGOTOG	CCOGGACCCC	CTOTCTTCTA	<b>acorractoc</b>	_
S	TTCCCCAGGT	CCTCCT000C	gacaccaca	<b>OCCIONITICO</b>	DOMOCTOCOC	COCAGGAAOT	•
	1000000000	OTCOTCOOC	COCCCTCAT	CCCAGCCCTC	TOACOAGGTC	CTGAGCGAGT	•
	TCGAGTTGCG	OCTOCTCAGC	ATOTTCOOCC	TGAAACAGAG	ACCCACCCCC	AGCAGGGACG	•
	CCGTGOTGCC	CCCCTACATG	CTAGACCTOT	ATCCCAGCA	CTCAGGTCAG	COSOCCICAC	•
ŧ	CCGCCCCAGA	CCACCOCTTG	GAGAGGGCAG	CCAGCCGAGC	CACACTOTO	CGCAGCTTCC	•
₹	ACCATGAAGA	ATCTTTOGAA	GNACTACCAG	AAACGAGTGG	GAAAACAACC	COGAGATICE	٦
	TCTTTAATTT	AAGTTCTATC	CCCACGGAGG	AGTITATION	CTCAGCAGAG	CTTCAGGTTT	•
	TCCGAGAACA	GATGCAAGAT	<b>ACCULTAGONA</b>	ACANTAGGAG	THECATOR	CCANTINATA	•
	TTTATGAAAT	CATAMARCCT	OCAACAGCCA	ACTICALANT	CCCCOTTCACC	AGACTITIOG	~
ž	ACACCAGGTT	OCTGAATCAG	AATGCAAGCA	GOTGOGANG	TETTOATOR	ACCCCCCCTG	•
2	TOATGCOOTG	ancrocucae	GOACACTOCCA	ACCATODATT	COTOOTOCAA	GTGGCCCACT	2
	TOGAGGAGAA	ACANOGRATIC	TCCAAGAGAC	ATOTTAGGAT	ANGCAGGTCT	TTGCACCAAG	2
	ATGMACACAG	CTOOTCACAG	ATAAGBCCAT	TOCTAGTARC	THEOCOL	CATOCAAAAC	Ξ
	<b>9504TCCTCT</b>	CCACAAAAGA	GAMAACGTC	AAOCCAAACA	CANACAGOOG	AAACGCCTTA	Ξ
6	AGTCCAGCTG	TAAGAGACAC	CCTTTOTACG	TGGACTTCAG	TOACOTOOGG	TOGANTOACT	Ξ
ခွ	GGATTGTGGC	100000000	TATCACCCT	TTACTOCCA	COGRGANTEC	centrocac	2
	TOCCTCATCA	TCTGAACTCC	ACTAATCATO	CCATTOTICA	<b>OACUTTOOTC</b>	AACTCTOTTA	=
	ACTICTAAGAT	TCCTAAGGCA	TOCTOTOTOC	COACAGMACT	CADTGCTATC	TOTATOCTOT	Ξ
	ACCTTCACGA	GANTOMANG	ANTIANTIA	MONACTATCA	GGACATOOTT	OTGGAGGGTT	=
30	gradatated	CTAGTACAGC	AAAATTAAAT	ACATAAATAT	ATATATA		

Seq ID NO: 457 Protein sequence Protein Accession #: NP\_001191.

PCT/US02/12476																																									
	120 180			120	300	120	9 7	9 9 6	200	006	1080	200	1360	1380	1500	1620	1740	1860	1920 1980	2040	2220	2280	2400	2520	0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2260	2880	000	1120	3180 3240	3300	3420	3540	3660	32.00	3840	1960	000	50	520	4380
	SI GEFELALLSH SPHTERILES INIYELIKPA			GCCCCGGCCC GCCCCGGCCC	AGGACAGCAG	TAGTTGTGGA	GACCTOTGCA	TCAGGTCAAC	TCAGCCCTGC	CATTGAATGC	CATCGATCAG	CTCCCGGGG	DOATGOACT	CATCCCCATC	TAAGCATCAT ATGTGAATGC			TOATGAATOT	CTTCAAGTGC	TOATACTOCAC	TTCCCCG0T AGAACCCTGC	POGAGTAGGT ATGTGCCAAT	CTATGAACCA	ACCAGGGTAT		TOAATOCTOT	TOTOROGOTO	TCGCATGGGAG	SANGTECCEC	RGCTAACCGA AGCATTTCCT	STOCKGOATT	TOAGTGCGAG	DESCRIPTION	CATGATTOGA	AAATTCAGAG	GROATCOROT	DOGGAATOT	GAAGAAGGGG	CTOGATTOGA	OTGTAGGATC AGGTTTCACT	сстстотала
	41 		-	TOTGGCTGGG CGCCCAAGCC CTGAAGGCGG	CTCCTACTO	TTTOTAGANA	TYOTGOACA	STOTECTE	CAGCCCAGCC	ATCTOAAGA	CTCTCGATG	CTOGGGCAT	MCTTTOCAT	TOTOGGGGC	CARCTACCO	ATCTTCATCA	ATATTGATGA	TUGANGTET	ACTIGACTOR	CAGTGAAGG	ATGGTTTTGG	TECTOATAT	CAACAGTOG	ОТАСОТОССС	TOANTOTTC	CTCTGAAATC	TOTTAATOA	OTTT GOATAT	COAGTOTCA	TOWNTOCAL	ACATCGACGA	CTGCATGGA	TOMCACTOA	AATOTOTOA	CCCMOTOCAC	ATOCCOCCA	TCTGCATGTT	GTTACTCAGT	GCAGAGAAGG	CCTGCTCCCA	MACATANA
	REPARABECH FOR PREPARE FOUNDER FOUNDE FOUNDER FOUNDER FOUNDER FOUNDER FOUNDER FOUNDER FOUNDER	99.2	ī-	CAGCETCETC 1 CAGCETCETC C	CCAGATTCC A	ATTOTCCCOA ACTTOTTCCA O	ATTOGAACTT A	ATCGCCCAAC AGGACAGGCC	GAGATOTOTO GAGATOTOTO GAAGCTTOCC	ACTACTCAGA A	TCAACAGATO		DANTATCOCA O	OCCCAGGAG O	CCACTOTCT O	GATTOTATAG	CATGCATTO	GAMANCE O		ATGGATGGAC O		TCCACGGCC 1	COTTOTAATT C		TCTTCATT	AATGGAGCCA	ACOTOTOAAO A		SCATCCACC CTTGGGGGCA	AAAGACATCA A	ACATOCOMA O	OTCAATACAC (	DOCACCTOTO 1	AGAMATOGA		DATACTOR A	ATTCAATA	TOTCAGCTOG		TACCOCTOTO	MOTOTOCAL
	21 	18.1 NH_001999 16.	=_	COCCABOCT C	TOTOTOCOCTO	AAACCAGTGC )	CAGTGCAGT O	AGAGGTTAC A	CATCOCACT	ACAGAGGAAC 1	TOTCHANCE TATOTANCE	CTOCTOTONO	AGOTTCTGAG GAGTCTCTGGT 1	CAATGGCTAT G	ACCCTGTATA	TOCAMATOON	ACCAAGGAA	ACTACAGAT O	CTTGGCTCCA 1	CATGAATGGG A	AGGAATCAAG A	TTCAGCTGAA 1	TOOTAGTTAC C		ACCTTOGA	GOTGAATATT	AAAGGTGTT	GATGGGACT	TOTOGGGGCG G	CCACACACTO 1	OCHOCAGAACT )	TOGATICATO A	CACCAGGGGG	CATCTCTC	ATOMACCOA	AACATCCT (	ATOTCACCTA A	CATTIOCCAC	AGGAAGCTTC	CCCCCCCCCA	CATCTTGAT
86443	11 LLLPQVLLGG RDAVVPPYNL I RPFFNLSSIP I	ISB DNA sequence   Accession #: NP   Ince: 18736	==	AGGGAGGCT C	COAGGCCCAA	TTCCCOTCC	AATCAATTCA GCCAGTGCCA	TCAGAATGG	DOGCOTOGG TCATCCCCAA	DOTCACA .	TTCCTGGGAT	AATGCAGTG	MATTECAGO C	TOCCATOC	CACTOGACT A	ATAMGCAGGA 1		OCTITIONATI A	CAGGATTTOT	CCCAGGCCT (	AOTCCCAATG	TOCARAMA 1	DANGARETTO T	TCCCGAAA	CTGCAGAAA	OCCOCTOTOA O	TOCCAGGAT	CCTTACOTE	CAAGTGGGA 1	TTACTOGGCG G	TETAGOGNA O	CTATGAÇÃO	CCCTCTCCT	CCCTGAGTGA		ATGAATOTOA /	ATTECATOR /	AGGGATCCTT	MATATCCC )	AGTGTATTGA :	тисстасте
WO 02/086443	MAGTROLLA C FOLKQRFTPB F LPETSGUTER TANSKPVTR F	Seg ID NO: 458 DNA: 1 Nucleic Acid Accessi Coding sequence: 1		CTCTGGGGGC A	CCCAAOTATC O	TOGARDACOC 1	DATGACCACT O	TICACTOGAT	ACCACTOGAC C	AGATOCCTO O	TECAGCATCA			TTTBCCCCM CCTCCTTGGGGGGGGGGGGGGGGGGGGGGGGGGG	OCTANCETT O	AACATGGGTT		TOCATCCC	ACMCTACCA A		ATGCGCAGTA C	ATCACTOTOS A		GATAACGGAT 1	GTCAATGGGG	ATCCAGGACA	CCAGAGGGC 1	TOCCCTORNS O	ATGGATGCCT O	GOOGNTOTTC 1	AGTGGCTTTG C	TOTCCTGACC 1	CAGTOTACOTA		GATATTGATO	GCAGACATTO 1	ACATOCATTO	GAGACACA	OCCICATOR	ACCOCATO A	COTTONTOOCT
	٠,	01		2		23		22		30		ý	3		9			45			2		55			09		7			20			75			20		. 50		

各

9
•
7
Ň
=
ñ
•
ಜ
5
↸
٤
u
Ξ.

										•
	0996	9720	9780	9840	9900	9966	10020	10080	10140	
	CITACOCAGO GIDOGOTIGOS ICOTONIDOS ACTOTAGOCA GOTOMAGAAC COCOGITICOS	TOGTOCATT	AAATCATGCA ATGCAGCCAA	TCATTAATAC	AGATOTITOT	CAGGATOTOC	NACCCNGNA CCTOTTTCCT GGACCAGTGA	COTCOCAAC	TATTOTTAT	
	OCTUNICAC	INCORDERS TETTAAATAA TOOTOEATIT	MATCATOCA	TITAGATIT	TOTOTATGAA AGATGTTTOT	TISCITING CATITANAN GATATIGIAC CAGGATGICC	CCTOTATICCT	CCTOSTTOTT (	TITIONGOTITI	
	ACTOTAGGCA	THEOREGIA	ATOTOCAMC 1	Serren Se	INTAGITATA CACCATATOC CICATITITAT CATAGCCIAT	CATTANAMA	MCCCMGNA	<b>GOCCAMBEA CATGERGOCT</b>	TACCCAGTAT	
	TOCTCATOCT	TTCTCTGGG 1	ITATOTICA AGITATITICA GGATIGCCAT A	CANTATATO TIGITIGITOT TOTTITIANC (	CICATITAT	TECTTIANT	ATTANGAGE ACOTATICENT TATTETICES	<b>QQCCAMACA</b>	TAACCAGTTA 1	cerece
086443	OTOCOCTOCO	TOAMAGGGA ACACCTGGCA	AGTTATTTCA	TOTTOTTOT	CACCATATOC	CANTEMATT CATOTITAGE	ACCURATOCAT	TATOTOMAT (	CANDATTAG 1	ANANAANACT
WO 02	000000000000000000000000000000000000000	TTGAAAGGGA	ATTATOTICA	CONTATATO	TUTAGITATA	ACATEMAT	TATTANGAGE	COMMICTICA	CTGTGCTGAC	TTAATAACTA
			•	,	n				•	2

PCT/US02/12476

Beq ID NO: 459 Protein sequence Protein Accession N: NP\_001990.1

2

15

	=-	17.	ï.	<b>7</b> .	11-	
MCRRRRLCLO	LYFLHIGEN	LWAQCTAGQP	OPPPREPRE	QPPPQQVR5A	TAGSEGGPLA	9
DCPC6RPNMC	TC8500185T	DVLRDPNVCG CGSKS100CS	SR PHSYCCPO VRCAGGGTCA	DDHCOCOXOX	IVPICAGNECA	120
ENGCONGGRE	IAOPCACVYG	PTOPOCERDY	RTGPCPTOVN	NOMCOGGLTG	IVCTKTLCCA	340
RCPACHKOSS	TTOKCEDIDE	CHIPOICET	GECONTVGSY	PCVCPRGYVT	STDGSRCIDO	9 9
RTCHCFSGLV DWCG18GC8G	NGRCAQBLPG	RMTKMQCCCB	PGRCMGIGTI	PEACPVROSE	BYRRLCMDGL	450
GPIITGLIIL	NOTIDICKH	ANLCLNGRCI	PTVSSYRCEC	NYGYKODANG	DCIDVDECTS	240
NPCTNGDCVN	TPGSYYCKCH	AGFORTPTKO	ACIDIDECIO	HOVICIOIDRC	VNSDOBPOCT	009
COAGFELTTD	GRACYDHDEC	CHCPPOTAVO	CINEDGEPKC	ICKPOPULAP	NGRYCTOVDB	9 20
AVTKSBCCCA	NPDYGFGRPC	OPCPAICEAE	PHOLCSBOVO	ITVDGRDINE	CALDPOTCAN	90
GICENTROSY	RCNONSOYER	DASGRACIDI	DECLYNRULC	DMCLCRNTPG	BYSCTCPPGY	640
VPRTETETCS	DINECESNPC	VNGACRUMIA	SPACECSPOS	KL88TGLICI	DBLKGTCWLN	006
PECYCENGE	WATERSEC	CPEGITING	CERCELDIAC GRACIDIBAR	OCYT.KWIEDR	TUEDVNECEV	980
HDACCCAVGA	AMOTECEBOP	KPOTKEYETL	CPRGAGPANR	CDVLTCRPPY	KDINECKAPP	1080
CHCTYCKCRN	TIGBFKCRCN	<b>GCFALOMBER</b>	NCTDIDECRI	SPDLCGSGIC	VNTPGSPECE	1140
CPECYRSOFM	MUNICIPATION	CERNPLICEG	OTCVITEG8P	OCD CP LCH SL	SPSREDCVDI	1200
NECELEDINIC	MACACAMATO	TYCCSCNOON	DATPOROGET	DIDECMINAD	SENTOCINES	1250
TCIDVNECDL	NENICMPORC	ENTKOSFICE	COLOYBVKKO	TTOCTDVDEC	SIGAHNCOMH	8 2
ABCLAIPGSP	KCSCREGNIG	NOTKCIDIDE	CENGTHOCSI	NAQCONTRGS	YRCACSEGIT	1440
COGLICEDAD	ECAGNINACE	MODELANDGA	YRCECEMOPT	PASDERSCOD	IDECSFONIC	1500
POLYNOMING	WINCI COOK	SECONTIGUACI	OLUSCADELN OCTUBIONION	CVRGLCVRIP	WANDADOON	1620
PPVNSTRYYT	LCPGGEGPRP	NPITITEDI	DECOELPGIC	OCCIVITION	SPOCECPOOY	1680
YLSEDTRICE	DIDECTAND	VCGPOTCYNT	LONYTCICPP	BYMOVNGGHIN	CHDMRKSPCY	1740
RBYNOTTCEN	ELPTIVITION	CCCTYNYORA	CNKPCEPCPT	POTADPIKTIC	CALIBORTEDI	1800
HTGKAVDIDE	CKEIPGICAN	<b>GVCINOIGBF</b>	RCECPTGPSY	NDTILLVCEDI	DECSINGDIALC	1860
ORNADCINSP	GSYRCECAAG	PKLSPNGACV	DRNECLE1PN	VCSHOLCVDL	NHOISOCICHIA 10100000000	1920
GOVCRNGRCF	NEIGSPRCIA	NECYBLTPDG	OCIDINECY	ALPGSCSPGT	CONLEGGERC	2040
ICPPOYBURG	ENCIDINECE	EDPNICLFGS	CTNTPGGPQC	LCPROFYLED	MURRICPOTRO	2100
BPCPTNPBND	KCSVPKAPNT	TKAKCCCBION	POECHICOPCE	LCPKDDEVAP	<b>QDLCPYGHGT</b>	2160
VPSLHDTRED	VNECLEBROI	CENGOCINTO	GS PRCECPMG	YNTOYTONG	VDTDECSIGN	2220
POGNETCTIVE GYALSEDOWN	IGSFECACUS	DARAGE COMMAND	CONTRACTOR	LICALROSS	PGSYECTOPI	2280
CRTKPGICEN	GRCWIIGEY	RCECNEGROS	SSSOTECLON	ROGICEAEVL	OTICOMABES	2400
RNLVTRSECC	CDGGRGWGHD	CELCPLPOTA	ОУХИСТЕРНОР	GYTTDGRDID	ECKYMPALCT	2460
NGOCININGS	PRCPCICUOYT	TOISOTSCID	LDBCSQ8PKP	CNYICKNTEG	BYOCECPROY	2520
VLQEDGKTCK	DLDECOTIKOR	NOOPLCVNTL	OGFTCKCPPO	FTCHHTACID	NNECCSOPLE.	2580
COGRETICENT	POBPACECOR	NACOSASCON	TIGENTIAL	HRECHIGGONI	LOGY RCGCPQ	2200
BIOVPCATGCS	NTEGGYLCOC	PPGYYRVOOG	HCVSCHOPNX	COYLSLOTEV	DEENALSPEA	2760
CYECKINOYP	KKOSROKRSI	REPOPTAVEO	ISLESVINGS	PVNDACPNLGH	LOSKEHILBL	2020
APAIQPLANH	INVISOUND TAYAR	DEVPRIHORN	GL9YLHTAKK V	KIMPGTYTLE	ITSIPLYKKK	2880
BHANDUMAND	DOI DEVOIDE	ADERTANDALE			•	

Seq ID NO: 460 DNA sequence Nucleic Acid Accession 8: NM\_013172.1 Coding sequence: 63..617

			0	•	200	٥			0	:	•	0		2	•	8	
		_	Ξ	=	ä	ä	Ŧ	Ţ	Ŧ	š	8	5	5	F	2	8	
		TOACT	CCTGC	BACAAGGCCC	20000	AGAGG	PAGCOCCTTA	TCTGTTAGG	<b>PCCTTTCAGT</b>	9	COTTOCATAT	ATOCAGOCCC	AGAGO	ATCACTOTOC	Ş	CTCACCCCCO	
	Z _	58	ACCCTGCTG		AACCOGGGG	ACCCARGAGO			1001	ACTOCCTO	8		AGGCCAGAGG		AGAGAGCACT		
		GAGGACCOGC COCACTGACA	CCTCTTGGGG	CCCCCCCCA	TOCCTCCADO	OCTOGRAPTICE	GTGCMAACC	CATCMCCBC	GGAGGAAGGT	COTCACACTC	DANGCAGTOT	TOTOCTAGGA	TAMACCTAG	precororac	AGTOTOGOT	TOCTITANTO OGGATOTACE AGAMACECAE	
	<b>;</b>		_										•	_		AGAM	
		CCCAGGCCCC	CCCTOCTTCT	AAGGTGCCAT	CCCAGCAGCC	GOGNOGAGOT	AGCGAGACTG	OTCO CACCAT	ACATCODGAA	CTACCATGAT	TCACACGTGT	CACCCAGCA	CTTACTTOCC	CTTGTGCGTA	GAGAAAACAC	MATACC	
	<b>#</b> _											_	_	_		OGGA	
		OCCITCOAAA	ACCONTOCCAG	AAAGGGTCCC	ACTCAGTCGC	OCCATOCCCO	MATACCTOA	COCTOCACA	ATCCCCAGGC	MOMMATTCA	NAGRAGAGAG	AAATCCAGGT	PACCAGATT	CAGGAGCCTG	TAGACACCA	TAME	
;	<b>1</b> –	60				_	_							~	1360	1001	
:		TCAGCGCCAC	CACAGCCTAC	AGGGAAAAAG	CTCAGAGCAG	GOCCOCACT	DACOGRACOC	CCACGAGGAA	CTCTTTCTAC	CTOCAGCCC	ACCTACCAAG	OGATTAAGCC	AGACCTAAAA	<b>POCTICETIOD</b>	procording	TAAACATATC	
	=_	5	_				_	_		ğ		GGATT	-		_	-	
TO		CCCCCCAC	TATCAGCOO	OGCTOCTOA	<b>IDCACAATGA</b>	DOCCOMOD	CCTGCATGT	AGCAGACCAT	SCCAGTGCAA	CTOCTCCTT	<b>NCTACAGG</b>	CATCGATTT	MODANGICCC	ACCCCCAGC	TOCOTOCCT	CCTATATE	
		8	GTATE	8	AGCAC	9	S	AGC	5	ğ	XC	Š	NOG.	ž	ATCCC	t	
5			:	٠				9	õ				,	င္သ			

11 21 31 41
SERANTVA LALLATILA ABRIKKOGO GUPEPEDA GEOSEGUEDE (COGNETARPO ENVESCODE LANTSKYLK ROWCKTOLK CTHEROCOS 1
COGNETARPO ENVESCODE LANTSKYLK ROWCKTOLK CTHEROCOS 1
COGNETARPO ENVESCODE LANTSKYLK ROWCKTOLK CTHEROCOS 1
COGNETARPO ENVESCODE CHECKET TWOTLACOR LOPPTKKKKY VI Seq ID NO: 462 DNA sequence Rucleic Acid Accession #: Ros sequence Coding sequence: 1..2733 တ္တ 33 6 55 8 8 25 ဓ္က 65 2 75 83 2

8 2 3

361

vo
-
-
rì
-
7
0
S
•
₽
$^{\circ}$
Ξ.
_

	CTCAGTTTGT CTCAAATGAA TAA	ATCATECTAA	33
2640	AGGAAACTC ATCADATTTA TCTGCCAAAC CCAAATTCTC AAAGCTTTC AAAACAAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCCGACAAC	ACCACTOC A	
2580	ACTICIOTIC AACAAGITOT CIGCCITAAG		
2520	TOCATTCCAG GGATTTTTTA TCTTATGCTT		2
2460	ANTAGGAACA ATAGTOGACA GCCAGAATCT	_	č
2400	COCCUTOGO AAGAGCTCC TCATTCTGAC	GATCACAAGG (	
2340	TAGTICICAC AAAGCICIGO AGGCGACTO TIGGGGAAAG ACTGAGICGG	grootectec 1	
2280	TOTTIONCOCT GCACTOGCTA TRONDOCTOT	AGCANACCAC 1	
2220	GATOTOTOTT GOCTTAACTO	ACCCAACCTA	₹
2160	OCCISIONTA TOSTOCCT CICATIATAT CIGICATTAC CATTOCIOTO	STTOGATTE O	Ş
2100	ACCOGNICAT CCTCOTOTIC CATCACATOD CCCAGCATIT GAIGATOGCT	CTOCTOCCTT 1	
2040	ENCACTICIT CTACCICIC TIGHTCHTC GANGCICAT GCTTGGCATC	STOTTCHTA O	
1980	GTGAACCCTT CTGGAGTCTG	D DITTOTTATT	
1920	GOTGAACATA OCCCTGTCCC TCTTGATTGC	CACACACOTC	<u>≏</u>
1860	TEATCATCEA GECTTTETT TOGMECKEA TTAMAMAM CCAMACTCT	ATTTANDCC 1	:
1800	INDIAMAND GATCACCIAT GROGOACTOD GTATCTCCAT TGGAAGTCTC	ATCTTCCCC0 1	
1740	CYCACTTGAC CTCCTTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA	TOCCAATOTA O	
1680	GRANCHATEC ASSCRIBERC CTASTIGNATE ANACTICARDA CATCOTERCE	CATTICCAGE	•
1620	ABATAGAGTE AMECTIGAGE CAGECTEATT GTGTGTTTG GGATTTCAGT	TITITITICG	2
1360	CTOTOATATC CACGOTTATT CAMACTATT CCATAMATCA AGTTTTCCTA	OTCAATGGAC (	•
1500	COTTOACTICT GOOGUACATT CTACCCOTTT CCAAAAATOG AAATGCTCAG	AGCATOGCCT O	
1440	POTTANTIDO GECADACCAA TECCADADAT COCTECCADA AACTATENTO	ADAGGCCOTO 1	
1380	ATGTGTCCCC	CTCANAGGG	
1320	ATTEATTEAE TREMANDER TTECHETEA	CCTCTOMATT	n
1260	INCTAGADAC ATTAGADAAC ATCAGCACTC TOOTGCCTCC GACAGCTCTT	AGCTCACOOT 1	•
1200	CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC	ATCCTTAATT O	
1140	TCAGGGTGTC CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT	OCCADOCUTT 1	
1080	ACAGTGGGGA ATCTGGCTTC GGTGGTGTCG ATTCTGAGCA ATAITTCATC TCTGTCACTG	ACAGTGGGGA	

Seq ID MO: 463 Protein sequence Protein Accession #: Eos sequence

	1X 60	•	180	•••				11 480							
#-	LLGVTYRDSK	WPPPSCLDPQ	BALYEKYANG	AEKAKTALHK	<b>GWOVIRETC</b>	TLENISBLBL	ISTLVPPTAL	PORSLPETII	QPHCVPMDPS	VOLGISIOSL	VNPSGVCTA	LIIBVITIA	RPTVGERLSR	<b>GPFILCPOI</b>	FSHTGDSSC
₽_	HLGPVEEYOL	LOCICEDENT	RFTNDLLM88	SELLSAIEN .	GNITAKCESS GWQVIRETCV	TVGNIASVV8	SSRLLETLEN	RGRVL IGSDQ	PPSKIESNLA	IPPVVKWITY	PIVGATVDIT	VGPCLGYGCP LIIBVITIAV	VVLLVLTKLW	VIPALLNAPO OPPILCPOIL	NPLQNKGHYA FSHTGDSSDN
<b>n</b> _	KKELI WITKK	TTDCNSLAGV	KINGTPKINE	GYEVVGSSSA	YTLPCBSOYR	<b>SVIIRQNPBT</b>	TVLLREEKYA	MCPONTSIPI	UNDPVIBTVI QNYSINEVPL	ILMSPFVPBT	ALSILIADVM	HEMAGRILMMA	ALAIVAVNPV	IVDSQNLANH	SAKPKFSKPF
#_	PLGKKDGIKT	<b>GLIRIIRAKA</b>	SOSVNPCERT	TOPRNOSTVA	VPGPGSKDDB	PEMIVGNATE AAVSBPVONE	ILNBASVIN	LKRGYSYOIK		COCTHLISFS	HTRRIGMNI	LLAYRLILVE	BKPLLAFWP	KBLLILTPLL GLINGFGIOT	QTEKONSSDL
<b>=</b> _	PPTPTDGRGG	LLKPPLLWSH	PECECHLAMIL	RIOGPESVQV	VPGKAQCAD1	PSHIVGNATE	MEDVISIADN	WKG! PVNXSQ	LPVSKNGNAQ	LUNETODIVI	WKOIKKSOTS	LPPWIMMIALDI	DVCNLNWSNG	KBLLILTPLL	NKLEALBSWK
	MKVGVLALIB	EXPLERNFLK	NCYLHTAGAL	TRIGLKKAYB	LPPLEDGBPR	LSLLEZLINON	ABHFRVSNST	PLNFSRKFID	<b>EMABLTLON!</b>	HLOWNDAGCH	11CL 1 EALF	VPPTHPPYLB	TOPSNTYXRK	DOKATITRVG	LOSKLROLLF
35				,	<del>\$</del>				•	3				:	သ

Bed ID NO: 464 DNA sequence Nucleic Acid Accession #: AB035089.1 Coding sequence: 9845..10219 

;							
		=-	<b>17</b> –	ī-	<b>\$</b> _	- 21	
S	OGGCA TGCAG	_	MATCCATAG	TOCAGATAAA	GCAAGGAGGA	AGAAGAAGA	9
3	CAGTTCTAGT	AAAAGGGAGA	ACATCAATAT	AGGATGTTTC	TTAGCAATAG	MANAGANGG	2 2
	TOOTITION	_	AMTATOATO	TCTOTCCCTG	GCAGTGTTGG	CAGAGTAGGA	2
	AGGADGAAGG	GAGGCAAGAG	ATAATATCAT	TITCICIOTO	CTCCAACTOT	ACTTACATAT	300
;	GAGACTATTT	CCCTCTCTGC	TTTTCAACC	TTACTOGAGT	TOTATION	CATGAAAACC	360
S	AAGAAAGGAA	-	тстиотте	AGOTTOTTCA	ATGTATACAT	ATCTATATOR	420
	<b>STAGACAGAA</b>	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTOTTATITE	ATGCTTGAMA	6
	AATCTCCTCC		TICCCTATAG	ATTOCCACA	GCACATAATA	AGAAACAATA	340
	AATAAAATGT	TOTOTTOPOL	TTOTTACTTA	ACAATOCTGA	GAMMOTTTA	CAGCCTTCAT	9
ć	AAGCAAGTGA	_	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	9
2	<b>OTAATGACAG</b>	GATATTCCT	GAAAGTGTAA	TTCCCATTG	AGGATTTGTT	TITANTIC	720
	00ATTCCT00	AGCCIATGAA	GTTGGTGTAT	STITATIONAL	TATCARGAGA	CATAMOTTOG	980
	CAAGTOTTCA	TATOCAAAA	CTTCTTGGA	TITCHGAGIT	CTCTOTOGCA	ATATATOACA	9
	TCAGGATATG	-	CACACCAGGA	TATOTOCHIT	CTAGCCTOTC	TATCACATGC	300
ì	TAGGAGAACT	ATTTAGGAAC	AGAMAMAT	<b>GCCTGAAATG</b>	ATTACACT	TOAACTCATC	960
C	CAAGCTTTCT	CINNITIAN	GCANACTCCT	OCTUATITIES	AGITAGTACC	TTTCCTTANG	1020
	TICARCTIC		10000010	AGACOTITAG	CCATAOTOTO	MATICICIT	1080
	CCATAGATTO	OTCCCCTOTA	ACCCCOOTIT	OTCTCA9CTT	OTTATCCTOT	Trrincing	1140
	CCTCCATTCC	CAGGATGAGC	TTOTTOCTTC	TOTOCTATOA	GACATTAGAT	TOTITION	1200
ć	TOOTACCOOA	GTAMTCCAT	CCTACTCCAA	TAGAGGAAGG	<b>DECENTATION</b>	TCTTATAGOO	1260
2	CTGGATGCAG	ACTCAGCTGA	GAAGACCATT	ATTCATTTA	DOMETICAL	ATCTCABATA	1320
	THICCICATO	THICHTHIC	TTCTATCTT	GGATTTTAG	TOCATOMOS	CCCCATTAGT	1380
	CTATTCCCC	ACTTCAATCA	OGGRACTTAT	ACCTCTTAAA	CTCATTCAGA	DACTCHANAC	140
	ATATATAT	ATACAGGAGA	CCTAAGAAGA	<b>OCATOTOTIO</b>	GGGGTTGAGG	MACAGGCAG	1500
è	STEAGAAATT	TCCADATTOO	AACACACT	tectricite	CATCCAGCCC	CTACTTOOG	1560
2	CCTATGEGET	TCTCGCACCT	TOTTOTAGAT	AAATCTCCCT	TOACTITION	ATCTCCTCAC	1620
	MAACAAACT	CACOGCTGGT	GETANANAGE	<b>ACCCATANCE</b>		TTOGGGAGAA	1660
	TOTTCGAGAAA	TCAGAACTCT	ATTCACOGEC	GOTTOGAATO	2000000	CAGNATICIA	1740

	9	120	180	240	300	360	420	680	340	9	999	720	780	940	900	960	1020	1080	1140	1200	1260	1320	1380	9	1500	1560	1620
	AGAAGAAGA	AAAAGAAGG	TAGATITUGI	CAGAGTAGGA	ACTTACATAT	CATGAAAACC	ATCTATATOR	ATGCTTCAAA	AGAAACAATA	CAGCCTTCAT	AAAGGCATTA	TITANTITCE	CATAMOTTOD	ATATATGACA	TATCACATGC	TOAACTCATC	TTCCTTAAG	MATTCHCTT	retreene	TOTTITOT	TCTTATAGO	ATCTCAGATA	CCCCATTAGT	DACTCHANG	MACAGGCAG	CTACTITICAG	ATOTOCTOAG
<b>4</b> –	GCAAGGAGGA AG	TAGCAATAG AA	GOGACAGOCT TAK	acantomoa cac	TCCAACTOT AC	TOTATION ON	ATGIATACAT ATC	CTOTTATTIC AT	GCACATAATA AGI	GAMACTITA CAC	ACCAATCTAT AN	AGGATTTGTT 11	TATCANGAGA CAT	CTCTGTGGCA AT	-	ATTRICTOR TO	NOTENOTACC TT	CCATAOTCTO AN	DITATCCTOT TT	GACATTAGAT TO	POCATTITION TO	DOMETICITY AT	DCCATCACO CO	CTCATTCAGA GA	SCOOTTONG AA	CATCONACCC CT.	TA CTTTTOTO AN
<b>3</b> _		-		_	_	Ξ.		_	-				-	_	_	-	-	_	-	-		_	•	_	_		•
<b>-</b> -	TOCAGATAMA	ADDATOTITO	DATCAGGAND	TCTOTCCCTO	TITCTCTGTG	TTACTOGAGT		CACATATAT	ATTOCCACAA	ACAATGCTGA	ATATTTCTTA	TTCCCATTG	OTTINIONA.		TATOTOCHI	GCCTGAAATG	OCTUATITUDE .		OTCTCABCTT	TOTOCTATOA	TAGAGGAAGG	TITICATITAT	DATTTTAGO .	ACCTOTTANA	OCATOTOTA		AAATCTCCCT
<b>z</b> -	AMTCCATAG	ACATCAATAT	ACTTATAGA	AATATGATG	ATAATATCAT	TTTCAAACC	Terrorres	TACAGTAATT	ITCCCTATAG	TOTTACTTA	LATCTADGAG	DAAAGTGTAA	CTTOOTGTAT	CTTCTTGGAA	CACACCAGGA	AGAAAAAT	DOMACICA	10000000	ACCCCOOTTT	TTOTTOCTTC	CCTACTCCAA	GAAGACCATT	TTCTATCTT	OCCANCITAT	CCTAAGAAGA	AACACAGC	TOTTOTAGAT
	CCATCGGGGA /	AAAAGGGAGA J	TAGGGAGAG A	AGCATACAGT 1	GAGGCAAGAG 7	CCCTCTCTGC 1	AGCTAGTTAG 1	T CCTTGGGAA 1	ACTAACCAGT 1	TCTCTTGACT 1	COTCCACCA.	GATATTICCT (	AGCCIATGAA (	TATOCAAAA (	TCCARTCTCA (	ATTTAGGAAC !	CIMMITIM	ADDGCAMCC :	OTCCCCTOTA A	CAGGATGAGC	GTAMATCCAT (	ACTCAGCTGA (	TICTITIE.	ACTICABICA (	ATACAGGAGA (	CCADATTOO !	reredeader.
=-	OCCATOCAC CC	CAGTICTAGT AN	COMONOGAL TE	PRODITITIONA AG	AGGADGAAGG GA	CACACTATTT CC	NACHARGONA AC	STAGACAGAA TO	AATCTCCTCC AC	NATANATOT TO	AAGCAAGTGA GG	STANTOACHO GA	DIGATTCCTOG AG	CAAGTOTTCA TA	TCAGGATATG TO	TAGGAGAACT AS	CARGOTTICE C		CCATAGATTO OT	CCTCCATTCC O	COTACCODA GI		meeter to the	A BOODTIAL	_	•	CCTATGIGIT TO
	-00	5	ş	200	AGGA	8	ADA.	9	ATC	ATA	7	E S	DOAT	CARG	TCAG	1700	3	Ē	Ş	Ĕ	ğ	E	Ĕ	Ê	ATAT	Ē	ĝ

TREGULATION STREETS TO THE STREETS T <del>우</del> S 

15 AGRICATION CONCOURT CONTROL OF A CONTROL LENVILINE IDOLQULEK LIASKUZET ELÖNGETV DILIPRINE SETDLOTTA TRONNIPRO BOLDSORTUS HISTORYUM KAPUSTED VENANTAV VELSSBERI SETCHIPLA FIREGRADE LLYGARSE 8eg ID NO: 466 DRA sequence Nucleic Acid Accession #: NM\_001910.1 Coding sequence: 50.,1240 S 

WO 02/08/413

ONDOARDA TITRICARD CONTROL MITTANDA MITTANDA GEOCODA, 1915

MATTERIANA CALTUTOR MICHITAL CONTROL MITTANDA CHECADALA 1915

MATTERIANA CALTUTOR TOWARDA MITTANDA CHECADALA GEOCODA, 1916

MATTERIANA CALTUTOR TOWARDA MITTANDA CHECADALA GEOCODA MITTANDA CHECADALA MITTANDA CHECADALA MITTANDA CHECADALA GEOCODA CHECADALA OTTO CONTINUOS DESCRIPTOS DE CANTINUOS DE CONTINUOS E CONTINUO DE C

TACCUCTCE GGACCEACA GODALACEC ACCORDER CATCAGORDE ACCORDER ACCORDE SLENKLRARS OF PTVIPOTGS W DOVSVEGLTV V DLWFSVYMS E PCSEGGOAIV D PYTLSPTAYT L Seq ID NO: 468 DNA sequence Nucleic Acid Accession #: NM\_018058.1 Coding sequence: 119..1575 WET.LALLY LIARCAGO LAPPUSABRE SI SECONDAL HYLDREYON TISTICATION OF PROSESTING POSSESTON TOSLICATION OF POSSEMANY TRANSPORT PRINCIPLY TOANDOM POSTETION PRINCIPLY HEPOGUALL COVINGEN POPTETION P 

8 2 2 2

M VLLGAKÜNTA QQISKVLAFU E LELANKLPUB KTYOPLOSYL K NLPPOGTIGN DTTLVLVNAI N PALLEDVQAK VLEIPPKGKO

K KEKENHIFYB PIBITBALGH VA VHHOPOKLIT EPHKETDAYB L. BEBAKKINSM VEGOTHEKIK M P WENTYTKSV QMORQTHEFN F.

MISLEBANTK PHYDLPGOPR K GVTENITEKA ATTEVDRECH VI DAIKKPYOTG VESTOPANAP EI YPKGONENKP KKENIKEEKP M

Seq ID MO: 463 Protein sequence Protein Accession #: BAB21525.1

11120 11120 1120 1120 1120 1120 1120 11	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	180
CCCCCCCCA TATOTICO TACONOCCO TACONOCCO CONSTITUTO ACCONOCCO CONSTITUTO ACCONOCCO CONSTITUTO ACCONOCCO CONSTITUTO ACCONOCCO ACONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACONOCCO ACCONOCCO ACCONOCCO ACCONOCCO ACONOCCO ACCONOCCO ACCONOCCO	S1   CACAPILIENN   LOMSTEGENE   REKODELIE   RINMILARVD   SAVETYRED   PTVGTPMEAT   LPLIHRES	11  THAGGGGGT THAGGGGGT THAGGGGGT THAGGGGGT THAGGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGT THAGGGGGT THAGGGGGT THAGGGGGGT THAGGGGGGT THAGGGGGGGGGG	SVACVDRKGS
AGACCAGG CONTOCOGG CONTOCOGG CONTOCOGG GOTTOCOGG ANTICOGGG ANTICOGGG ANTICOGGG ANTICOGGG ANTICOGGGG ANTICOGGGG ANTICOGGGGG ANTICOGGGGG ANTICOGGGGGG ANTICOGGGGGGGGGG ANTICOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	41       S\$ASDIPCDN   GRNNDPIKLY   BLSVFREWO   AHTGLOUGH   AHTGLOUGH   SSINCOLLETS   S	1   1   1   1   1   1   1   1   1   1	ROVABLITAGR
ACCICACTO TOTOCCTOS TOTOCCTOS TOTOCCOSTOS TOTOCOS TOTO	11   COVECTILS   NEGENCTIVE   IPENIATES   ILSHGESPAG   SOLLEGREP   APLETPRIAS   PAPPEPELL	11 CICTORITIC CICTORITIC CICTORITIC CICCONICTOR CONACTOR CONACTOR CONACTOR CICCONICTOR CIC	DILEDEVNVA
	P_66528.11	1   Carteriors   C	LPKPRNDRWB
SECTION OF THE PROPERTY OF THE	11 10 11 11 11 12 12 12 13 14 14 14 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	11    NECTROOT  INTERPREDED  INTERPREDED  INTERPREDED  INTERPREDED  INTERPREDED  INTERPREDAD  IN	PEGVATYTDX
2448884444444444	Protein Accessing State	##	RIYFLUTTANA

ଓ

. . 8

							~~~~			*******	****
OGRGVGVGPI DPNRDGKVDI LEIPPNHIAY DLILEHUSEN OGSGYLCTMB DPAPLECOGO NEDGACVGT	s1  -     oosraaaccc	ACCOACCTO TOACCTCCAC ACCTCCCAC CTTCTCCAC GCTCAAGCCT GOACTTTTCC						GENERATION CCAGGGTTCT TCTGATCCC CCACAGCTAT GCGAGGTGC CTGGAATGGC CTGGAATGGC CTGGAATGGC CTTGACAAT		TCACTACCAC CCAATCACTA GOOTCCAATC TACGGGOTCC GGGCTACAGG	AGANAMANG TACCAGGAA GOTCETTANG GOACCTTANG GOACCTTC CAGGGAGCT CAGGGAGCT CAGGGGAGCT CAGGGGAGCT CAGGGGAGCT CAGGGGGAGCT CAGGGGGAGCT CAGGGGGAGCT CAGGGGGAGCT
AAEAGVSKYT HGHGRGYALA 1TADFUNGS VIDPDGGGG KGOAHLA ID KKPRDETLG HKKPRDTLG	41 	OOTACAATOO TCGCGGTCAA TCGGGGTCAC CCAATAATOC ACAGGCCTOT TCAGCGGAAG	TTCTTCTANG ATMCCOOTO ACTTGCCA ACTTGCCA ACTTGCCA ACTTGCCA ACTTGCAAATA ACTCACAAATA	ATOGRAGICA CAGCAGCTTT TTCGAACAGC CATOTTACTA CCCAACACTA	CCACTOTOOT TOTCCAOATO CTCCTAOAOA CAOOAAGAA CAOCTCTCOO	OGCCTCTTON TTCTOGACAT ATGCACCACCA GCTCCTCTGA AGGTCCTCTCA	AGAMT CCANT TTCCTA	COURTCACE CACTCACCT TCCTCROCTT TCCTCROCTC GCCTGATGAC ACCACCATGC TCCTCATGCCATC TCCCCTTCCC TCCCCTCCCATCC TCCCCTCCCCATCC TCCCCTCCCCATCCCCATCCCCCCCC	TAACAGCTO CAGGGCTO GUAGGACG CGACCTCTO AAGGGCCAC CCAGGAAAA ACTACCAGG	CHOCOTICAN OCTACOGOT AGGGCTACO GANAGGGGC CCAGGAANAG ACTACCAGAA	ATCACTACC CTCCATCAC GGAGGTCCA ACGGAGGTT ACGGGAGG TCCGGGAGG GGATCATCG GGATCATCGA GGATCATCGA GGATCATCGA GGAACGTGGA GGAACGTGGA
ARGILALEDV AAABAGVDDP PENEDROTODV EPENEGOTOV RGAKVVLYTK BGENGVLYTK ATYGGYRGYI ATYGGYRGYI	H 31 1 TGCTCTOGTT	TCCTCTCCACA CTOSTSACA GOSAACSCCA TTCCTCACA CTCCCACACA CTCCTCCACA	CCAGACCAT ANOTICCACA TOTOCCAGC TACTCTATCT ANOGCCCTG ANOGCCCCTG ANOGCTCGCCTG		OCCACCAGO GACAGOCA CAGCACCTGC GACGAGATC GACGAGATC GACGAGATC	AGCTGCTTGA GGGAAGTTC TTCCCCCCAG				MAGGGGTA AGGAMAGOG TACCAGGAA TCACTACCAG CCAATCACTA GGCTCCAATC	
HEROPEASDL HERODGTPYO VRPERPODAL VPRTETOAFA DODWYSENYA VCPEDEFOVCY	A Bequence salon #: FGENESHH 4794 21 31 3 	CCCCCCAT CCAGAGCGG GGACGGCAG GGAGATCTAC CCCTTCTGGG CCTCCTGGGGT		AGATGAGGAG COGGCAGTTC TOGGATGCCC CAAGAACCTA TTTCCCTGCC GACACATGGA				OFFIATORO CTCCAGTOCC TCTGCAAAA GTGGTCTGC COTGGTTGT ATAGGCACAA ATAGGCACAC		ACTACCAGA ANTCACTACC GTCCANTCAC CGGGCTCCAA GCTACAGGGT AGGGGCTACG	285222233
186443 AYGNVGE DNENGPE LYLGNGE VIRREN OGPNEN BRASEVE TPTAAA	472 DNJ d Acce ence: 1 11 CGGGAG	ATGACGGGG ACGCGCTGGG ACGGCCGGGA ACGGCCGGGA CAGCGCAGGT CCCCTGCAGG	ACCTANGO CCTACACCA ACCTANGO ACCACATOC CCCTCAGA CCCTCAGACA	CAGAGGGGG GCTGGAAGGA CTGGGGCAGC ATTTGGCTGA CAGCCACC CAGCCACCC CTCAGCTAAT	AGGCTTGGG GGGAGGAAAG GTCCCTGGAG CTCCCATTTT CACAGGAGTG	CCCTGGCCTGCC CTGCCCTGCC ACCAGATGGA GGAAAGCACG	ACTISTOGETC GCAGTGCCTC GGGGCGATGG TTCACCTCAA CTGGTCCTTC	ATCATOGITT AAGGCTTGGC CACCCTGCCT ACATGTCCT AAAGAGTCAA TCTCAACC TCTCAACCC	OCTCCATCCT AAGGTTTAAG CAGGTCCCCT GGAATGCAGG GAAATGCAGG ACAAAAAGG TACCAGGAAA TCCAGGAAA	GOCTCCAATC TACGGGTCC GCGCTACAGG AAAGGGGCTA AGGAAAAGGG	TCACTACCAG CCANTCACTA GGGTCCANT CAGGGGGTGT GGGGGGGTGT GGTGCAGT GGTGCAGT TCTACACCAA GTGAGTGGA TTACACCAA TTACACCAA
25255555	Beq ID NO. Nucleic Acto Coding seque	AGGGGCTCCT GTTCTGAAGT TCACCCTACT ATCGACGGGG CACAGCAGC CCACCTACA	CTCAGCATO CTCAGCATO CTCAGCATO GCCTGTGTG GCTTATGTG GGCTTTGTG	GONGAGAC TOCOGOTTO CAGAGOGAG TCCAMAGC GOGCTTCTC CCCTTCTCA	CTGATGGCTG CTGAGAGGCT GAGCTGGGAG CTGGGAGAAC CCCAAGGTCA	CTCTCCCATC GTGCCGGGAG CTGCGGTGAA TTTAGGCTCA	TCCACACC TCCACACC GCCTTCATCG CTAGCAGAAAAA	CCACATTGCC TYCTTGACGC CAGGGGCCC ACTGCCTATT TYGTCCTCTG CCCCTCGCGC CCCCCCCCTGCCCCCCCCCC		AGGGGCTACG AGGGGCTACG CCAGGAAAAG ACTACCAGGA AATCACTACC GTCCAATCAC	
ر د	15	20	30	35	40	45	20	55	59 07	75	85

9
-
-
2
_
ñ
0
ō
=
=
=
ì.
v
۵.

								-
	4360	977	4500	4560	4620	4680	4740	
	GGACCCAGCC	GGACACCAAT	CACACCTAT	CAACGAGGAT	GAMICCANGO	CITITIOCIA	CACCCTTCTC	
	MENACECA TOCTODARE CETETACCE COGRATORO ACACACTICA GOACCONDEC	CACTEGRADT OTGECCAAGO AFFETCCCAG CAGANAATO GCCAFFGCAF GGACACCAAF	MATGCATCC AGTICCCATT COTOTOCCCT CONOACMOC CCOTATOTOT CACACCTAT	DAMACTACA OCTOCCOCAC CARCAGAAG TOCACTCOO OCTACGAGC CAACGAGAT	DICACAGECT OCOTOGOTAE TOAGETAGGE TETAGGEATA CAATGACGTG GALACELAGG	CCAMANDO AGCIGCAACT TICCCAAGGC ATCTGCACCC CCOTCTGGTC CITITICCTG	ECOSTISCE SACTICATE CARAGRACT CASCICCAGO CIGATECCAG CACCCITATE	The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
	COCCATCACO	CACCALALTO	CONCACAGO	1000000000	TCTAGGCATA	ATCTGCACCC	CAGCTCCAGG	
	CCTCTACCCC	ATTCTCCCAG	COTOTOCCCT	CACAGAAG	TOAGCTAGGE	TTCCCAAGGC	CAAAAGAGCT	
111780	TOCTOGAGAT	OTOGCCAAGG	AOTTCCCATT	OGTOCCOGAC	OCCIDOCIAC	AGCTGCAACT	ממשפטים.	-
11/280/CO OW	ATGAACTCAG	CCACTOCAGT	DAATBCATCC	CONNECTACA	SECRETACE	CCCANANGO	CCCOGITICCC	-

CAGANACTC CAGGIATTCC AGANGCCAA GTGTATGAC AAGATCAGA ATAA Beg ID HO; 473 Protesin sequence

20	Beg ID NO: Protein Ac	8eq ID NO: 473 Protein sequence Protein Accession #: FUENESH predicted	n sequence	Mcted				
2			<b>12</b>	<b>=</b> -	.· <b>=</b> _	- 23		
2	BPYYALRDRO	CEGWAGLAGP GNA LOVTACE	I DCDCREEIY	ESSRYNGPHI.	VLXYDRAQKR	LUNIAVDGRS LHRNRPVI.KD	120	
	PPTTPAGLLG		SSLCQASPDS	ROGERVPVPC	CROGLRPTHE	PRPPLLRPKS	8	
ç	GAVOPDALIE		GILALROVAA	EAGVERYTEG	PEHTASP810	BISCRIEGER	3 20	
3	BKSHLADKNL	POPPCYYBVC	APSPARPPPA	RESEALATIVES ROAPOHYPVA	PLYTOLATHO	REAGREAREV	420	
	PHPRAPONDP ELOGPWEGAT	KCKGRHAEPG OHLPARELYD	LMAEALGANP	ALSTTVVPGG DCDPGRRRDS	LRBWEESROK PKVTOECHLV	GOAMSRCALR ATMPALGGLB	540	
25	GPGRVAKREI	-	LEHPLVPNPP	SCLRPLEAGE	VPGAALPGNP	GNIVLDHAKA	009	
ì	BATHODSKSP		1LGSSSASD1F	CONTRACTOR	PHYRODOTEV	DANASAERRI	720	
	APIVHLICHE		LARTOPSSSC	CPWHARLLOA		PTRIGGRPYS	780	
:	PLTOGLASSA	HRRTLSLQG9	QUAPPCLIAR ALADEMENTS	APCVLOSLIP	TAYYIVLMBA	· I PESLATHBY	940	
ဓ္က	SPKPGMPGPV		DOBLETPINN	IAYRESSANR	LFRCSTLARG	BSSLTAGGRN	98	
	OCCEPTA I RR	_	KVNTGPLAKK	<b>OXCRADEDWA</b>	ROCCHACOSE	AKEPABATAG	1020	
	ROKONVAQSV ROPITTRICKO	PRIGAPODIK YGVOSLPCKG	PHYHKKGLQG	DITTREGYG	VOSLIPCKGAT	GENHYOEKGL KGATGSNHYH	1080	
36	RKGLRAPITT	RKROYOVOSL	POKCATOSNH	YOUNGLEGPI	TTRICKGYOLD	SLPGKGATGS	1200	
3	NHYOEKGLOO AMGENHYOEK	GLRAPITTRK	VOSLPOKGAT	GSNHYQEKGL KGATGSNVIR	REHEDPLIER	YGLOST.PCKB	1260	
	<b>GRGTOGWTD</b>		LEHCESMAQP	LSVFRGNQGP	NAMMLRVVPR	TRFOAFARGA	1380	
	KVVLYTKKED	-	GYLCEMEPVA	HFGLGNDEAB	BVEVTNPDGK	MVSRNVASGE	1440	
9	MISVLEILYP		PLECCOCFSO	QENCHO/DIA	<b>ECIGFPTVCP</b>	RDKPVCVNTY	1200	
⊋	DEVRCRTNRK		CSRGYEPNED OTACVOTELO QLOAAPSTLL OKAPOIPEAO	BRHTMTWKPR VYEQDQE	PICKELQLEQG	ICTPVWSPFL	1560	

Beg ID ND. 474 DNA sequence Nucleic Acid Accession in NM 003661.1 Coding sequence: 1..1152

45

		<b>:</b>	- 23		<b>7</b> .	- 27	
Ş	ATGAGTGCAC	TTTCCTTGG	TOTOGGAGTO	AGGGCAGAGG	ANGCTGGAGC GAGGGTGCAN	GACCOTCCAA	9
ž	CONNECTTO	CAAGTOGGAC	AGATACTGGA	DATCCTCAAA	GTAAGCCCCT	CGGTGACTGG	120
	<b>ACTION DOOR</b>	CCATOOACCC	AGAGAGCAGT	ATCTITATIO	AGGATGCCAT	TAAGTATTTC	180
	AAGGAAAAG	TOAGCACACA	GAATCHBCTA	CTCCTGCTGA	CTGATAATGA	OCCTODALC	340
	<b>OCATTCGTGG</b>	CTGCTGCTGA	ACTGCCCAGG	AATGAGGCAG	ATGAGCTCCG	TAMBETETO	300
į	GACCACCTTG	CAAGACAAT	GATCATGAAA	GACAMAACT	OGCACGATAA	AGGCCAGCAG	360
S	TACAGAMCT	<b>GOTTTCTGA</b>	AGAGTTTCCT	COUTTCAMA	STEAMSCTTCA GOATAACATA	OGATAACATA	420
	ADAAGOCTCC	GTOCCCTTGC	AGATGGGGTT	CAGAAGGTCC	ACMAGGGAC CACCATCGCC	CACCATCOCC	9
	AATOTOGICE	CHOCHCHCT	CAGCATTTCC	TCTGGCATCC	TOACCCTOOT	COCCATOGOT	3,0
	COOCCOCC	TCACAGAGGG	AGGCAGCCTT	<b>OTACTCTTOO</b>	AACCTGGGAT	GOAGTTGGGA	9
•	ATCACAGCC	CTTTGACCGG	GATTACCAGC	AGTACCATOO	ACTACCOANA	DAAGTOGTGG	9
3	ACACAAGCCC	AAGCCCACGA	CCTGGTCATC	AAAAGCCTTG		ACAAATTGAA GOAGGTGAGG	720
	CACTITITICS	<b>GTGAGAACAT</b>	ATCCAACTT	CTTTCCTTAG	CTGGCAATAC	TTACCAACTC	780
	ACACGAGGCA	TTOGGNADGA	CATCOSTGCC	CTCAGACGAG	CCAGAGCCIA	TCTTCAGTCA	6
	OTACCOCA'TO	CCTCAGCCTC	ACCCCCCOO	<b>STCACTOAGC</b>	CAATCTCAGC	TOMAGOOOT	900
,	GANCAGGTOG	AGAGGGTTAA	TOMACCCAGC	ATCCTOGAAA	TOAGCAGAGG	AGTCAAGCTC	960
3	ACCGATOTCC	CCCCTOTAAG	CITCHICH	<b>STOCTOGATO</b>	TAGTCTACCT	COTOTACGAA	1020
	TOWNSOLD	TACATGAGG	GGCAAAGTCA	GAGACAGCTG	ADDADCTONA	GAAGOTOGCT	2080
	CAGGAGCTGG	AOGAGAAGCT	AAACATTCTC		AACAATAATT ATAABATTCT	GCAGGCGCAC	1140
	CONGMICTOR	8					

Seq ID NO: 475 Protein sequence Protein Accession #: NP\_003652.1

2

	22 60	180	360	
15	I FIEDAIKY F	RGILTLYGWO		
₽.	 	SYVHKOTTIA MVVSOSLBIB E	Lrraranlos uphabasrpr Vlovytlyve skhlhedaks	
п.		QKVHKGTT IA BTNDYGKKW	Lerapanlos Vlovyylyyb	
່ ສຸ	QNVPSOTOTO		TRGIGKDIRA I TDVAPVSPPL V	
=-	ISALFLOVOV RABEADARVO (ERVSTONIL LILITDREAWN (		LELAGNTYQL ILEMSRGVKL MMYKILOAD	
4-	MSALFLOVGV	YRNMFLKEPP LAPPTEGGSL	EPLOENISNP EQVERVNEP6 OZLEEKLNIL	
	25		80	

Seq ID NO: 476 DNA sequence Nucleic Acid Accession #: NM\_014452.1 Coding sequence: 1..1968 85

. 15

1114 114 144 144 144 144 144 144 144 14	11000 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 11100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 10	11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11,680 11	4 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000	180	66000000000000000000000000000000000000	11020 11120 1120 1120 1130 1130 1130 113	1680
CACCACCADA CACCACCADA CACCACCACA CACCACCACA CACCACCACA CACCAC	ACAGAACCTA CCTGCTGCTG GAAAAGGGG CATGACTCCA TATCCTGAAG TTGCAATGCC GCGGGCCTAC GCGGGCCTAC GCGGGCTAC GCGGGCTAC GCGGGCTAC GCGGGCTAC GCTGATTAGC GATGAAGCCG GGTGAACCGG GGTGAACCGG		10TYRHYDRA OPCHWPALEK CARGIFBDVP PRPEHMETHE TLPHLQVVHH PPHIVLFLLL CAGHGIDILK	LPDIA.	S1 Inceccada CCCCAOTTCC GCCGCCTTO TCTCCCAATO GCTGCCGCCTO	ATTCTCAGA TGGCAGAGC CTTCTGCA CCTGCCGTC TACCTCATC GGAACATG GGGAGCAA GCGGAGCAA	Adcritting CARANTEINC CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON OTOCONO CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRACON CONTRA	CONCACCTAC
CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CANCOCAN CAN	ACATECTAR THOROCTITY COAGAANTE ATOOTATOA ATCAGTTTCT CCGACCACA OCCTGGCCA GCCCAGCCC CTCGTGGGCT GCCCAGCCC	COCHCECTTAT OTTOCTTAT OTTOCTTOCA TCANGAGECA TCANGAGECA TCANGAGECA	41   AQPEQXASNL NGIEKCHDCS TETEDVRCKQ TEPSPOTAIF BRACKEDVNK BRACKEDVNK BRACKEDVNK BRACKEDVNK BRACKEDVNK ANACHTER	BP I PBPHAKL KKOTVLRQVR QTLLDSVYBH	41 	Addresses Todaccaeaa Addresses Addresses Todaccaea Occcator Atorccicc Cottooroot Cottooroot	TOCAMORCCE GOOSTIGATOR AUTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA ATTOCTACIOCA GOCCTIGANOC ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ATTOCTACIOCA ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN ACCIOCAN	AGGCAGTGAG
CCCCCCCC CCCCCCCCC CCCCCCCCCCCCCCCCCCC	CCCMANAGO CCCTANTAN CCCTANTACT ANGOLACIO TOCANTACT CCCTANGOCA GOOTACACA GTCCANGOCA GTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CTCCANGO CT		11 LLLLOPLSTTT CPVOTFTRHE PVGMOVRKG COTLPSF858 PKGUPRONTS PKRGHPRONT KAGLKKSFTP	LPMBPBURB Bracspitke IIGVKSGBAB IIGVKSGBAB	11 CGCCGGGGGG CGCTGTTGCG GGGGACGGG GGGAACGG CTGGCGGCC	CTGGGCTCTG GCCCTCTGG GCACTCTGG GCAGACGCA CAAAACTACA GCAGCCTTCA GCAGCCTTCA GCAGCCTTCA GCAGCCTTCA GCAGCCTTCA GCAGCCTTCA GCAGCCTTG	CTCAACTOCC  ACCTTCAAC  CACTTCTAAC  CACCTCCAAC  CCCCACAAC  CCCCACACC  CCCCACACC  CCCACACC  CCCCACACC  CCCACACC  CCCACACC  CCCACACC  CCCACACC  CCCCACACC  CCCCCC	CACCOCATCA CGGCTCCACA TTCTCATCGG
COCCOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CATCANGGGG TIGACATTIG CATTOTIGAN GATCTACTAC AAGCCATIGG TITICTICCAN CATCCOCOGE AAACAGTT CAAACTAGTT		ATATMIAGBL ATATMIAGBL TNTBLRVCBB NATCAPHTVC KPGTKETDNV GGKSSTPIKG GRKSSTPIKG PRODPSATE	NUMED TTQLETDKLA LPP NLIRC DGTSSGSSAL SRN SEIPQ ASDKLORLFS III (A sequence sesion 8: XM_04533	21 GCGGGCCGG CCCACTTGAC CCCACTTGAC GCCCACGCGG GAGGAGCTGG	CAGCCTCCCC CAGCCTCCCCCCCCCCCCCCCCCCCCCCC	CGAGAGCTCC CAGGAGTTCC CAGGAGTTCA CAGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GCTGTGCTCA GGTGTGCTCA GGTGTGCTCA GGTGTGCTCA GGTGTGCTCA GGTGTGCTCA GGTGTGCTCA GGTGTGCTGCA GGTGTGCTGCA GGTGTGCAGTGCA	TGGTGACGGC GCTGCAGATC
(1)/(186443) (1)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(186443) (2)/(	CCAGEACGOC TTACATCA TTACACTOGA AUTOCOAGTOGG AGATTGCTOC AGCACTOGAC AGCACCOGAG TCGAACTOGAC AGCACCOCAGACTOGAC AGCACCOCAGACTOGAC	ACADAACA CCAGCOGCT CAGCOTTTCC ACTAGACC TOGACTCTOT 177 Protel	11   LASCSKIARR LASCSKIARR PAGTYVSEHC CTCPPGWPQB DCLSGNLVVI MMSTESNSSA RKLEMEATG RKSSKILKKG	LINED LLING EIPO	2000 2000 2000 2000 2000 2000 2000 200	ACCECCACA ACCECCACA ACCECACA ACCECACA ACCECACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA ACCECTACA	ACATECHAAC ACATECHAAGG TETGEAAGC TETGEAGC TETCCAGC CTTCCAGT ATTCCAGT ACACGTACAGA ACACGTACAGA ACACGTACCAGA ACACGTACCAGA	TCCTGGGCAC TCATTGAGGA
WO 02/0  MTGGGGACT  OCCOLOGICA  OCCOLOGICA  ACCOLOGICA	GGCGAGAAAT CACAAGCAT GACAAGCAT ACCCAGAAC CTTOTAGCAG ACTOTAGCAG ACTOTAGCAG ACACCCAGCAG ACACCCAGCAG ACACCCAGCAG ACACCCAGAGC	TCCCCACAGG GACTCTACAT AAGAAGGACA GATGAGGACA GACTCACGCCCC CAGACCCTCC Beq 1D NO:	1 HOTSPESSTA TGQVLTCDKC LPCAALIDRE SSWMKCKAYT VPSSTYVPKG QQOPHHRHIL VLVVIVCSI	ALRGHRANDV VEKIRG SPODNAKGPP VDESEP DDMLHFLAPE ELRVIE Seq ID NO: 478 DN Nucleic Acid Acce Coding sequence:	1 derergeech Addiscrand Addiscrand Adreedeed Adreedeed	TOGGCCTCA TTCGAAGCTG CTGTACGTGG CTGTACGTGG CCCCGCGAT TTCAAGGCATC AACATGGAAGC AACATGGAAGC AACATGGAAGC	ACCTTODIC TITITITICA ATTOCCOCA TICTTICATO TICTTICATO TICTTICATO ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST ACMATISMOS CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTOST CAGCARTO	GATOTECTET
\$ 10 15	20 25 25	30	45	55	09	65	75 80 85 85	3

=

	KEVTPBALV JASSRVOPP APOGRVNOM KLUARKES TVALKUJPK SQIEKEVVER KLIGNARG ELVKELQHSC TFODGRTATI GGELKADOR NUNARPEJRK KTHOCHÍDVL PRESAGISKÉ TVARIVKYDL KFRÁSVFTGA SRRVLEPSAL GGVA
	LV LAGRE BH FIVAL RG ELTO FG WEVEL WE TYRR!
	KEPVTPBA VYLAREKK YLILEYAP KGELKIAD PPFEBASH BRRVLPPB
•	PROGRAMMA INTERNATION   PAGESTANDE   PAGESTA
086443	AQCESSIVE PRESCRADES LETLOCKUE EXPTERALV LEGISSKOPT ANOCKNOSS AQCESSIVE PRESCRADES DE PLEGORIOS VILLEGISKUS FULLOLING EQUESCUTOR PRESCRADALM CHURKVIHOD INPENILLOLI RESERVAND EXTRELOGES TROOPCATION RESLADALM CHURKVIHOD INPENILLOLI RESERVANDO HENVADEUR RINCOTIDIU RESLADALM GHURINALICH VILLEGIAND PERSANSE TRIBUTINDOL REPARTORIO DOLISEIJANI REPEZIPLAJON VERIFINANDA RERVIAPRALI GOVA
WO 02/08644	MACKENSTPW 1 SEGTPDILTR 1 CLRRSTEIGA 1 WEELADALMY PPEMIEGENGI 1 QDLISKLERR 1
	٧

\* 2 2 2 2

8eq ID NO: 482 DNA sequence Nucleic Acid Accession #: AK055643 Coding sequence: 38..1423

ន

		11-	-33	<b>1</b> -3	₽_	15 -	
15	AGAACGGCTT	CCGGCGGGAG	CTOTOCAGCT	CCTTATCATO	GGGACAATTC	ATCTCTTTCO	Ç
	MANGGAGA	AGATCCTTTT	TTOOCCAAOTT	DITACODDAA	TTTAGACTTG	TAGCAGCTGA	22
	CCGMAGGTCC	TOGARDATAC	1007777700	TOTANTANAC	TTGATATGTA	רספטדוסטד	180
	GCTTATCTGG	TOCAGITOTA	CTAATAGTAT	AOCTITAACT	<b>GCCTATACT</b>	ACCTOACCAT	?
ç	TITIOATCIT	TITAGETTAL	TOACATOTET	MINAGITAC	TOGGTANCAT	TUALGUARACC	0
3	TAGCCCTOTC	TATICATES	COTTTONAND	ATTAGAMENC	CTOCCTOTAT	TOCCTCCAC	2
	AGTCTTOOCA	CAGTTGGGAG	これにいいます	ATTANABAN	AGTGCAGAAC	OCTITION	Ç
	ACAGCCCGAG	ATACACACOG	GAAGATTATT	AGTTGGTACT	THOMOGUC	THOUSE OF	4
	CCTGTTCACO	ATCCTTCTA	TTCOGANTA	ACCTITION	TATOTCTCAG	AAGCTGCTAG	940
Č	TACGAGCTOG	CTTCANGAGC	ATOTTOCAGA	TCTTAGTCGA	AGCTTOTOTO	DAATTATTCC	9
?	GOGACTTAGC	AGTATCTTCC	TYCCCCGAAT	GAATCCATT	OTTITIONITIO	ATCTTGCT00	9
	AGCATTTOCT	CTITIOTATIA	CATATATGCT	CATTOMATT	AATAATTATT	TTGCCGTAGA	52
	CACTOCCTCT	<b>GCTATAGCTA</b>	TIGCCTICAT	GACATTTGGC	ACTATOTATO	CCATGAGTGT	780
	GTACAGTGGG	AMGICITAC	TCCAGACAAC	ACCACCCCAT	<b>STIATIOOTC</b>	AGTTOGACAA	9
;	ACTICATIONA	CAGGTATCTA	CCTTADATOC	AGTTTTAGAA	<b>OTCCGANATO</b>	AACATTTTTO	900
30	GACCCTAGGT	TITIOGCICAT	TOOCTOOATC	AGTGCATGTA	AGAATTCCAC	GAGATGCCAA	8
	TOMOCAATG	GTTCTTOCTC	ATOTOACCAA	CAGGCTOTAC	ACTICAMENT	CTACTCTAAC	1020
	TOTTCAATT	TTCAAGGATG	ACTOGATTAG	<b>OCCTOCCTTA</b>	TTOTCTOOOC	CTGTTGCAGC	200
	CAATOTOCTA	AACTITICAG	ATCATCAGGT	<b>MATCCCMATG</b>	CCTCTTTAM	ACCOUNTACTOR	1160
1	TGATTTOAAC	CCAUTTACAT	CAACTCCAGC	TAMACCTAGE	AGTCCACCTC	CAGAATTTTC	1200
35	ATTIMOACT	CCTGGGAAAA	ATOTOMACCC	AGTTATTCT	CTAMACACAC	ANACAAGGCC	1260
	TIANGGITH	GOTCTCAATC	ATOGACACAC	ACCTTACAGE	AGCATGCTTA	ATCAAGGACT	1320
	TOGAGITICCA	COAATTGGAG	CACTCAGG	ATTGAGGACT	COTTTTACA	ATATACCAAG	1380
	TAGATATGGA	ACTIVITATA	GAATTGGACA	ACCARGACCA	TOATAGACTC	TACTIVITY	140
:	TTATAAGGAA	TATTGACTCC	TTGGCTTCCA	ATTTATTAG	TAATCCAACT	TTGCATTGAC	1500
40	TOTTTAATCA	TITACTCTAA	ATCITAGATA	ATAGTAGTCT	TOTACACT	TCATOAAACC	1560
	TATOMACTA	TATTTTGTA	AAATGTATTT	<b>OTGACAOTGA</b>	AATCCTCGTA	AATGTTAAAG	1620
	CCTTTAAATA	COCTTCCTTT	AGAAAATOTO	TITCITIMA	TTTOOYTT	<b>OCTATICATIO</b>	1600
	GTTTTGTAGT	TOACTGCAGT	<b>STGATGTGAC</b>	CTTACCTTTA	TANGAGCCAC	TTCATCCACT	1740
;	AGATCTGTCA	CATTACTARG	ATACCATATT	acrimina.	TCCGAGACOG	AGRICATION	1800
45	TOCCACTOTO	CCCGGCCAAT	ACATTATTAT	TAACTTAAOG	CTOTACTTA	TTAGGCTTC	1860
	CTTAGITTT	DITIONAL	GTTTTTO	ATOGAGICTC	ACTICTOTICGE	CCACCCTOOA	1920
	ATGCAGTGGC	ATGATCTCAG	CTCACTGCM	CCTCTGCCTC	CTGAOTTCAA	ATGATTCTCC	1980
	TGCCTCAGCC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTT	2040
•	TGTATTTTA	GTAAAGACGG	<b>GOGATITICAC</b>	CATOTTOOCC	AGOCTOGICI	TOWCICCIO	2100
သိ	ACCTCATGAT	CCACCCACCT	TAGCCTCCCA	AAGTGCTGGG	ATTAGGTGTG	AGCCACCGCA	2160
	CCTGGCCGAT	ATTITCTIA	ATGAAATTA	TAMATATOCT	TCTTGAATAA	TACACATTIT	2220
	CCCAAAGGGA	AAAATOTCTG	TTCAAAAGT	AAAGGTCTCT	TITATAGGIT	TTCCAACTT	2280
	AATTOCTAAA	TITITION	AGOTTCTCCT	GAATTATGTC	TTACAACTA	AMAGCAAAA	2340
	TTTTAGCAG	MATTITIOGA	ATACATTCTA	TCTAGGACAA	THAMIT	TAATTATCAA	3400
ડ	DATTTTOTT	AMOTTICIC	TOCTITIONA	ATTTTAGTAC	ATTTCIMAT		
	Bed ID No:	483 Protein sequence	* secuence				

Seq ID NO: 483 Protein sequence Protein Accession #: BAB70980.1

KALTATURA MARMALD PREPLIALILI LILLIAPPPP TALLERISE DEGESERPL FORTINGEN WAS PROFILED FOR THE PROPLICE AND THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILE FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE PROFILED FOR THE

Seq ID NO: 480 DNA sequence Nucleic Acid Accession F: NM\_004217.1 Coding sequence: 58..1092

09		=-	<b>11</b> –	<b>#</b> -		121	
9	MCTIHLPRKP TAYTYLIPD ESASRPLEOP ESASRPLEOP GLEYCHIPGUNSVYS VAIRRDANEO MOLLETONIC	GCTHLPRE DESPONDE ETRUNADES ÉNCLILIFOY NICTOTULA MOSSTHSIAL SENÉRICOS ENFORCALS ETRUNADES ÉNCLILIFOY NICTOTULA MOSSTHSIAL SENÉRICOS ENFORCALIS EYENÉRES VERSENERS VAVERANTOS BALALAMPT SENÉRICOS ENFORCATIONS VALORISMINES ANTOREANTOS BALALAMPT SENÉRICOS ENVILOTIPE NICTOCIALLI SEVETICOVI. SENERETEL OFSELACIONA SENERICOS ENVILOTIPE NICTOCIALLI SEVETICOVI. SENERETEL OFSELACIONA SENERICOS ENVILOTIPE NICTOCIALLI SEVETICOVI. SENERETEL OFSELACIONA SENERICOS ENVILOTIFO NICTOCIALLI SEVETICOVI. SENERETEL OFSELACIONA SENERICOS ENVILOTIFO NICTOCIALLI SEVETICOVI. SENERETEL OFSELACIONA SENERICOS ENVILOTIFO NICTOCIALI SEVETICOVI. SENERETEL DISPUESTO SENERICOS ENVILOTES SENERICOS ENTRE SENERICOS SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE SENERICOS ENTRE	ETRLVAADRR TWATLRKPSP TWATCRNUP PVLIDLAGAP HVIOGLDKLI HVIOGLDKLI RVIOGLDKLI RVIOGLDKLI RODDERSERV	WKILLFOVI YYBPGFERLB TWLBIRWKPP ALCITYWLIB REVBTLDOVL IPLIOMIRPA	NLICTGFLLM VLAVPASTVL ATVGEASTS IMMYPAVDTA EVRNEHFWTL LLGGFVAAM	MCRSTMBIAL MOLGALFILK MIGGINVADIA BAIAIALATP GFOSLAGEVH LAFEDHHVIP	
5	SEMUNDOLOV	BSMLNDGLOV PGIGATQGLR TGFTNIPSRY GTUNRIGORR	TOPTHIPSRY	GTINK I GOPR	9		

Seg ID NO: 484 DMA sequence Nucleic Acid Accession %: PGENESH prodicted Coding sequence: 1..900

GOCCOGAGA MARCACTE CETGBACCCE AGCECTECTE CECETITETE TETAMORING 6
GOCCOGAGA MARCACTET COCTOGACE ANGOSTOCIE ATTRACECTE 13
ANDOCCETC COLVETICE COCTOGACE ANGOSTOCIE ANTOGATOCIE 13
ANDOCCETC COLVETICE COCCAGACE CACCATOCIE CANGOSTOCIE ANGOSTOCIE 13
ANDOCCETC COLVETICE COCCAGACE TETAMORING CANGOSTOCIE ANGOSTOCIE CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC CACCATOCIC C

	_	_	_	_	_	_	
	ATOCCOCCOC	אדשככשבנשכ משפאמבושאם במאמשכנשאם לכשכככככשב הכשמשכנכל מאכככנדככם	Самадессама	coccccac	recoocce	GACCCCTCCC	ű
	CCGCGGCGGC	COCOCCOC GINGCOCCC CCCAGAGCTG GCCATCAAGT GCGTGCTGGT GGGCGACGGC	CCCAGAGCTG	GGCATCAAGT	CONTOCTOR	GOCCGACGGC	ä
	OCCUTOGGC.	SCHOOLGES AGAGCAGCT CATCOTCAGC TACACCTOCA ATGGOTACC COCOCOCTAC	CATCOTCAGC	TACACCTOCA	ATGGGTACCC	COCCCCCTAC	=
္တ	COCCCACTO	COCCCACTO COCTODAÇAC CTICTCTGOT ACOTACOTIC AATCOCCCOT GCOOCCOCOT	CTICICICION	ACCTACGTTC	AATCGCCCGT	acaaccacat	ž
	9007720000	ADCTRICACIO GOOCTOTACA COSSOABET BOSSCOASCO TCTCOSCOSO ADSCOCADA	CCGGGGGAGCT	00000000000	101000000	ADGGCGCAGA	Š
	GOACCCCGGG	JOACCCCGOO GAGGAGAGTO GAGCAGGCCC COAGGTGGCC CTOGTGCGGC CCAGGACGCT	GAGCAGGCCC	CGAGGTGGCG	CTOGTGCGGC	CCAOGACGCT	Š
	CTTCCTAACT	CITICATARET CAGGCTCTCC COGCCCCCC CCTGCAGTOC AAGTCCTGGT GOATGGAGCT	CONCOCCACC	CCTGCAGTGC	AAGTCCTGGT	COATCOACCE	2
	CCCCTOCCC	COGTGCCC TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTCC	DOACACAGG	GGACAGGAGG	ATTITIOACCO	ACTTOOTTCC	ŧ
œ	CTTTOCTACC	ETTIOCTACE COGATACEDA TOTETTECTO OCOTOCTICA OCOTOGICA OCCEADETICE	TOTOTTOCTO	OCOTOCTTCA	<b>acataotoca</b>	accessorace	8
	THOMACA	THEMAMON TENENDAMIN ATGESTIGES GAGATOSTICA COCACANOSE CENDOSCOT	ATGCCTGCCC	GAGATOCOCA	COCACAACCC	CCAGGGGGCCT	ŝ
	000000000000000000000000000000000000000	CHANGE OF STREET AND ADDRESS OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF	-	-	-	Carried and a	;

										•
720 780 840		120 240 240	•	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	999	80 120 180		60 1120 120 120 120 120 120 120 120 120 1	600 650 720 720 780 900 900 1000	11200 11310 11310 11310 11310 11310 11310 11310 11310 11310
OCCUACIA GAAGUAGTA GAACTUAAT CTTCOTTTGA		S1 TCMOTPARY RGGAQAAQDA ACPSWQPSS QPQAQGIAEK RWKKFPCFV		1 accertece descande consequent cettractae cettractae cettractae cettractae cettractae daaccasses aarccasses	ATTTGACTCG TGCCAAAGGT A	S1   YTCNGYPARY SYVQPESPQN AQGLAEKIRA KPPCPV		51 	GCACAAAAGC AGCTGCCCAC TGCACCTCAG CCGTATAAAA ACCTCGAGA ACCTCGAGA CCGAAAATCC GAATATTAC GAATATTAC	INTEGRATED AND AND AND AND AND AND AND AND AND AN
CTCAGGGTCT AGAAGAACTT SOCTGGAGAA AGATCTTCTG		41   AVGKSELIVS OPROCDWSRP LCYPOTOVFL DQGGREGPVP AKGVRTLSRC	٠.	41 TCCGGGCCCC GCOTGCTGGT ATGGGTACCC TAGGTACGCG ACTCGGTC TAGTCGGGGCC TAATCAGCT TGGCCGGAAA	TGAAGGAGT AGAACTGAA SCTTCGTTTG	41 		41 CAGAACCTCG COTCCCTGGC CCAGAGATA AGCACCAGC TCACCTTCA ACTCGCAC ACTCACACC GCCTGCACC GCCTGCACC	COATAGGACT GAACAACGG GAGGCACCC GAAGCAGCC COOTTITIC COOTTITIC CACTOCCCAC ACTOCCCAC ACTOCCCAC ACTOCCCAC ACTOCCACA CAGATCCACA TCCGCCAT TGAAAACAAC	TOCATAGO ACCAGADA CATCOTOCO CATCOTTCC AMCENCAT TOMITICAL ATTACOTTA TATTCCTOTO TATTCCTOTO TATTCCTOTO COCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOTOCO COCOCOCOCOTOCO COCOCOCOCOTOCO COCOCOCOCOCOTOCO COCOCOCOCOCO COCOCOCOCOCO COCOCOCO
CAACCCAAC OCTTAACC CACAACCC CACAACCC	edicted	31 GIRCYLVODG GAGYBAGGIR GQEDFDRLINS RDDVNVLIQL HYARLEKKLIN	063832.2	11 CCGCCCCGC COGCCCCGC CANTICTICA CANTICTICA ACCTICATO ACCTICATO GCTCANGTO GCTCANGGTO GCTCANGGTO	CAGAAGAACT COGCTGGAGA AAGTTCTTCT	31 	014398.1	11 CCCCACACTG GCCCTTCO TTTCCACAAAA AMACTGTCA GATGGTCATA ACACCCAACA GCCCCATATT TCAACCGTCA	OCAACHTAN CATOCOCOAG OTTCTAACO GACAAGAAT GCCTCTGGAA TTAACCATCT TTAACCATCT CAAACAGCAG	TTTGGAMTA ATCOTGGTT CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE CONCRETE C
CCCGATGCC TAMPTICTON TOCCATTAMA CTCCCGCTTAC	n sequence POZNESH pr	21 	P S	21   CCAGAGCTO CCCAGAGCTO CCCAGAGCTO CCTCTCTOTO GGGATGCTTC GGGGAGCAT CCAACCCCG GGGGGCGA	AGCCTTGA CCACAAAG CCGCTGGA CCGCTGGA	21 PRRESAP IELMDTA VGTQADL AILSAIE	9000 14 NA			MATTANCHA MATTANAGTO MATTANAGTO ATTANAGTO MATTANAGTO MAGATANA TIMACANAG MATTANAGTO MAGANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATTANAGO MATT
02/086443 og occorances er ocracraces og cratrerea te receaeces	485 Protes	11 	6 DNA e	11 	TTGAGTGCTC OTGCCATTGA TCTCCCGCTG 187 Protes	11 	ND: 488 DNA sequ : Acid Accession Requence: 6413	11 	OTANCEAANC ADANGCETOA GCACAGETOC TCANGACTOC TCANGCECCA TCANCECCOA TCANTATTCA TCANTATATCA ANCATGANCT ANCATGOOGT	THEATTHEA MATCHOCTO AMTCHOCTO ATRIANATA CCCCASAGA THEATCHOCTO THEATCHOCTO THEATCHOCTO TECNOTITE TOWNSTRAN TOWNSTRAN TOWNSTRAN TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA TACATORIA
WO 02 GACCAGGGG ATCGGAGCT TTTOACTCGG GCCAAAGGTG	Seq ID NO: Protein Acc	1 HPPRELSEAR RPTALOTPSG LPNSGSPRPA PQNITEKNLP IRACCTLECS	Seq ID NO: 48 Nucleic Acid Coding sequen	ATGCGCGG CCGGGGGGG CCGGGGGGGGGGGGGGGGGGG	TGCTGCTACC GCTATTCTCA GTGCGCACCC Beg ID NO.	8121	Seq ID NO. Mucleic Ac Coding sequ	GGGCCGATT CGGCCCGATT ACATGCCC CACATGGCA ACTGCAGA ACTGCAGA ACTGCAAA ACTGCTACAA ATTACTGAG GTTACTGAG GTTACTGAG GTTACTGAG	ACTOMICCO ACANCOSTC CCATCSTCAC CCATCSTCAC TACTTCACA TACTTCTOT TCATATATA CANSSATCA STOASTSAC STOASTSAC STOASTSAC STOASTSAC	THOMOGEN CONTOCANTO CONTOCANTO THOMOGENATO ANTOMOGEN CONTENTATA ANTOCATO ANTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONTOCATO CONT

WO 02/086443  OTTOTAM TOTITIAND THANGOAG MANGARGA MICHGETHA TATTITIAN 2220  CTRAINCAIR COTORIGINA MATHERAN TO TRAINANT ATTORESHO. AND TOTOTAMA AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND TOTOTAMA ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO. AND ATTORESHO	20 Protein Accession 8: NP_055311.1 41 51	PRELIGIO MOL 430 ENA sequence  PRELIGIO MELLA MEDIA MOLTANIA  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GOTTOWNOS ACCOMANCE ON MIXED TITLEGIAN BOATROCH CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL	Seq ID NO: 431 Protein sequence Protein Accession 8: MP_005400.1  1	1 11 11 11 11 11 11 11 11 11 11 11 11 1
\$ 0 \$	:	35 6 45	60 55 50	65 7 7	

WO 02/086443
creatages certectree cuernoca areacerto autacomo 1100
regionare certectree excurace cuernoca areacerto autacomo 1100
rectautor autacorre erocanosa neutrales en travertera acuadore 1100
rectautor acradente recognica erocanosa cunacitar retroradas 1100
conculares acuados areacanos erocanos autacorre contrata 1100
certectro acuados erocanosa erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos erocanos

ន

Seq ID NO: 495 Protein sequence Protein Accession #: NP\_002072.1

<del>6</del>

S

PCT/US02/12476		
660 720 720 720 720 840 860 1112 860 1124 1125 1126 1136 1136 1136 1136 1136 1136 1136	120	1100 1100 1100 1100 1100 1100 1100 110
TECOLOACIA CETEGORANTO CETEGORANTO CECOLETOCE ANGOLOGIE CONTENTANA CATTIANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA CONTENTANA C	51 	ELECTRONICO DE CONTROLOGO DE C
TCAGANGGE TANGGCCTT TCTCTTCT TCTCTTCT TCTCTTCTT TTTTTTT	41   YLQOPKVNLE   QDXGPAFIRE C	enconcecue currentele
ENGENERAL MACCECTED MEDIACOCT MACCECTED MACCECTED MACCECTED MACCECTED MACCECTED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACCETED MACC	OLVAG SENRK QEDE	20000000000000000000000000000000000000
CAGCOATIGA ARACCACIO CCOACCOC CCOACCOC CCOACCOC ARACTACA MATTACA MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC MATTACAC M	P_000568.1 21 21 BETRICLENV TWAPDEGVAV	adactraca datactraca contropera decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporate decorporat
R6443 DACTEMBRO SULTEMBRO SULTEMBRO SULTEMBRO TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE TOTOGRADE	Parotei 1. TRESUMOAP RESUMOAP WCLSCYREG WEADOPVSL 94 DNA se Accession	COMMONTORY  CONTRACTORY  CONTRA
WO 02/086413 OCTATEGROUS CHETHER CTRETECRA TOTALE TOTALECRATOR CANTOR CTRECTORY CANTOR CTRECTORY CANTOR CTRECTORY CONTROL CANDON TROUBLE AND AND AND AND AND AND AND AND AND AND	Seq 1D NO. 493 Probection Accession 1  1  1  1  1  1  1  1  1  1  1  1  1	adertaceas adertativar consolication and and and and and and and and and and

	Seq ID NO: Nucleic Act	5 8	sequence	. 2.0291	:	-	
ಜ	Coding sequence:	Jence: 40.1511	011				
		<b>:</b> -	<b>7</b> -	#-	<b>\$</b> _	S -	
	GOGGCAGGCA	ATGAGAGCTG		OCCUANOCA	TGAGTGACAG	ACCCACAGCA	8
32	GGGGTCTGGA	CTCMOCTT		OTCACAGGG	AATTICTOC	CATGCTTAIT	1 1
	TITOTICICO	TCAGCCTOGG	ATCCACCATC	Actodopto	GACAGAMA	GCCTTTACCO	2 5
	TTTGGCCATA	TCAGCGGTGG	_	CCTGCAGTGA	CTOTGGCCAT	COTOTOCACC	3 2
40	AGGAAGATCA	DCATCOCCIA	OTCTOTOTTC	TACATCGCAG	CCCMBTOCCT	GGGGGCCATC	420
2	ACCATOGITC	ATGGAAATCT	TACCOCTOOT	CATOGICTCC	TOADTTOADT	GATAATCACA	2 5
	TTCAATAGCTT	TACCALTED	ATTTCCACC	TOTGATTCCA	AACGGACTGA	TOTCACTOOC	9 9
4	ACTOOTOCCA	OCATOMATEC		TTTGGACCTO	CAGTTATCAT	GOGANATTOO	130
£	TATGAGTATG	TCTTCTGTCC	ACATOTTOAA	ATCATAGGAG	CTOTOCTOGC	TOCOTTON	9 2
	AAAGCTGCCC	AGCAAACAAA	AGGAAGCTAC	ATGGAGGTGG	AGGACAACAG	GACTCAGOTA	8
Ş	GAGGAGAGA	AGGGGAAAGA	CCAATCTGGA	GAGGTATTOT	CTTCAGTATG	ACTAGAAGAT	1020
2	GCACTGAA	GCACACAAGA	TAGAAATOTO	CTGTCCTCAG	ATTTCCTTCC	ACCCATTANG	1080
	GTCTAMCAA	TAAATATTTC	ATAATTACA	AAGGAGGAAC	CONTONIO	TATTOTOM	1200
į	TCTAGTTACC	TTTCATTAAC	ACCMITT	ATOTTCTTAL	CARCATTOO	TIMOTOTIO	2 2
S	CCTGACAGAA	CTCMAGACA TATTTGAATA	COTCTATCAG TTTATTCTAT	CTIATTCCTT TAAACTGAGT	CTCTACTOGA	ATATTOGTAT C	1380
99	Seq ID NO: Protein Acc	Seq ID NO: 497 Protein sequence Protein Accession #: NP_001641.1	n sequence				
		: ::-	11	<b>14</b> –	7.	<b>16</b> -	
65	MEDRPTARRW GTERPLPVDM AQCLGAIIGA	GREGALCTRE VLISLEPGLS GILYLVTPPS		TOAFMKAVTA I SGGH I NPAV HCNLTAGHGL	BPLAMLIPVL TVAMVCTRKI LVELIITPQL	LSLGSTINMO BIAKSVPYIA VPTIFASCDS	9 2 2 6
	KRTDVTGSLA AVLAGGLYBY VLDVDRGEEK	LAIGPBVAIG VPCPDVEFKR KGKDQSGEVL	Hlpainytga Rpkgapskaa 88v	GOTKGSYMEV	av i monnedh Ednreqveto	WIYWVQPIIG DLILKPGVVH	28
29	Seq ID No. Nucleic Act Coding sequ	Seq ID NO: 490 DNA mequence Nucleic Acid Accemsion H: 3 Coding sequence: 1:.1744	Tuence 1 #: AB020684 744	4.1			
75		- = -	<b>1</b> 2	<b>=</b> -	₹_	<b>.</b> ۳	
	CCCCCTTGTC TTGGTACCGG	ATTATACAT ATTATACCA AGAGGAGAAG	TAMAMANTT AAATAATGGA GACTCAGTCC	CTTGATTGGT	CCTGAGGTAA ATTCAAACCA TGTGAAGGAT	TTTTGGCCAG AGATATGTTG	9 2 2
80	CATATATGC	TATGTTGCTG	TAATTTTAT	TTTANATOCA ATTAGGAGGC	CTAATOATOO	TOTTOTICT	200
	CTCATATOCA	TTTCTTOTTC	TTCAGATGTT	OCTADTOACT CATTTCCAT	CATATTOTOS	GGGCTACMA TGCTTCCTTG	5 5 5
82	ACTITION TO TITION TO TITI	GATATATOTA GATATAGATOT ATTTGGGGTA	AATTACTOA AATTACTOA TTCCCAACTC TTCTGGCAAT	GATCATTAT ANTOTATTAT GAAACCACAT	ATACACATOA ACTTCTTATT TTCCTGAAAA	TATATOTTOT FTFCTCTTOC ATGCTTCTTC	12668

·c
-
Z
_
=
G,
_
š
∍
$\geq$
_
C
~
_

780 840 900 960 1020 1140	1260 1320 1320 1380 1440	1560 1680 1740 1900	1980 1980 2040 2100	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	25 60 25 60 25 60 27 60 27 60	2820 2980 2980 1000 11180 3240	100000000000000000000000000000000000000	3860	12260
TCATACTEAA ACTTACTAAC CAGCGGAGTT TTCCAGTGT TTTACCATGCT TTTACCATGCT	TTGGATGGC TOTCAATACA ATTTGCCCCA TTGCGGTGC ATCATCCACA ATAATCGGAA	ACATTCTAGA TITGGGATGI AGGATTCCAA TIGTAANGA	TCANATAGAA ACACCTTTAT TATATACCTTO AAAACACAGT GOGCTOATTT	ACTTGACTTT AACTTGAGTT GTTTTACTTC CATTATTAAT TOGCATTATC	TTTANAMA TTTANAMA ATTTANTA ACTATTTAN TCATTANA CANTANACA	TATATTTA TAATTTOOT TITAGTTTT CCTTGTATGA ATGAACCTC TATOGCTGA ACCTCATTO	GAAGCACGC TCCCTGAAG TTCTCATTTG GAAGCAGCC GAAAATGGG	AGCAGTTACA GTAATTTCCT ATTAAAAATA GCTTTTTCCA	TOGCCACAG TOGCCACAG TOGTAGCAG AAATAGCTA ATAGCCTCT ATGAGAAAT TATGAATTTT
TTTGGAACTG CATATTGGCA TATACCTGTG AACATTATTGC GAATATTGGGG GGAGAGAGTAA	AGACAGCTAT TTAGCAGCAA GAGTTCAGCA GATGCAGTGT CCCATTGTGA TACTCAATGT	OTGAACTATT ATGCCTGAAA CTCTTGGTGA GTCCTAGAAG	ANATOACTT ANATOACTT TGCAAATOAO CTGTATAAO GACAATGTAO	TOCCTCT TOC CCCTOTCATC CTATCTOTTT TTTCCTOCC TCCAGCATA	CTTCCCATA TATTCTTOGT AATOTTTAT TTTAGBAAA TOATTAGACA	ATGAGTTTT CCTTATGTTA COTCCTC TCTTGAATT CTTCAAAACG AAAGCTGAC CAGGCAGATT	TECCTCAAA GAATGCTCCT TEGCCACTGT AGAMATAGG CAACAGTCCA	GTGTACATCC CTCACCCCCA GGAAAAAAGC ATATAAATTA	TATGCAGCG CAATGCAGT GCATATTOT AGAAGCATC CTTAAAAAG AGTGATATTA AATGTATTTA AAAATCATGA
TTTTTGGTTA AGATGAGGT TACTTTATTG ATACACANG GATTATTAGT GTTTGATCAT TATTTAATT	GATCTGCTCA GTTTGCTATA TATTGTAGGG TACTAGACA TGCACTTCGG	AMOTTAMA TOUTTOCAGE CTTATOTAC TOTTTACAM GAACTACATC	ACTITIATAG TCTAATTATA AAATTTGCTA GCAAAGCTAC GGACAATTCT	TICTITITIC TCATGICAGC CTATATAAAA TTAATGAAGC	CICTTCTCCT ATCAAGTACT AGCATTATTC TAATTATAGT AATGTATATT TTTCTTTTAC	ATATGATA AGCCTTAG AGTATATT TTCTACACC AATGAGAT AATGAGAT TTCTTAACCA	CTGAGGAGTG CAGCTCCCAG TTCAGATTTG TCCTAGTTTT CGATGATGCA	GTGGCTGATT TTATATTITT ATTCTGTATA ATTAMMGTA	ACCTOTATED TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOATGOOCH TO GOAT
TTCAAGGATG TTGATATTGC AGGATTTTTGA CTCCACTGA TTGTTAGAAA GAAACACCA CAGCCTTGG	TOGCATCACT  OTCCTATIOT  CCCAGTGGAA  TCAAATATAA  TTAAGCTCTC  OAGCCAGAAC	GAGAACTGAT GATCCAAGCC GGAAAACTCC TCCAGAACAG TGCCTACGGA	TATCCOMAA TGAATOTCAT GCACCCTTTA GCTAAAGTGA TGAAAATACA	TOCCCCTTGC AGTTCTTCGG GGAGTOTTTG TGTTCTCTTG	CTTGCTCTCT TTGCATTTTT TCTCATTTTT TTTCATGTTT TCTAGAAACT CATGGTAATT	AATCTAMGA TATAAGACA TATAAGAAT TITOAAAAT AATTIGIOTO TAGGGTTTTA CAGCTTCTCT	GCTGCAAAGG CCTAGAGCCG GGCAGCGTTC CTTAGGCTTT	TCACCTGAGT TACATTTATT ATAAGTAGAA GCTGGGAACC	AGAGGCTAA AGCATCCACA OTATTAAAG AGAAAGTAA ACAAAGTTOG ATATAGTTTT AAGTGATATT
186443 TTATGOOTTA TCTANATTT TTAGAGAA GANAGAGA ACACATOCTA ACACATOCTA	ATOTOTOTA OTACATCCTO ALTCTOCAA ATAGATOGA ATOGCAAOTO OCAGOCTTGA	DANGTRANDO TOTOTANDA GCCANTOCTO ACCACTOTAT CATGACCTGC	TTOTCATT CTATTCAT TAINTTGT	GAACTATTAA AGTGATTGTA GGGCAGACAT TTTTGTTCTC GGACCTTGTG	CTCTCTCTCT OTTTACTCAT ACTOTATTT CTTTAAAGTT ATATAGTGCA GACTOTAGTA	TGCTGTCAAA TGCTGTCTT ATCATTTTAAT CTTAGAAGTTT TTTAATTATA	ACATAACTCA TOTOCCACC GAGGGACTCT GATTTTATTT GATTAAAAGC	TICATTOTTOC ATTATACTTT TICACATOTA	ACTTTCOAGG ACCACTOTOG GTACAMAC CTTTAGTAG ATTTCOAMA ACCAMAMAN ACCAMAMAN ATCAGGATA
WO 02/1186443 TGARTAGE TETAMO ATROMATE TTAGE TGARTINE GAMMO TGARTINE GAMMO TETATAGE TETATO TETATAGE TAGE TTAGE TTAGE TTAGE TTAGE TTAGE TTAGE TAGE	GACACCACA CTTTTGCAAA AGGTTCAGCA AGAAGAACTT CATGCCCACG					CTTTANGAT TCTANANGC TTCTCCTAT ATTTTCTTCTAT ATACCTCCAC	_ : : : : : :		
٧	9	15	20	52	8 %	. 9 40		20	92

Seg ID NO: 499 Protein sequence Protein Accession #: BAA74900.1 65

	9	130	180	240	900	360	420	480	540	
21	IESCEGLGDP	MYTPPLRESP	IABLPAVYVV	KPHPLKINVS	TLLYTCAAEF	PDHGELVYBA	PAILAAMSIQ	ALRPIVNHPH	CCSMPRINDV	
<b>=</b> _	NLYPEVILAS WYRIYTKIMD LIGIGTKICM TVTRGEGLSP IESCEGLGDP	IYOTYLSGER LOGLYTVICE FFREGECTRY I	OPAQPVLLTQ :	MLLTSYYASS LVIINGILAN	SKPPSYMOTO	KOOTHVRKHO	ILIMALIKLFL THINCYMASL ICSRQLFONL PCKYNPCATV	MPTHASVKLB	ESWCVRRSKP (	
<b>1</b> -	LIGIGARICA	LOGIVITALCE	LYROSLIALC ISWVPPMLPW (	MLLTBYYA68	WLFOTVILK YLTSKIFOIA DDAHICMLLT	LVVFVAIVRK IISDMICVLA	ICSROLPONL	TKPDAVFAGA !	KLKVNYYILB I	
<b>:</b> -	WYRIYTKIND		LYROSLIALC	INTHMISTA LCPVLMPGNS I	YLTSKIFGIA	LVVFVAIVRE	TPHREVMASE	EEFIENIKAB .	kivysmyskk areevrreli klrunyyilb Lonluvdsk phfttvpqnb vyrvlevvrb	
<b>=</b> _	NLYPEVILAS	LNGLAMALPP	LVTHILRATK			YTKTLLPVV	ILIMRLICLFL	INGEPENLPO	KIVYSMYSRK LCNLLVXDSK	
	PLVINTLERP	ACPYVAVIPI	BYPPLVLOML	GYIDICKLRK	ELBLAVIOC	DPMBKBTPLR	LOLLAYTALG	GBANLOTOWN	YEDAGLRART EDPAKAGKTP	
	ę	?				į	C			

Seq ID NO: Soo DNA sequence Mucleic Acid Accession N: NM\_001276.1 Coding sequence: 127..1278 80

	9	120
11.	C CCTGTCTAGG	CTCTGCTGCA
<b>:</b> _	GOGANGNOCC	CCCTGCCCTO
<b>-</b>	ACAGGGCTO	GCAAGGGA AGAGGCCACA CO
<b>#</b> _	TAAAGGAAGT	2
<b>:</b>	GACAGGTATA	CTOSCAC CASSASCEST O
	AOTOGAGTGO	TAGCTGGCAC
82		

	WO 0.0	03/00/2413					
	GCCAGAATOG TGCTCTGCAT	OTOTOAAGGC ACAACTGGT	GTCTCAAACA	OCCTTT0T00 ACCAGCT00T	TCCTGGTGCT CCCAGTACCG	OCTCCA0TOC GOAAGCCOAT	
~	GOGAGCTOCT GCCAATATAA ATGCTCACA	CACTCAGATOR CACTCAGAA CACTCAGAA	CATCGACCGC CATCGACACC CAGGAACCCC	TTCCTCTGTA TGGGAGTGGA AACCTGAAGA	ATOATOTOAC CTCTCTTOTC	CTACAGCTTT GCTCTACGGC TOTCGGAGGA	
	TOCATCAAGT	CAGTACCGCC	ATTCCTGCGC	ACCCATOGCT	£8		
01	OCCEMATITA ICTGCOGGA GATTICATIA	TAMAGGAAGC AGGTCACCAT GCATCATGAC	CCAGCCAGGG TGACAGCAGC CTACGATTTT	AAAAAGCA TATGACAT CATGGAGC	CCAAGATATC OGCOTOGGAC	CCACACACTO CCACACCCTO CACAGGCCAT	
15	24CA91CCCC TATGCT9100 CCCACCTT00 TCA99ACC90	GOTACATOTT GOTACATOTT GOAGGCCTT GAATTCCAGG	CACTCTGGCT CACTCTGGCT CCGGTTCACC	GCTCCTGCA TCTTCTGAGA AAGGAGGCAG	GTAAGCTGGT CTOGTGTTGG GGACCCTTGC TCGGCCACACA	CANCACTUAC GATGGGCATC AGCCCCAATC CTACTATGAG	
	GCACCAAGG	OCAACCAGTO AGGATAGGCA	GCTAGGATAC	GCCATGGTAT	AAAGCGTCAA		
20	GCCCCTCTGG GCCCCTCTGG GCCTCAGTCT			CACACAGCAC GATCACCTGC AGAGGTCCAC	GGGGGCCAAG CCTGCTGAGT AACACACAGA	GATGCCCOT CCCAGGCTGA TTTGAGCTGA	
25	GACTICOGGAT GACTICOGGAT TOOCAAGGGA TOGCAAGCTC	TAGTACACAC ATTICTTCAA TATCACCAAG	AGGGATGGGG TTGTTGATGA CTCCCTGCCC GAGCCNACA	TTATGGGAA TTATGGAA CCTAGCCTC TCCTACAGA	AGTTTACAGA CTTATCAAG CTCATTACAAG CACAGTGACC	COCCATOTA TCCCCAAGC GACACCATT ATACTAATTA	
30	ACTICCCCTT CUCTTTGCTT TCTTCTGGGT ATGTT		CAGCTGCTCA	ATAAAGTACA ACCCCTGAGC			4 2 2 2
35	Sag ID NO: Protein Act	Sol Prote	In sequence NP_001267.1				
3		<b>11</b>	<b>%</b> -	<b>:</b> -	<b>\$</b> _	51	
<b>9</b> ;	MGVKASOTGF I SNDH I DTNB KSVPPFLATH GKYT I DSBYD VGYMLALGAP DPLRGATVHR GSFCCQDLRP	VVLVLLQCCS WNDVTLYGNL GPDGLDLAML IAKISGHLDP ASKLVMGIPT TLGQQVPYAT FLLAQQVPYAT		WEQYRECDGS KTLLBVGWN TTLIKEWKAR AWRGTTGHHS BTGVGAPISG GESVKSKVQY	CFPDALDRFL PGSGRFSKIA PINEAGPGKK PLFRGGEDAS PGIPGRFTKE LKDRGLAGAN	CTHIIYBEAN BNTOBRRTFI QLLLBAALSA PDRFSNTDYA AGTLAYYBIC WALDLDDFQ	
<del>.</del>		502 DNA sequence id Accession #: Ni uence: 181669	*'	006474.1			
20	1       GCTGCCTAGG	11 GTCTGGAAAG	21  -  -  -  -	31  -  -  -	41 5000CTCCT0		
55	TCCCCCAGC ATGTCGAAGG GAAGGAGCCA GTTGCCATGC	TOTCAGCTCT TOTCAGCTCT OCACAGCCA CAGGTGCCAA	GCTCCTCCAG GCTGCTCGGC GCTCTTCGTT GCCCAGAAGAT AGATGATGTG	CCCCAGGAGA CCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG	TURCECOURT OCNACACTO COTOCCTOTO CTACAGOTT GAACCAGORA	AACOGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT	
9	AMERCESSET GAGGATCTGC GCCTCAAACG GTTGAGAAAG GCCATCGGTT	TARCACTCT CAACTTCAGA TAGCCACCAG ATGGTTTGGTC TCATTGGTCG	OGTGGCACA AAGCACAGTC TCACTCCACG AACAGTGACC AATCATCGTT	AGTGTCAACA CACGCGCAAG GACAAAGTGG CTGGTTGGAA GTGGTTATGC	OTOTAACAGO AACAAGTCC ATGGAGACAC TCATAGTTGG GAAAAATGTC	AAGGGCACA ACAGACAACA GOTCTTACTA GOTAGGTAC	
65	TTCTGACTCT	OTOGCCCTOT CAGATTCCAC TOGTTCTAA	CCCTGAGCTC	OTTTTCCAA	GATGACCCTO ATTAACCGAG	GANGACCIT	
92	Seq ID NO: Protein Acc	3 Protes	In sequence NP_006465.1				
75	1 	11 	21   EGASTGOPED EDLPTSESTV AIGFIGGIIV	31 DTETTGLEGG HAGEGSPSAT VVMRKMEGRY	41   VAMPGAEDDV ASNVATSHBT 6P	S1   VTPGTSEDRY EKVEGETQTT	-
8	Seq ID NO: Nucleic Act	504 DNA sequence id Accession #: E uence: 62695	. 8	quence			
\$	1   CACTGCTCTG TATGATCATC CAAGATGGA	AGAATTTOTO TTAATTTACT ATTTTCATA TCTOCCAAT	21 	AACAGGCTGT GCTATGGGAA GCTTGAACGA	1 TACTICACTA GACACTCAAG GCAGCGGTG	S1 CACTGACGA GATGGGGATT TOTACCACAGA	
	TOAAGGCGGC	CATCHOOCIA	CTTACAAOCA	CTAGAGGCA	OCCIONANA	TOCATTICA	

929299

92929

9 82

TOTATION OF CONTRATOR TOGENAGO CHOUGHED TACCCATE TOANGOOD 186
COCCAACTE CAATTOOL AMERICAN THTEATTE COANGOOD 186
COCCAACTE CAATTOOLOG AMERICAN THTEATTE COANGOOD 187
TOANGANG CAATTETA ANTENCOO CTECCAAL GARGACAN THE CAATTOOLOG TOANGOOD TO TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD TOANGOOD T

HILLYLFLL L EGGHLATYKO L ERWDAYCYNP H DLEDDFGCLA D QIKYVAMDFV B

Seq ID NO: 505 Protein sequence Protein Accession N: Eos sequence

NH\_007115.1

Seq ID NO: 506 DNA sequence Nucleic Acid Accession #: K Coding sequence: 69..902

<del>\$</del>

\$\frac{1}{1} \text{TABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZP} \text{ABARAVEZPAP} \text{ABARAVE

eq ID NO: 507 Protein sequence rotein Accession #: NP\_009046.

Seq ID NO: 508 DNA sequence Nucleic Acid Accession 8: NM\_001044.1 Coding sequence: 129..1991

Seq ID NO: 510 DW Nucleic Acid Accel Coding sequence: 

deargeree docteactor receesant rosecoant ассотаск Асототог даакиссе Аситока мосства тестотот актесаас статска стасктае тестотом астатски сседавая тессетта аламаете тетовам актысска тессетта аламаете тетовам актысска 

Acceptora Acceptora dispersion dispersion from American Progression Companies Chalculum constantion and progression General Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confession Confessi

MATRIAGGO NETECCEDE ARACADAN CALCECCEGO MARACATER METECGOAD
MODANTER CETROAGGA CANTENCE ANAMERICA CHANTERA ANAMERICA CONTROLLA MANAGAGO SET CHANTENA MANAGAGO SET CHANTENA ANAMERICA CONTROLLA CANTENTE CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTROLLA CONTRO

2

2

2

	ACCACACTGA	TOCCATCCTC	CICTCIOCAT	avcacaoror	TTCATAGAT	CTTANADAGE
	ATOGACGAGC	TOGATOTICAG	GACTCCCACT GCTGCCGTTT	CACCOCACACA	ACTITICIOCA	COUTTITI
•		TTATTCTCOT	GATCTTOGCT	OCTOTOTTTC TO COLOTITE	CTOCTOTOCT	TTTAGTOOTO
•		TOGAGANTOT	CAGCCCOTCA	CCCTOOTTCA	CCCACATCAC	
	CAGGGCCTGG	OCATCATTCA THE STREET	ATACATCATC	ANDMAGGAGA	acrecy toke	CTATACTICA
Ç.			AGCCUANTIC	ACCTCCOTOG	AGCTGCTCAG	
21	CCCAGCTOTO	DOCTORATO	CTTCAGAGAC	TATCACATOA	CATACACAGA	CAACACCCC
	CTTGTTCTCO	ACAGECTICAA	CTTGAACATA	CAAOTOOC	AGACAGTCOG	DATTOTTOGA
•	AGTGGCACAA	CCCCCAAAGTC TCTTTATTGA	TOAGGTGGAT	ATCTGCATTC	TCAGCTTGGA	AGACCTCAGA
15		CTOTCATCCC	ACAGGATCCT	arccrantra	TAGGTACAGT	AAGGTACAAC
-	ATGAGAGACA				CAGAAGTCAC	AGAMATOGA
		CAGTAGGGGA	ACGTCAGCTO	CTTTOTOTOO	CCCCAACCTCT	TCTCCOTAAT
20	_	CCATCAAAGA	TOCCTIONS	COCTOCACTO	TOCTOACCAT	COCCACOOC
	TTGACAGO	TTCTCAACTG	COATCACOTO	CCAGATTCTO CCAGATTCTO	AAAATGGGAA CATTTGCGAT	OCTOATTOAG OTTACTAGGA
	GCAGNAGTCA	CATTOTAG				
25		Seq ID MO: 513 Protein sequence Protein Accession #: Eos sequence	sequence			
			ដ	:		.15
30	- Autobase		-	-	  -   ADVOVEDAGE	1.00avredut.
		RLTVDTLPPL	BTYDSSDTNA	KRFRVLADES	VARVGPEXAB	LEHVVWKPQR
	TRVLMDIVAN ALAMAINYRT	TICI IMAAIG AIRLKVALBT	PTVL/HQ1LO LVPENLVSFK	OTERTSON'N TLINI SVGEV	VOIGLCIALP	LPEAALPCPL
		CANYAPPILO	PTALIGISVY	VIPIPVOMPH	AKLNSAFRRS	ALLVTDKRVQ
CC .		LINYAWEKS	PTNT IQDIRR IAMFNVMKPB	RERKLLEKAG	MAEANVSLAR	PIVSTIAIVL
	PRYITOPEDP	DTVLLLANAT	LINEHEABRK	BTPKKLQNQK	RHLCKKORSE	
•		POEVDATORA	AKYLOK ILOI	CONVOSOKSS	CLAALLOONO	
40		I PHONVRENI	LPGERYDHOR	YOHTVRVCGL	OKOTENTAKO	
	NESOGORORI LQFLESCDEV		OLYLLDDPLB KOTHKELMES	RCRYAKLIHD		GKTVVLVTHQ HLYNAAMVEA
		DAGIIGYLLB	LPTVPLPLLM			MTCGPGGNRT
45		GRIJANAFSKO	MELOVALPE	HAENPLOOPP	MVPILVILA	AVPPAULLVV
	SKGLSCBYIL	LRIPHROVOE QLEGLLOVCV	LKKVENVSR8 RTGTETQAKP	TOWELLREY I	OCCUPECTHP	KKESCITITE LKVOTCPIDM
		YOMRYROHTP	LVLDSLATAI	QSGQTVGIVG	RTGBGKBSLG	MALFREVEPA
50		KLOABVTENG	TOWERON AND	LCVARALLRN	BKIILLDEAT	ASMOSKTOTL
	VONTIKDAPK AEVRL	GCTVLTIAHR	LATVLACOHV	LVMENGKVIB	PDKPEVLAEK	POSAFAMILA
	CN CT TAB	K14 PMA Rec	90000			
55		Nucleic Acid Accession 4: 231560 Coding semisors: 1-966	4. Z33560			
			. ;	;	,	. ;
;		<b>a</b> _	<b>=</b> _	ä	<b>:</b> _	ň –
09		CCATOTACAA	CATGATGGAG	ACOGAGCTOA	AOCCGCCCGG	CCCCCCACCAA
	AGCCCGGACC	OCOTCAAGCO	OCCATOAT	OCCTTCATOO	TOTOGLECCO	CGGGCAGCO
	-	CCCAGGAGAA	CCCCAAGATG	CACAACTOOG	AGATCAGCAA	acacerdage acacerdage
65		TGCACATGAA	GGAGGACCCG	GATTATAAT	ACCOGCCCC	GCGGAAAACC
		TOMONADO	TANGTACACO	CTOCCOGGO	GGCTGCTGGC	CCCCGGCGGC
	ATGACAGTT	ACGCGCACAT	GAACCGCTGG	AGCAACGGCA	GCTACAGCAT	
	ATRICACTORICT		CCCGGGCCTC	TACAACTCCA	TOACCAGCTC	GCAGACCTAC
		COCCACCTA	CAGCATGTCC	TACTODONOC	AGGCACCC	
	TCTTCCTCC	ACTICCAGGGC	DOTEMBRE	OCCOGGGACC	TCCGGGACAT	DATCAGCATG
<i>SL</i> .		DOSCORAGE	GCCGGAACCC	GCCGCCCCA	OCKARCITICA SCACE CITICA	CATOTOCCAO
2		COGACAGCGA	ACTOGAGGGG	DONGMANTT	TCAAGAAA	ACCAGGGALA
	TOCCAGGGGT	OCAMAGAGG	AGAGTAAGAA	ACAGCATGGA	GAMAGCCCG	TACCCCAM
80		515 Proteir	e seguence			
	Protein Ac	Protein Accession #1 CAAB3435	2AAB3435			
	-1-	<b>a</b> _	a_	<b>-</b> 22	₽_	- 51
82		TELKPPOPOO	TEGGGGGWBT	AAAAGGWQKO	BPDRVKRPM	AFMVMBRCQR
	RIOGOGIAPIO KTLAKKOKYI	rkaqenpka akeeebkrla abwelleete krpfideakr Ktlakkdkyt leggelapga nskaegygva aglaagyngr	ABWKLLSETE NSMASGVGVG	KRPFIDEAKR AGLGAGVNOR	LRALKINGEND KOBYANDONON	DYKYRPRRT SNGST6HHODD

131 41 51

LICEROPER DELIGIONES DE L'ANGELES 
Seq 1D NO: 512 DNA sequenc Nucleic Acid Accession #1 Coding sequence: 1..3978

各

45

တ္တ

25

65

8

S

82

Seq ID NO: 511 Protein sequence Protein Accession #: NP\_001207.1

25

30

35

ত
Ē
3
~
=
Ģ
9
2
۳
$\sim$
ż,
×
-

300		2 60	3000	120000	
Убосотром Алрякснию	•	51   AGCTTOTATO AGGNATGNA	MAGATAGTA ANGCACATGT GTAAATAATT TOAACAGCC GCAGAAGGA AACTTCCTAC. TACCAGCTCC ACAMATCTG	COTATATIC TO AACOCO CAGATTETT ACTATACTO ATCCCTIANT TAANTATCA CTCTTCTACA ATTOTOGITT COTTTTCAAA TAANTCTAAA	
KARYDVSALQ, PRISATSSOTY WROSPTYBNB YSOQOTPORA 888918RAPCQ, AQDLADMIBH YLPGARVPER AAPBRLAHNSO H		41 			
Ynemteegty Agdl,romi bh		31  - GATGGCAGGA TCTGTGCTCA	ATTOCAUTET GRAGETTOTT GTTGACALTA		CONT
	8eq ID NO: 516 DNA sequence. Mucleic Acid Accession 8: U91618 Coding sequence: 29541	21     GCTGAAAGAT   GCTGCTGGAG	TOCTAATOT TTCATGAAGA TTCATGAAGA	AAGTCATAAA GAAGACCCTA ACATGTGATT TGACAAACAC CTAATAGAAA	AATGGGGC
WO 02/086443 0LOYPORPGL NAHGAAQNOP LGSHGSVYKS BASSSPPWYT ITYOSOPVPOT AINOTLALSH	Beg ID NO: 516 DNA sequence. Mucleic Acid Accession 8: U9 Coding sequence: 29541	11     TTOTTAGANG   CTGGCTTTCA	ANDATOACTC ANDATOACTC ACAGGAGAGA GGCTTTAGCT		AMMANAMA
WO 02/ QLOYPOHPGL LGSMGSVYKS IIYQSGPVPGT	Seq ID NO. Nucleic Ac Coding seq	1   coancttoac catoctactc	AGCATTAGAA TCCCTCTTGG AGCTGAGGAA TGCTTTAGAT	AGAGAATAA AGAGAATAAA ATTATATTO	TCTTCMMAA
	S	10	15	20	

Seg ID NO: \$17 Protein bequence Protein Accession #: AAB50564

	9	120
	CAGHKIQLV CHLLLAFSEM SLCSDESEEM KALEADFLITN HTTSKIEKAR VPSHKMTLLM .	CHSRAPQHVB
₽.	MHTSKISKAR	WLTIYQLHKI YILKRDSYYY
	KALEADFLTN	TALDOPSUEA
	J BLCSDSEEEM	KELVARRILF
:	CHLLLAFSEW	VCSLVNNUNG PAERTGEVAL BELVARRILP TALDGFSLEA MLTIYGLHKI CHSRAFQHMB LIORDIIATG NDKNGKERVI KRKIPYILKR GLYGNKPRRP YILKRDSYYY
	PRAGMKIQLV	VCSLVNNLN6
	30	

Seq ID NO: 518 DNA sequence Nucleic Acid Accession 8: NM\_06536.2 Coding sequence: 109..1940 

:		<b>=</b> _	<b>-</b>	<b>=</b>	<b>=</b> _	- 51	
<del>\$</del>	ACCTAMACC	ACCTABANCE TISCAROTIC ASSANGAMAC CATCISCATE CATATICAMA ACCIGACACA	AGGAAGAAC	CARCTIGGATC	CATATTGAM	ACCTGACACA	ĕ
	ATGTATGCAG	HIGHATSCAD CAGGETCADE GEGAGEGAAC EGGAGGETEC ECTACAACAE GACCCAAAGG	<b>GTCAGTGAAC</b>	TOGAGGCTTC	TCTACAACAT	GACCCAAAGG	ž
	AGCATTGCAG	ACATTOCAD OTCCTATTTO CAACCTOAAG TTTOTOACTC TCCTGGTTGC CTTAAGTTCA	CAACCTGAAG	TTTOTOACTC	TCCTGGTTGC	CTTAAGTTCA	ž
	GAACTCCCAT	ANCTICICAT TECTUGGAGE TOGAGTACAG CITICAAGACA ATGGGTATAA TGGATTGCTE	TOGAGTACAG	CTTCAAGACA	ATGGGTATAA	TOGATTOCT	7
:	ATTGCAATTA	ATTECANTTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG	ACCTGAGAAT	CAGAACCTCA	TCTCAAACAT	TAAGGAAATG	Š
3	ATAACTGAAG	ATAACTGAAG CTICATTITIA CCIATTIAAT OCTACCAAGA GAAGAGTATI TITCAGAAAT	CCTATTTAAT	OCTACCAAGA	GAAGAGTATT	TITCAGNAT	ž
	ATANADATT	ATAMADATIT TAMINCCTOC CACATODANA OCTANIMATA ACAGCAMANI MAACAAGAA	CACATOOMA	OCTANTANTA	ACAGCAMAT	MANCANGNA	Ţ
	TCATATGAMA	ICATATGAMA AGGCAMATOT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA	CATAGTGACT	GACTOGTATO	CCCCACATGG	AGATGATCCA	48
	TACACCCTAC	TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAT ACATTCATTE CACACCTAAT	GTGTGGAAAA	GAGGGUAAAT	ACATTCATT	CACACCTAAT	š

	_	_	_	_	_	_
<del>수</del>	ACCTAMACC	ACCTADADCE TECCAGETIC	AGGAAGAAC	AGGAAGAAC CATCTGCATC	CATATTOMA ACCTGACACA	ACCTGACACA
	ATGTATGCAG	CAGGCTCAGT	GTCAGTCAAC	TOGAGGCTTC	TCTACAACAT	GACCCAAAGG
	AGCATTGCAG	OTCCTATTTO	CAACCTGAAG	Trrotoacre	recreation	CTTAAGTTCA
	GAACTCCCAT	TCCTUGGAGC	TOGAGTACAG	CTTCAAGACA	ATGGGTATAA	TOGATTGCTC
,	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAAACAT	TAAGGAAATG
3	ATAACTGAAG	CTTCATTTTA	CCTATTTAAT	OCTACCIAGA	GAAGAGTATT	TITCAGALAT
	ATAAAAATT	TAATACCTOC	CACATOOMA	GCTAATAATA	ACAGCAMAT	AAAACAAGAA
	TCATATGAMA	AGGCAAATOT	CATAGTGACT	GACTOGTATG	GCCCACATGC	AGATGATCCA
	TACACCCTAC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAT	ACATTCATT	CACACCTAAT
	TTCCTACTGA	ATGATAACTT	AACAGCTGGC	TACOGATICAL	GAGGCCGAGT	OTTOTOCAT
2	<b>GAATGGGCCC</b>	ACCTCCQ171G	GOOTGTOTTC	GATGAGTATA	ACAATGACAA	ACCTITICTAC
	ATAAATGGGC	AAAATCMAT	TAMBTGACA	AGGTOTTCAT	CTGACATCAC	AGGCATTTT
	<b>GTGTGTGAAA</b>	MOOTCCTTO	CCCCCAAGAA	CCCCCAAGAA AACTGTATTA	TTAGTAAGCT	TTTTAAAGAA
	OGATOCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	CTTCATGCAA
:	AGTITATICET	CTOTOCTTCA	ATTITIOTAL	GCAAGTACCC	ACAACCAAGA	AGCACCANAC
ş	CTACAGAACC	AGATOTGCAG	CCTCAGAAGT	CCATGGGATG	TAATCACAGA	CTCTGCTGAC
	TTCACCACA	OCTITICCCAT	GAATGGGACT	GACCTTCCAC	CTCCTCCCAC	ATTCTCCCTT
	<b>OTACAGGCTG</b>	OTCACALAGT	GOTCTGTTTA	<b>GTOCTGGATG</b>	TOTOCHACKA	GATOGCAGAG
	OCTOACABAC	TOCHTCALCT	ACAACAAGCC	GCAGAATTTT	ATTTGATGCA	GATTOTTCAA
,	ATTCATACCT	TOOTGOCAL	TOCCAOTITC	GACAGCAAAG	GAGACATCAG	ACCCCAGCTA
3	CACCALATTA	ACAGCAATGA	TGATCGAAAG	TTGCTOCTT	CATATCTGCC	CACCACTGTA
	TCAGCTAAAA	TCAGCTANA CAGACATCAG		CATITOTICA GOOCITAAGA AAGGATITGA GOTGOTICAA	AAGGATTTOA	GOTGGTTGAA

	TCAGCTAAAA		CATTIONTCA	GOOCTTAAGA	AAGGATTTGA	OCTOCATICAA	
	AMCTGAATG			ATCATATTAG	TGACCAGCGG		
	250111111111111111111111111111111111111	ATTOCTTACC	CACTGTGCTC	AGCAGTGGTT	CACATTO	COCK TAGG	
;	CTGGGTTCAT	CTGCAGCCCC	AAATCTODAG	GNATTATCAC	<b>OTCTTACAGG</b>	AGGTTTAMAG	
S	TCTTGTTC	CAGATATATC	ANACTOCALT	AGCATGATTO	ATOCTTTCAG	TAGAATITCC	
	TCTGGAACTG	GAGACATTTT	CCAGCAACAT	ATTCACCTTO	AAAGTACAGG	TOAMATOTO	
	AACCTCACC	ATCAATTGAA	AACACAGTG	ACTUTOGATA	ATACTOTGGG	CAACGACACT	
	ATCITAC	TTACOTOGCA	OCCAPTOOT	CCTCCTGAGA	TTATTATT	TGATCCTGAT	
6	COACCANAAT	ACTACACAAA	TAXTITIATO	ACCUATCTAA	CTTTTCGGAC	AGCTAGTCTT	
2	TODATTCCAG	GAACAGCTAA	CCCTGGGCAC	TOCACTTACA	CCCTGMCAA	TACCCATCAT	
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCMCTCAGC	TOTOCCCCCA	
	OCCACTGTGG	MOCCETTOT	GGAAAGAGAC	AGCCTCCATT	TTCCTCATCC	TOTGATGATT	
	TATGCCAATG	TOWACAGG	ATTITATOCC	ATTESTANTO	CCACTOTCAC	TGCCACAGTT	
ì	GAGCCAGAGA	CTOGAGATCC	TOTTACOCTO	AGACTCCTTG	ATCATOGAGE	AGGTGCTGAT	
c	<b>STTATAMAA</b>	ATGATGGAAT	TTACTCGAGG	TATTTTTCT	CCTTTGCTGC	ANATOGTAGA	
	TATAGCTTCA	AAGTGCATGT	CARTCACTCT	CCCAGCATA	GCACCCCAGC	CCACTCTATT	
	CCAGGGAGTC	ATGCTATGTA	TOTACCAGGT	TACACAGCAA	ACCOTANTAT	TCAGATGAAT	
	OCTCCAAGGA	AATCAGTAGG	CAGANATOAG	GAGGAGGGAA	AGTGGGGCTT	TAGCCCAGTC	
6	AGCTCAGGAG	acrectitic	AGTGCTGGGA	grecocto	GOCCOCACCC	TCATGTOTT	
ွ	CCACCATGCA	<b>AMATTATTOA</b>	CCTGGAAGCT	GTAAAAGTAG	MONDONATT	GACCCTATCT	
	TGGACAGCAC	CTOGAGAAGA	CTTTGATCAG	GOCCAGGCTA	CANGCTATOA	AATAAGAATG	
	AGTAMAGTC	TACADAATAT	CCAAGATGAC	TTTACAATO	CTATTITAGE	AMTACATCA	
	AGCGAAATC	CTCAGCAAGC	TGCCATCAGG	GAGATATTTA	COTTCTCACC	CCAGATTTCC	
,	ACGAATGGAC	CTGMCATC	<b>GCCAAATOGA</b>	GAMCACATO	AAAGCCACAG	TATATATA	
S	OCMATACOAD	CAATGGATAG	GAACTCCTTA	CASTCTSCTO	TATCTAACAT	10CCCA00C0	
	CCTCTOTTTA	TECCCCCAA	TTCTGATCCT	STACCTOCCA	GAGATTATCT	TATATTOMA	
	<b>OCAUTITIDA</b>	CAGCAATOOG	TTTGATAGGA	ATCATTTOCC	TTATTATAGE	TOTGACACAT	

	WO 02	WO 02/086443						
	CATACTITAA	GCAGGAAAAA	GAGAGCAGAC	AAGAAAGAA	ATOGAACAAA	ATTATTATA	2940	
	ATAMATATCC	AMOTOTOTI	CCTTCTTAGA	TATANGACCC	ATOGOCTICO	ACTACAMAA		
	CHACTACE	AAGTCAAATT	MCATCAM	STATE OF THE PERSON	ATOCATTOM	TTTTTTTACA	3060	
,	ATACAGATAA	CATTITACA	TOGINGATCA	ACCATACATE	TTOOCCOTAG	ATTABALLAC	3130	
^	OCTTACACTT	TOOCTATOMA	CUATATA	ANATTATTCT	TAMADAMAT	<b>STCTTTANG</b>	3180	
	GCANAGGGNA	<b>GCOTANAGIC</b>	COACCACTOT	CAAGGAAAGT	TATHTOTT	GAGGTGGAAA	3240	
	AATAGCCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAACTOTCTG	TOTOMACCA	3300	
	TCATTTAGT	ACTIGATTA	ATTENDED	TCTCCTTATC	TOTOCAGTAC	AGOTTOCTTO	3360	
	TTACATGAA	CATCATOCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAAG	CTCTTTACCT	3420	
0	CTTGCTATTT	TOTTATATAT	ATTICACATO	ACATETECET	OCTANTOCTC	AGAGATCTTT	3480	
	TITCACTUTA	AGADGTAACC	TTEACATA	TOOGTATTAC	CTTTOTCTCT	TCATACCOOF	3540	
	TTTATTACOLA	AGGTCTATTO	MITTATTO	TATOTAGET	TCTACTCCC	TCAMGCAGC	3600	
	TTTCTAAGTT	TATTGCCTTO	CGTTATTATG	GAATGATAGT	TATAGCCCC	TATAATGCCT	3660	
	TACCTAGGAA	4						
S								
	Seq ID NO.	Beg ID NO: 519 Protein sequence	aequence					
	Protein Accession	cession #1	N: NP 006527.1					
			1					
	-	=======================================	21	31	7	51		
5	_		_		_			
	MTORSTAGPI	CALKITYTLLY	ALSSELPPLO	AGVQLQDNGY	NOLLIAINPO	VPENONLI BN	ç	
	INEMITTABLE	YLPNATKRRV	PPRNIKILIP	ATMIXANDINGK	IKORSYEKAN	VIVTDMYGAH	730	
	GDDPYTTOYR	OCCINECTORY	PTPNPLLADN	LTAGYGSRGR	VPVHEMAHLR	WGV PDSTYRND	90	
,	KPPYINGONO	INVIRCEBDI	TOIPVCERGP	CPOENCIIBK	LPKEGCTFIY	NSTONATABL	25	
S	MENOSLASSVV	EFCNASTHWO	EAPYLONOMC	SLRSANDVIT	DSADPHHBPP	MOTELPPP	900	
	TPRLVOAGDK	•	KMARADRILLO	LOGARETTLA	OIVEINTEVO	IASPOSKUSI	360	
	RACLHOINSN	DDRKLLVBYL	PTTVBAKTDI	SICEGLACE	EVVEKLAGKA	YGEVMILVTS	420	
	CODKLIGNCL	PTVLSSOBTI	HBIALGEBAA	PNLEELSRLT	OCICKPEVPD1	ENSHBHIDAP	9	
	SRISSOTODI	POOHIOLEST	GENVKPKHOL	KNTVTVDNTV	CHETTAPLYTH	OASGPPRILL	340	
0	PDPDGRKYYT	MAPITALITPR	TABLMIPOTA	KPCKWTYTLN	NTHHSLOALK	VTVTBRABNB	9	
	AVPPATVEAF	VERDSLHFPH	PVMIYANTYO	GPYPILNATV	TATVEPETOD	PVTLRLLDDO	9	
	AGADVINOG	IYSRYPPEPA	ANGRYSLKVH	VNHSPSIGTP	AHS I POSHAN	VVPGYTANGN	720	
	IOMNAPRKEV	GRNBEERKMG	PSRVBSOGSP	BVLGVPAGPH	PDVPPPCKI1	DLEAVKVBZE	790	
	LTLSWTAPGE	DPDQQQATSY	EIRMSKBLON	IGDDFNNAIL	VNTBKRNPQ0	AGIREIPTPS	840	
^	POI STNOPEH	OPNOSTHESH	RIYVAIRAND	RNSLQSAVEN	IAQAPLFIPP	NSDPVPARDY	8	
	LILKGVLTAM	GLIGHTCLII	WITHTLERK	KRADKKENGT	KLL			
	Seg 1D NO.	520 DNA sequence	quence.					

	NM_000228	1
Seg 1D NO: 520 DNA sequence	Acid Access	Coding sequence: 823600

	e1	=-	17	<b>1</b> -	<b>\$</b> _	15 -	
;	GCTTTCAGGC	GATCTGGAGA	AAGAACGGCA	GAACACACAG	CAAGGAAAGG	TCCTTTCT00	
5	GGATCACCCC	ATTOGCTOM	GATGAGACCA	TICTICCICT	TOTOTTTTOC	CCTGCCTGGC	-
	CTCCTGCATG	CCCAACAAGC	CTGCTCCCGT	DODOCCTOCT	ATCCACCTGT	TOCOGACCTO	-
	CTTGTTGGGA	GGACCCGGTT	TCTCCGAGCT	TCATCTACCT	GOODCHOAC	CAAGCCTGAG	~
	ACCIACIOCA	31418	מאיניים מיניים	ALGAMATAL	SCHOOL STORY	200000000000000000000000000000000000000	•
S	CCTCACACT	ACTACAGTCA	CCGAGTAGAG	AATGTGGCTT	CATECTECO	CCCCATGGGC	•
3	TOGTOGCAGE	CCCAGAATUA	TOTOMCCCT	GICTOTO	AUCTIONACCT	GALAGUALA	•
	THECKOCTTC	MGAGTCAT	GATGGAGTTC	CAGGGGCCCA	1000000000	CATOCTOATT	• 4
	SAGGGCICCI	CACACT TOO	TANGACCIOS	COMPLETALL	ACT ACCION	TOTAL PROPERTY.	
	ער ורויייייייייייייייייייייייייייייייייי	TOTAL PROPERTY.	TAATOTACO	CONTINUE	GOVAGOTOCA	ACTTABOUT	
55	ATGGATTTAG	TOTCTOOGAT	TCCAGCIACT	CAMGTCAA	AAATTCAAGA	OGTOCOCCAC	-
	ATCACAACT	TOMORGICAL	TTTCACCAGG	CTGGCCCCTG	TOCCCCAAAG	DODCTACCAC	-
	CCTCCCAGCG	CCTACTATOC	TOTOTOCCAD	CTCCOTCTGC	AGGGGAGCTG	CTTCTOTCAC	-
	OCCATOCTG	ATCOCTGOGC	ACCCAAGCCT	000000000	CAROCCCCTC	CACCOCTOTO	•
S	CAGGTCCACG	ATOTOTOTO	CTRCCARCAC	AACACTGCCG	<b>GCCCANATTG</b>	TOAGCOCTOT	^ :
2	<b>GCACCCTTCT</b>	ACMCAACCG	GCCCTCCAGA	CCCCCCCCAAOG	GCCAGGACGC	CCATGAATOC	2
	CAMAGETGCG	ACTGCAATOG	OCACTCAGAG	ACATOTCACT	TARACCOCCC	TOTOTTTGCC	2
	accaaccaag	OCCUTATOO	AGGTGTGTGT	GACAATTGCC	GGGACCACAC	CCAAGGCAG	=
	AACTOTOAGC	<b>GOTGTCAGCT</b>	<b>OCACTATTC</b>	COGNACCOCC	OCCCGGGAGC	TCCATTCAG	Ξ
,	GAGACCTGCA	TCTCCTGGGA	<b>GTGTGATCCO</b>	DATOOOCCAD	TOCCAGOGGC	TOCCTOTORAC	=
ဥ	CCAGTGACCG	<b>DOCADTOTOT</b>	GTGCAAGGAG	CATOTOCAGG	CACACCCTO	TOACCTATOC	=
	AAGCCGGGCT	TCACTGGACT	CACCTACGCC	AACCCGCAGG	OCTECCACCO	CTGTGACTGC	2
	AACATCCTGG	OCICCODAG	GCACATGCCG	TOTOACGAGG	AGAGTGGGGG	CTGCCTTTOT	Ξ
	CTGCCCAACG	toorcoarcc	CAMIGIGAC	CAGTOTOCTC	CCTACCACTO	GAAGCTGGCC	2
5	AGTOCCAGO	<b>OCTOTOMACC</b>	grandeerac	GACCEGEACA	ACTCCCCTCA	OCCCACAGTO	7
2	CAACCAGTTC	ACAGGGCAGT	<b>GCCCTOTCGG</b>	GAAGGCTTTG	<b>OTOCCTOAT</b>	<b>OTOCACCOCT</b>	=
	<b>GCAGCCATCC</b>	OCCAGTOTCC	AGACCOGACC	TATOGAGACG	TOOCCACAGO	ATGCCGAGCC	3
	TOTOACTOTO	ATTTCCGGGG	<b>NACAGAGGGC</b>	CCGGGCTGCG	ACAMODCATC	AGGCCCCTGC	H
	CTCTGCCGCC	CTGGCTTGAC	200000000	TCTGACCAGT	accidedado	CTACTOCAAT	=
ž	COCTACCCO	Totacoroac	CTGCCGCCCT	TGCTTCCAGA	CCTATGATGC	<b>GGACCTCCGG</b>	=
c	GAGCAGGCCC	1000011100	TAGACTCCGC	ATGCCACCG	CCACCITOTO	OTCAGGGCT	2
	GOGCTCCAAG	ACCOTOOCCT	99007000	ATCCTAGATO	CANGAGTAA	DATTONGCAG	2 :
	ATCCCAGCAG	110000	500000000000000000000000000000000000000	ACAGAGCAGO	AGGTGGCTCA	GOTOGCCAGT	2
	CCATCCTCT	CCTCAGGC	AACTCTCCAG	GCCCTGCAGC	TOGATCTOCC	CCTUCAGGAG	3
S	GAGACGITOT	CCCTTCCOAG	AGACCIOGAG	ASTCITACA	CANCELLOA	TWICE CO.	₹ :
2	ACTATICIATIC	AGAGGAAGAG	SOCIAL PROPERTY.	GAMAMATAA	S CALGOLICA A	TELETERSON OCTOBRESHED	::
	ADDITION OF	TOCTONO.	ACCIACIANO ACCIACIANO		500000000000000000000000000000000000000		: :
	CACCO COCO	OCCUPATION OF	CLASC I CAGO	SACAGETEGA	CACACACACA	040000000	::
		TO SOURCE STATE				DESCRIPTION OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE	
š	A LOS CALLES	John Sand	TACOURT OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PAR	100000000000000000000000000000000000000		TOOL OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	
3	VICE COLUMN		100000000000000000000000000000000000000	ACCOUNT OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE P		CATOOCOCC	: :
	Character	AGCIGCAGGG	GGGCTTCAAT	OCCUPACION OF	AGCOCACCAG	OCAGATGATT	. 2

WO 02/086443

-	
~	
_	
~	
_	
ェ	
n	
_	
_)	
_	

Sag ID NO: 521 Protein sequence Protein Accession N: NP\_000219.7

25

Seq ID NO: 522 DNA sequence Nucleic Acid Accession #: NM\_001944.1 Coding sequence: 84..1083

S

11.20 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10 55 ઉ છ 2 75 8

AN OCCUPACION COMPANDO MACCONTRACO
CO TRETUCIONE TRANSPORTATION
AN ANTINAMEN TRATECIONE CONCUENTA
AN ANTINAMEN CONTECCION CONCUENTA
AN ANTINAMEN CONTECCION CONCUENTA
AN ANTINAMEN CONTECCION CONCUENTA
AN ANTINAMEN CONTECCION
ANTINAMEN CONTECCION
ANTINAMEN CONCUENTA
ANTINAMEN CONTECCION
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN CONCUENTA
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN
ANTINAMEN CONTENTION MATTETH, COACCIOLO DE COASCIOLO DE COACCIOLO DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA DE COACCIONA D Seq ID NO: 523 Protein sequence Protein Accession #: NP\_001935.1 2 23 35 <del>수</del> 2 20 3 5

Seq ID NO: 524 DNA meguence Nucleic Acid Accession 8: XM\_058069.2 Coding meguence: 1..1413

S

AGGENTAME CECEBOAN ANTANTE CELETRANCE CENTRALE ANTANATE CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN CECEBOAN C 55 8 65 2 75

Seq ID NO: 528 Protein seque Protein Accession 8: 919900

S

9 2 41 51 | CALEINKLPV TROKYBGNLM P REMPGGPVWR KMYITYRINN HKFILILLO ATASGALPLA KBKIQEMQHF LGLKVTGQLD =-

82

PC																
					:											
2 5 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		24 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	500000	2228	960 1020 1080	1260 1320 1380	1500 1560 1620 1680	1600 1860 1980 2040	2220	2400 2500 2500 2500 2500	2760 2820 2940 3000	3060 3120 3180 3240	3480 3480 3540	3660 3720 3780	1000	12222
PHAPDGKGGI DPKANNEPTY VTYGKILIP KYMLISNLRP DPGYPKLITK	ر	81 		TOGAGTTGAT TTGCACTCGG AACTGCAGAT AAATGACAAC TAGACCTGGT	TOTACATOCC AGACAAGTAC AGGCACATCA ACAAAATGCT	ACCTATAGAA AAAGGGAAAT TCTTTCTGTT AGTAAACAAT	ATATOTICOSA TOTOTICOSA TTOTATCACC GOTTOMACT TAGATCATGT	MATACTTCAA TOTTGATCCT TCCAGMATC ATATCAGMA CGGCCMGCT			TOGACCOA CAATTAGGTC TCACATGTA ATATTTTAA ACTGGTAAA	TITITITACO AOTTATOCTA AGAMATATTO TAMATTAMA	GAATATAGTT ATGAAATGAG TCCTACAATA CTGAGTCTAT	GCTTTGCAGT CGCCCAGCTA CGCCCAACCTA CCTGTTTCTA	GGGGAAATTG AGCTACAAA AAGGAAAGCC	ATCACTTO TATAMAGA CCAAGTAGGT GAGAGGCCAC CTAGGCTTGG
VVPARGAHDD GHSLOLCHSS LCDPNLSFDA RWQVFLFRDD HRYDERHQPM		41 TCCTGGCCCT CCGTCTGCCT ANAGGTGAT ATTTGGAGGA	CATTTACCAT TAGAACATCA CCAAGAGGAG	TAAGTGGACG GAAATCTATT CTTATGCGTC TAGAGATGA TGGAAAGTAG	GACACATTC GACACATTGT TTGGATTGAT CCACTTTCAG	TCTTACGAAT TTACCATTIT ATGAAGGTGT TGGAAATTGG TGAACAGAGC	CTCCAGCCCA ATAAGGCATA ATCCTANAGG TGGATAGGGA ACAAAGATGA	ACATTTAGE CCATACTTE CCCOTCTTC AAGACAGGE	TOCTTOCAL GAGTITITOG TTATATCAAA COCCAAACTAC	ATGGAGGGA GGGGGGTGG ACTGCAGATA CCATTAGAGG AATGAAGACC TCTCCAGCTG	TIMATIMIT CACAGIGETA AUGITCATT TCACCAGITT TAMACAGAC	TOCTCTTTTT ACATAGCTA AAAATAAACA AAGACTGAAT ACTACCAAAT	TITICIATAS AATATITAAA GIATAGITIG TGCATIATAA ATHITAAAAIA	CAGTAGCTTT GOGGAATACT GTGTTTTTTT ATCCTCTATT	AAAGCACCCT CAGGTCTGGG GGCCTGAATC	ATTANTITI ATTITIONIO AGANGGOONG CNAGGOONG ATACTITITIC
Kintomadil Niputavhet Lpnpomsepa Giranyetea Riyepudnoy	024423.1	31 	AAGAAAGAT ACTGTGCTGC CTCAGGCGTG	TTCTACTCAA AGAGACACTG GATTTGATTG CCCATCAGGG TTTGAAGTTT	AGOTCACCTO TATTTGGACA GGCCAGTTTT GATAATGCAC	AATOTGGAAA AGAGTCAATT AAAGAAACTA CAAGTGAACC GTGACAGCCT	AACTGCACTC AACTGCACT AACTGCATG TCCAAAATCC CTGGCAATAG	OTAMATGATA OCOTATACCO TICAOTITOC GATACAOCTO ATTACTOTAA	AAATGGCAA TTAGTATGTG CAAAACTTAA GGATTTATGA	GGAATGAAAA GAATCCTGCC GAGGTGGACA GGTGAAGAAT ATGTAATCAG GGGAAGAGGA	CCTTGACTTT GAGATAATGT TAATATTGTA ATTATGCTAC TGAAAATGT	CTAMAGCATC TATTAGTCCA GATAGTTTAA AGAACAATG CCCCTACTGC	GAAGTAGCAA TAATCAATGC TGAGGCTGGG TCTTAAATGC		ATTINGATED GATCTTACTO GACACTGAT GAGTGGCATT	TTCAGCOTGA AGAMTAGA GAACTTTGGG TGCAGGCCTT CGTCTGCTTC
NGNVTPLKPB EPWTTHSGGT LYGDPKENGR 18SLMPTLPS DAAV PRPRY		21 	AAOTGATCCT GCTOTCTGAT GAAAGAGGTT AGAAACTGTT		TUCCACACA GCAGACACCA AGTCTCTCAT AGACTTCAAT	AAATGCAATTG TOCCAATTGG CAGCACAGAC AGAAAACCGT AGAAAACCGT	TGAGGGGCCT GGGGTCAAAG AAGGTACAAA AATCATAACT TATTACAGTC			TATGGGATCA CCAGACCTTG AGGACACACA ACCCCGTCTC AATTGCATCA AATTGCATCA	ANGANGATEG CATECANA TTTCCANAA TCAATTTEA TTCCANAAG	ATTAAGOTCT OCTGGATAAA CACTTTAAGT OTTTTGGAAA TTGGGACTCA	AGTGCCCTAT ATATTATTAT AAACTTGAAA AGGCCTGGGC		CCACAMETT CCACAMETT CCCTTCTTCT	TCCACCATC AATAATABA ABACAGAGG AACAGGAAGA AAAGCAACAT
86443 Dya irkapov Ioddahrded Saddiroigs Serpktsvyl Poppivkit	HO: 526 DNA mequence c Acid Acception #: NP p mequence: 642590	11    - 	TCATEOGGTC GOGCTGTTGC AACAGACACA GACACACTAG	CAGCACAGAA TAAATTIGTT GTGAAGAATA CAGATCTGCC TCACAGAAGC	GCATTTTGCA TAATCACCAC TGAAAGTACA TAACAGTAAC	TTGTAGAGGA TAATTAACAC ATTTCAAAAT TGAATTATGA TTGCTAGAGA	GOGATCTGGA ACTTAGCAGT GCAATGGTTT TTCAGGGTC AGTTGTATAA	TCATTGCAA TCCATGGAA TCCATGGAGC GGAGCCTCAC TTCAAGAATA	GTACAGGAGT TCTTTTCTGT TTCCTGAAGA ATAGAGTGTG	TTTGTGGTAC ANGANGANA CCTGCAGGGG GTTTACTCA ACATAMAGA GTCCTCACTT	DAMAGCAGG TTAGCAGAAG ATTCTGGAGG GATTTTTTC TGCTTATCTT			TOTGOOMGO ATTICTOCAT GCTITTTOOT CATTITAMA	TAGLISACCA CTAGASOGAG AACCTAGGC CTCCTGACTS	CTCCAGGITT AGAATTITA TTOTCATTTT OTCCAGGGC
WO 02/086443 TPDRARED DIALKA LAUREDED DODAR KYODINTEL SADDIR ENDRYMLAN ERRYTE ENDRYMLAN ERRYTE PROFIDENTS	Seq ID NO: 526 I Nucleic Acid Aci Coding sequence	dachagrere codarcaco crancaco crancecro		GNATCTOATO AAAGAACCTT CCTGTGGATC GGATATTCAG CACCCTGTTT	CTGAAATACA AGCACAGGG TCATTGATAA	TATGAAGCAT GATAAGATT GAAATGGAC GTAAAGCCAC GAAGCGCAT		ACTOGAACAC GAATATOTAG GATGAACCTO AGTAGACTOT AATOCTGGAT	ACTTCAAGA ATAGCACTGC GOGAAACGTT CCTGGAGAACG	AGCCAGOTT GAANTGATGA ACCCTGGACT GAGTGGCACA TAAAAATTAA CCAAGATTAT	ATTIATIACA TITIOTCAGAC TOTATATIAT AGCCAGTTOT	TCTCAAACTC GATATTTTAG ATATCACATT AGTATCACTA ATGTTGCAGC	TTGGAGGCAA GGAAATAAAT AACAAAGAG GAAAAAAGAG GAGGAAATAG		ACTITAGAGG ATTGTCCTTA TTCATTTTT	
'n	2	15	20	25	30	35	04	45	20	55	09	65	92	75	08	88

															•	
4500 4560 4620 4680	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	8 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	5580 5640 5760 5160	8940 6000 6120		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6780 6840 6960 7020		4 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8 8 8 8 4 6 8 4 6 8 6 8 6 8 6 8 6 8 6 8		3	120 120 120 120 120	4 2 2 6 1 6 4 0 6 1	
ONODGATCAG CAGAGCTGAC AGAACAACA CTAAGAAGGT	מאמדאמרומי מאמדאמרומי	DAGACOGOGT TOCOTTTAAA ACGAATTOGA AGAACTCAGG	ATTRICTION TTTOCTOACT ATAMCTITIC CITTOTTCTCT	TATTATTAT ATATTITTAA ACAGAATOT TITGCAATOT AGAAACTTOG	DOGGGAGATOT TANAGTANTA TITTGCTOTA GGCTGGCATO	CATCACTATT TTTTCATCGO OTACACTGAC ANAGRAMO	ADCTATATOR TTCTATTOTA TAATAGTAAA	TCTGTCACTT ATTAANTCA TACCTANGT TGGTAANTT AAAGTTTGTG		S1   RVNLEECPRB VLLEHOKKYB YBIGGROUN IRVEDENDH SPGLPEYNPB SPGLPEYNPB HAPTFRONAY ETNEOVLGVV	CTPAQYVRI KILDREVETP YTDILAVDPO TVKDRAQAA VCGVFGATKE MONGOQETIE		S1   GCCGGCATC	ACTTANTOTA OTOCTTCAOD TGOTCAOTO ATOCTTCT AAAGMOOTA	ATGGGCACCT TCAACAAGTT TGGAGTTGAT TTGCACTCGG	AAATGACAC TAGACCTGOT GCATACGCGC TOTGCATCCC
ATCANGAGA CTGGTTGTGC CTTCTGGGCA	ACATETICEO TOCCCCCCC GROOCICCOA TCACCCTCCT	OTGATECOCC GOCCTTGTTT AGTTGATCAT AGGGGGAGAA	TAGTTGCTGA CCCACTGTGT ACTAGTGCCG CTAACCATCT				AMATCIAT TICCAGIANC TITITIGITIO	DANTCCTGGA TAGCTTTCTC TTAGTTAATA OTGAGGTAGT TTAGGGAAAT		41   SKLEADKIIG KRKOTOKEVT YBADLELELE YBADLELELE KYBILOGTER CIITVTDGND NOHFKISTDK	HVRDLDEGPB DE16G811F8 YVVICKPROG AGFGEYTIP1 ALLFSVLLTL QGFCGTWGSG		41 	CCOTCTOCCT AAAAGGTGAT ATTTGGAAGA TTCTAAATGA CATTTACCAT	CCAAGAGGAG CATTGTTTCT TAAGTGGAGG GAAATCTATT	TAGAGGATGA TGGAAAGTAG CGGACACAAT GGCTCTTTTC
		AATTTTTOT TCCTGACCTC CACCGCTCCC CATGTGTGAA	TCTGTMGCC TACTGAMCA CCMGACTTT TATAMACCT GTATGCCGA		AAAGTAATAT ATAAGCAAA ATATTAAGTT CTTTGCAAA GTATTAATGG		GATCATTICA AMATTICA OTTCATTICA			11     ACKKVILAVP   PFPLFILAGO   DEPOTATALO   OFFGLIGTST   VMFTILKGNB	TALNRALVTV LEDPKOWITI NDWPPEILOB TAARLSYOXN WAILAILLGI PWTQTTNWSS	· ·	31  -  -  -	GTGCGCGGAG GAAGCCTGCA GGCAGAGTTA GATTTCAGAG AAGAAAAGAT	CTCAGGCGTG GGCCCTTTCC TTCTACTCAA AGAGACACTG	CCCATCAGG TTTGAAGTTT AGAGATGAAC AGGTCACCTG
OCCUPATOR CACCTANTIT ATTROCAGA OTATECTIC	TAMAATTCTO TTTAGACTTA GAGGGACAGO GTTCATGCCA	ACOCCOOCT GOTCTCOATC AGGCATGACC TCATTTTGAA CAAAAGACA	ANTOGANTE ATCTACOGC TOCTACCTCC CTTCCCTOTT		TTGGATGCAT GCTGCTTAAA TAATAAAACA AAGATGATCA TGTCTTTGTT	TCATTAATAT TGAGTATCTA TGGTTATAAT ACCAGTGTAG ATTCTGCCAC	AMBTIGCTCT COTTANGACT NOOTTGAACC CTTCAAGAAT		in sequence NP_077741.1	21     TLV I FERDGE TARAVALEDK PCEMQENSILG VDRESYDVPD TVGVVCATDR LIMKVQDMDG KDLINTAMRR	APPARDIPRV RNGNGLRYKK GTLAVNIEDV GTLAVNIEDV RLMSLTKVND GRSTGVILGK GDDRVCSANG	sequence idon #: NM_001941	21    -  -	CCGGCGCTCC CCGAATAATT CAAATAATT AAGTGATCCT GCTGTCTGAT	AGAAACTOTT GAATTCCTTG CTATACTGTC TTATATAGAA	CCTCCCACTA AATTTATAAT TGCCACAGAC GCAGACACCA
02/086443- rrr recentered arr erenange ra aretanage	AATGCCTATC ATCTATOTOT GTCTCGCTCT CGCCTCCCOG	DCCCACCACC TAGCCAGAT CTGGGATTAC TTTAATGTAA	AGCCAOTITT GATCANAACC ACCAOTATCA	TTAATTTAO TOTAGOTGA TTTCCCCCAO TTTATAGGA	TAACCAAAAA TATTAACTTO TGGGGAGATG AAATAATTCT TACTCAATTA	ATTGCACA OCTTTACAGA TATTACAAGG TACTTTGAGG	CCCCTACAAA ATTTTAATAT TTOTOTATOT	ATGACATA GACCTTGAA CCAGCCTCAT CTGCCTGCAC ATATACTACC	527 Protein	11 	VNLEIGVNNE NGYKAYDPEN AIDNODRSCT RLEPTSCRAT NLIISHTEAP	528 DNA d Access ence: 64	11    -  -	CCGCTGGGCC TGATCTTCAG TAGAGGCAGA TCATCCGGTC GGGCTGTTGC	CTATOCAGA CTATOCAGA CAGCACAGAA TAAATTTGTT	GOGTOGTTTG GOGTOGTTTG GCATTTTGCA
	CTATGAGTAA TGAGGGGGA TTGAGAGGGG CTGAAAGGTC	TECCAMORO TECCAMORO TECCAMORO TECCAMORO TECAMORO TECAMORO TECAMORO	GCACAAATA TOTAACCAGA CCCACTCAGC TCAAAGAGCA		CTGCTTAAAA AATAAAACAA TTTACAGATG TTTAGAGATT GAAATAGAAA	TCATTATCAA TTGAAGCACA GTATTAAAAG ACAGGGGTTT CAGGCAATAT	GACAAGATGA GGAGTOTGCT AAAGCCTTAC ACCATTATTY	TTCACAGATA  TTCACAGATG  ACTTCACATG  ACTTCACAATG  ACTTCACAATG  ACTTCACAATG  ACTTCACAATG  ACTTCACAATG  ACTTCACAATG  ACTTCACAATAATAAAAAAAAAA	Seq 1D NO: Protein Acc	1   MAAAGPRRSV ADLIRESDPD KTRHTRETVL EPLILYIER PVFEAINH TQVITTVBHY RAPVEENAPN	KPLAYBEARO KENTAVGBKI KWELYN ITVL BPVHGAPFYP TKLLRVNLCE KRPPEDLAQO	Beg ID NO: 52 Nucleic Acid Coding sequen	1    -  -	CCGATGGCCG CTGACCCTCG CCTTCTAAAC TCTGCAGCA TACACAGCA	ATTCCTTACT ANTCCTTACT ANTCTATG ANAGANCCTT	CCTOTOGOATC GGATATTCAG CACCCTGTTT ACTACAGTGG CTGAAATACA
	^	01	15	70	22	30	35	40	}	55	99	9	20	27	80	85

.389

PCT/US																	
1020	1260 1260 1360 1360	11860 11860 11860 11860	1980	2220	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2640 2760 2760	3000	33300	10000000000000000000000000000000000000	1350 1350 1050	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4560 4560 4620 4680 4740	4980 4980 5040	5100 5160 5220 5280	5400 5530 5540 5540	5700 5760 5820 5880 5940	6060 6060 6120 6180
GACAAGTAC	AGCACATCA ACAMATGCT ACCTATAGNA AMGGGALAT TCTTCTGTT AGTANACAT	CTTGGTTACA ATATGTGCGG TGACCCCGAA TTGGATCACC GGTTGAAACT	AATACTTCAA TOTTGATCCT TCCAGAAATC ATATCAGAAA	STATESTAN ATTACTOOT SCAACTAN	CACACATT GGAACCATT GCATCATCAT CACTTACTCG TAATCAGAAT	AAGAGGATCT TOACTTTTA ATAATOTCAC TATTGTAAAO	AAACATCTAA AAGCATCTGC TAGTECAACA AGTTTAAAAA	CTACTGCACT GTAGCAATT TCAATGCAAT GGCTGGGGTA	OTTTAMATT ANTGORACAG GCAACTGGG AGATGAGGTG	CTTACTGAMA ACCTGATCAG TGGCATTGGC CTAAAGCAAC	AGCCTGAATT CTTTGGGAGA AGGCCTTCAA CTGCTTCAA CTGCTTCAA TGCCATTGA	OTCHOANTC OCCTOANCTO AGCCCTCCTT TATTCCTACA	GAGTGCAGTG TTTTTGTATT TGACCTCGTG	GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCC	ATAMACCTC TATGCCCSAA TATATTTTCA TATGAGTGTG GAATTTTTA	AAAATGCAGT GAAGTTACTT AAGTAATATT TIGCIGTATT CIGGCATGGA	ACATOTTC TCACTATTT TTAATCOOT ACACTGACAC
A TOTTOD A	TTCCATTCAT  CCACTTCAG  CCACTTCAG  TCTACGATT  A TTACCATTT  A TTACATTT  A TTACATT  A TTACATTT  A TTACATTT  A TTACATTT  A TTACATTT  A TTACATT  A	TOACAGAGC CTGCAGCCA A ATAAGGCATA T ATCCTAAAGG T TOAATAGGA		ATCCAACTCA G TCCTTGCAAT A GAGTTTTTGG	CCCAAACTAC ATGGAGGGCA G GGGGGGCTG G ACTGCAGATA C TGCATCGATG T		CAAAAATTA A AAGGTCTCTA A GGATAAATAT T TTTAAGTGAT A	GGACTCACCC GCCCTATGAA TTATTATTAA CTTGAAATGA			ACCATCCTTC A TAATAGAAGA A ACAGAGGGAA C AGGAAGATGC A GCAACATCGT C CAATGGCAAC T	CTTATHEGA O TOCAGGATGA O TTCCTTCTGC A AATTCTGATT TAGGETTAGAC T	GCACAGGCTTC 11 CATGCCATTC 11 CCCGGCTAAT 1 CCCGGTCAAT C CTCGATCTCC C CATGACCCAC C CATGACCCAC C	AMACAGTES A MACAGTES A GOAATTETET G TAACGGCTAC GCTACTECE C	TICCCIOTIT A GOTCTOCATO ANTICATITIC I ANTICATORIA O GAATGATITA G	GCAGCTGTCT A GCTATTAAAA G GCTATTAAAA G TGGATGCATA A TTTCTTGTTT ATGCTTATGG C	AATATTTOO A TOOGAAGAGA TAATAAATT ATAATAATT CATGAATAGT
ATTTOGACA 0	GOCCAGTITT OCCAGANA TATOCAGANA TATOCAGANA TANGANACTA ANGMACTA ANGMACTA ACANTIMACTA ACANTIM	GRACAGECT T GAATGCACTE C ATCACGGCT A AAATTGCATG A TCCAAAATCC T					TTATCTTTC CACTOGRATT A TAAATATGCT GAATATCCT TAAATATCCT CACTOGRAAGTT	TANAGAATTO O OTOTTOAAGT T TOTOTOTATA ATGCTANAAA	CTOTCCATT  COCAGONAL  TCTCCATCA  TCTCCATCA  TTTTAAAACTT		CAGGTTTCC A AATTTAAAA T TCATTTAGA A ACAGGCCAAC A GGGAGTAAAA G		TCGCTCTGAC G CTCCCGGGTT C CACCACCAC CCAGGATGGT CCAGGATGGT CGAGGATACAGG	ACTOMOCAA A OTOTOMOCAA A OTOTOMOCAA O CAGTTTATO T A ACCAMACET G	CCAGTATCAC T ANAACCACCT G TAATTTAGG G GTAAGGTGAA A TTCCCCCAGT G	TTATANGGAA G TTTTAGTATT G AAGCAAAAAT T ATTAACTTGG T TTGCAAAATT A	ATTATOOG A ATTOTAATOT T ATACATATOT A CACAGATATO
OPCICICAL 1	AGACATOGAT O AAATGCATTC A TGCCAATTGO A CAGCACAGAC AGAAACCGT	TATTCCCAGA O TGAGGGCCT O GGGGTCAAAG A AAGGTACAAA A AATCATACTA TATTACAGTC	CATTGAAGAT O ACCAALATTO O TCCATTTTAT T		CTCTGCCAT G TATGGGATCA G CCAGACCTTG G AGGACACACG		CAACTCCAG CAACTCCAG CAACACTATTA	TTGCAGCTCA T GAGGCAAAT G AATAAATGTG T AAAGAGGAAA A		TTAGAGGTA G GICCTTAAAC CATTTTCTC	TAAGTGACTC C TCTCCAGAGA A GATCAAGTTO T TTGTACAGTC A GAATATGGGT O TGCCTTTTCC T		ACACOGACTC T AAAGCTCCCC C TACACCCCC C TACACCCCC C ACTOTOTTAC CAAAGTCCTO O			TTTCTTACTT T TTAMCAGAG T TGCTTAMAT A ATAMACAT A GATGATCACT T	TCTTIGITOT A ALTAATATAT A AGTATCTATG A GITATAATTG
ğ	TOMMOTACA A TACACTACA A TACACTACA TACTACACA TATTCACAC TATTCACAC TATTCACAC TATTCACAC TATTCACAC TATTCACAC TACACAC  TTOCTAGAGA T GGGATCTGGA T ACTTAGCAGT G GCAATGGTTT A TTTCAGGGTC A			ATAGACTOTO C TITIONGCIAC T ANGRAGOAN C CCTGCAGGGG A GTTTTACTCA A		TTTTANAGC C TOGTANATCT C TTTTACGGAT A TATGCTANTA	ATTAMANTO T TTTGACTTTO O TATAGTTGGA A AAATGAGAAC A		CTCCTAGAGT T GAGATTUATT G TACANATTT C	GAGATTCCCT T CAGTTTGCTT T AAAAGAAAA G AATAGGTTAT T AGGCCACAAG G GGCTTGGCAC T			ATTGAAGTC A AATTGATCA A ACTCAGGGCA C TTCCTGCTGT A GCTCACTGCTGT A	TAMACTITUTE OF TENDENCE OF TEN	CAGARTOTTT T TTGCAATOTT T GAAACTTGGC T GGGAGATGTA A ATAATTCTAA G	CTCAATTATO T TOTCGACATC A TTTACAGATO A TTAGAAGGTO O	
WO 02/086443	TCATTGATAA T ACTTGTATCA T TATGAAGCAT T GATAAGATT T GAAATGGAC TAAAAGCCAC	GANGGECAT T GTTCATGTGA G ATTANAGAA A AATAGAAATG G ATTGATGAATG G ATTGATGAATG			CCTGGAGGCG A AGCCAAGGTT T GAAATGATGA A ACCCTGGACT G GAATGGCACG G		CCANTITATA T AACAGACAC T TCTTTTTTT T ATAGCTAGT T	ACTGAATTAA A ACCAAATTCA T TCTATAGGAA TTTAAAATG	ATTATACTO A OTAGATAMAT TAGCTTTGCT TAGCTTTGCT TTTTTTTCGG OATTATACTCGG OATTATTTTCGG OATTATTTTGGG OATTATTTTGGG OATTATTTTGGG OATTATTTGGGG OATTATTTGGGG OATTATTTGGGGG OATTATTTGGGGGGGGGG	TAACCATOTC C OCACCCTOOO O OTCTOOOAAC 11			CCCCCCCCC TO CCCCCC TO CCCCCCCCCCCCCCCC	CTTOTTTCC G TOATCATACO A GOODGAAAAAA TTGCTGAAAT ACTGTGTGTT		TOTMATATA C GCCOTTTOTT T TCCTTTTAM O TACAGATOTO O TAGAGATTAN A	ANTAGAATA C ATTATCAART T GAACCACAGC T ATTAAAAGTA T
•	رم در	01	. SI	2	25	8	35	6	.x o t o t (	200	55	94881	995	5	25	8	<b>\$</b>

	086443 ctttdagdac castettgat casteataa cetacaaco tttaatatad	CACTA TOTON ACTON TOTON TOTON	AGGGGAAAAC ACAGGATAGA GCTTCACAGT TCATTTCAAA AATTTCAATT	ATGACTTAAA GAATCTTTC AATCTATTAG CCAGTAACTT	MADAMAGCA ACTITIMITA CCCATECAGO CTATATCAMA CTATTOTAMA ATAGTAMAT	6240 6300 6300 6420 6420
ACCEDATACH TUGANGCAT TTCTGTGTGA GAACAATGCC ATAGAACACT GTAGTTGGAT TATATATAT	THE ACCOUNTS COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE COTTEMENTS THE THE THE THE THE THE THE THE THE THE	אמדאר דלאדר דדמאר אממא ארקדא	TOCATAGA TCCCCCTA TCCCCCTA TUATAMATA TIATAMATA	GATATTOO ATCCTOATO OCTTCTCA AGTAATATA GAOGIAGTTO	TCATAATGAT TOTCACTTAC TAXAATCAAT CCTAAAGTAC GTAAAATTAT AGTTTGTGCA	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Beq ID Proteir	No: 529 Protein asquenc	ence 932.1				
1 ) MAAAGPRRSV ADLIRSEDPD	11 21   RRS RAVCHILL TUIFFROGE BEDDO PRULMOGEY TARANLEDK	SKDGB ALBDK	31 	41    - 	\$1   RVNLEBCFR\$ VLLEHQKKV8 Y81 GGBGXJR	9 6 6
eplalpyier Pyptrainp Tovittvshy Rapvernaph Kplaybenro	DTGNLFCTRP EVLESSRPGT LOREVVDKY8 VBILRIPIED VWLEIGVNNE	CATOR CATOR CONTO CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CA CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CATOR CAT	LIAYASTADO DEPOTRATEL OPPOLIOTET WPTILKONE TALMRALVTY	YSADLPLPLP KYBILOGTPR CIITYTDSND NGHPKIBTOK HVRDLDGGPB	I RVBDENTNH BPOLFBYHPB NAPTFRGNAY ETNEGVLGVV CTPAAQTVRI	*****
KENLA KNELY RPVHG TRLLR KRPPE	KRELANGSKI KOYKANDER KREMCLAYKK KRELYNITYL AIDKODRSCT CTLAVNIEDV BRYGANETF ELBRIDERER RLWELTRVNI TKLLKVNICK CTHPTQCRAF SRSTOVILGK KREPDELAGO VILIBATER ODDRYCZBAG KANCANOWIE STOPANEWER	ATEDY TROND TROND TROND	LHDPROWITI NDNPPRILQE TAARLBYOKU WAILAILLOI PHTOTINNBS	DEIBGSITE YVVICKERG AGFGETIFI ALLFSVLLTL QGFCGTNGSG	KILDREVETP YTDILAVDPD TVKDRAGQAA VCGVFGATKG MKNGGQETIE	20025
DRMP6	TYNYEGROSP	X	<b>GEEDGLDPLAN</b>	NLBPKFITLA	EACTICA	
Seq 1 Nucle Codin	Seg ID NO: 530 DNA sequence Nucleic Acid Accession #: NM_COding sequence: 72842		016583.2			
	n-		8-	<b>\$</b> _	- 51	
GOAGT TAAGA CCATO ATCCA	Adadadada GATGTTCAA GTTTGGAGGC GCCCTTGAGT GTCTGGGGGGC	SGACA COTTOC MOSTIC SOGGA	GCTGCTGAGA TCATTGTCTT CCCTGGACCA TTGCAGGAAA TTCTGGAAAA	CCTCTANGA CTACCOCCTG CACCCTGCCC CTTCACAAT CCTTCCCCCC	TTAACCAA TTAATOTAA GCCCTCAGCA CTGGACATCC	92222
CAGTO	CACTANTEC TOCCOTANG ACCTANGE AACTOCCT TOTCAGAGG CCCATATOC TOAGACTAC TOTCAGAGG TOAGACTAC TOTCAGAGG TOAGACTAC TOCCATATOC TOAGACTAC TOCCATATOC TOAGACTAC TOACACATAC TOAGACTAC TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGG TOAGAGGG OAGAGGG OAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAGGG TOAGAG	20100	ACATAAAGGT ACCOTCTCTA GTGCAAGTCT GAGATAAGCA	CACTOACCCC TOTCACCATC OTTOACCCTO OGAGAGOATC	CACCTOCTOO CCTCTCOOCA OCTOTOMOC CACCTOOTOC	25253
AAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CCCCCCCAT TOMOSTET CTGGGCGCCCCTTGGCCCTTGGCCCTTTGGCCCTTTGGCCTTTGGCCTTTGGCCTTTGGCCTTTGGCTTTGGCTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCGGGGGG	ACTOR CTOCT CTOCT TTGCC NTOTO	TCACAGGAT TCACAGGAT TCCACGACT AAGCTOCTTC TTCCTCCCA	CTTOWNTAMA TCTCAGAGGC ACAGTTTGTC CCAGTGCTCA GGAACCTGC AAAATGGCT	TEGARGATCA ATCAMBATCA CAGATGACATCA CAGATGACATCA CACATGATCATCATCATCATCATCATCATCATCATCATCATCATCA	720 780 900 1020
Seq ID Proteir	NO: 531 Protein se	quence 57667.1				
1 - M	11   YGLLAQTHAQ	791.00	31   Tepennipae	41   PL&PTGLAGE	S1   LTNALSHGLL	9
8000L VQ6PD TH8PQ TH8PQ	BOGINGIER LPLICIENTO GOTSCOLLOS VQSPOCHELY VITELOINE VATFLYCASE THSPOSLQIS LLDCLOPLPI QCLLDSLTOI DIVMLIHGL QPVINY	NGASL NGASL BLTGI	LIGIKYTSY IS LRLAVKLDIT LMKVLPELVQ	GLENTIDIKY ABILAVRDKO GRVCPLVNEV	TOPOLLEGISL ERIHLVLADC LRGLDITLVR	2 8 2
Seq ID Nucleic	NO: 532 DNA sequence Acid Accession #: sequence: 115,,2223	ş	4363.1			
1-025	11  -  -	CAGAC	31  - CAGACAGTCA AGGACAGAGC	41  - CAGCAGCCTT AGACAGCAGA	S1  - GACCATOGAG GACCATOGAG	8 8
DOT PET POS	тетостеско систеское сионатия телитета сионатия сисосори телитета сионатия выоспист тетосться сисотиямия ститовия стемения сисокают ссилясям сетостам семения	DOTAC COOCO CAGOO CAGOO	ACCCCTOGC ACTGCCAGG CTACTTOTCC GTGGATGGCA GCCGCATACA ACCCGCATACA	AGAGGCTCCT TCACTATTGA ACATCTGCC ACCGTCAAAT GTGGTCGAAAT ACACGTCGAAAT	GCTCACAGCC ATCCACGCG CCAGCATCT TATAGGATAT GATATATAC CTACACCCTA	######

TOTOLOGYANDA CONCUENCA CON

9

15

ន

Ś

	V IIGCOIALT AECIFVEDO HELPPALEAT DEDDIYGAM I MOSSMILLA FFILMTYNA FFVAGITAA TORDFTERN O HENNGYTKYN DRIANGDINC GWADEDWOK TESANSTERN Y MIRACKLUVP GYTHWOCTE LISGEMENIA WCYAMPGFAI V	· <b>\$</b> -	N. TACACAGAC COCCETORA GEOLOGICA TH ACCEPTAGE CAMERICET CETALCACA TH ACCEPTAGE CAMERICET CETALCACA TH ACCEPTAGE CAMERICET TO ACCEPTAGE ACCEPTAGE TO THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCEPTAGE THE ACCE	TTANGCCTOO CTCCTOCCCC ICTOCTTOAN ADATACTOM GOCCOCTOTT GOCTACAGO CCCTTCTTCCTCC ATTCMOGNATION	. u.	TOTOPUR COOTYGAND PROCODYTOO YSYKOODKYN ALAPPU RCLAOTOCRO IKKCEOSCO MACPYPO B M 001793.2		DOCCOSTCOC GACAGCTOCT CTCCCCTTC CTCCTCCTTC COGOCGOTC STCAGGGAAG	ACTOATAAT GATGACTTCA AAGGAAAGG AATCCATTGA GATTGGGTG GTTGCTCCAA CTGAATCAG CTCAAGTCTA	SCCEGGGGCA GACAGCCCC FITGITGAAI AAGCCACTGG FITGITCAGAG AATGGTGCCT SCAGAATGAC CACAAGCCCA GTCCTACCA GGTACTTCTG	ACCTACAT GOGGGGGTU CCCATGTTC ACCATTCACT CCGGGAAAA GCCCCTGAGT TCCCCCC ACGCCATGG TTTTGACCC CAGAGTACT AGGCTGACG GTCACTGATC	ATCATOGOC GOTOACCACO GOCATCCTO ACAACCAGOA GOTOTCACO OTOGAGOAGO AGOTOCCA GAGGCATCC	ATTOTACCA ACAGTOGCC ACTIONA ACAGACTC ACCACTOGC ACGGGACCC CCCTCAGCCC COTCAGATCA	MACATETA TOGACOCA MACATECTO ANGCAGATA GASCAGETO ACOGTATEA CECTOGACEC TOGACOGATO	TO CENTRATING AND TRANSPORD AS CONTRACTS IN CONTRACTOR CONDICATION TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT	TATCTURE GANTESSORA BACGGATTA CAGTECCEC SAACTOST CAGTECCEC CAATTOST CAGATOST GANTESSA ANTOTOST FTGCTOA ASSCRAFT FTCTTAGGC TCCTOTOST TCTTAGGC TCCTOSTOR
	WO 02/086443 MAXDHETVRC POOLLIPOR IGITVOICE CLEVICIVO PLAGMERY OF CHANTHER DADYPWPRQC CVANNIKEP LCATPWYLLO INPTHRIE	Seq ID No. 516 DNA sequence Nucleic Acid Accession f: NM 002618.1 Coding sequence: 120473	CAATACAGET ADGUATTAT GETGACTGE ATAMGATEG TGAGGGCGG CAGGTTCTTAT AGGCAGCTGT CAGGGGGT TCAATGGACA AGATCCCGTT	COCHADACE ANTICAMENT CENTETECS, CTCOMENT CANTENACE TECANACE CANTENACE TECANACE CONTICAMENT CONTICAMENT CONTICAMENT SECTION CONTICAMENT CANTENACE TECANACE TECANACE TECANACE TECANACE CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTICAMENT CONTI		HRASPLIVY VPLIAGTLVL EAAV AGEVKGVG TKOGSCPIIL IROAV GEG ID NO: 338 DNA sequenci Nucleic Acid Accession 9:	Coding sequence: 712560	MAGGGGCA CTCTGCAGC CTGCTGCAGC	CTGCCCTGGG CAAGAGCCAG TGGCGAGCT ATCTTACGAA TGCAAACGT ATCTTACGAA TGAAAATGGC AAGGGTCCCT	AGACACCANO ATTICTACA CTICGCIGIN GAGAGGARA GATTGCCAAG TATGAGCTCT CCCCATGANC ATCTCCATGA GGACCCTTC CGAGGGAGTG	GACACCACO GATGAGOTTO COTAGOCAA GACCAAGO CACCATCAGO GTCATCCCA CATCCAGGO ACAGACATG GATCCTGAT GCCATTAAT GCCATTAAT GCCATGAGATTA	CAACTCACCA GESTSSCOTG TACCATCACC ACCACCCTG TTTTSARGCC AAAAACCACG SCTSAASCTC CCAACCTCCA ACCTSTSTTT STCCCACCTCA ACCTSTSTTTT STCCCACCCTCA	CATCCTANA GACCCAGORA TUTOGGACC CTCAACCTO GATCTTGAC ATGACATO ACTGATTAT	CCCTTTCCAG GCCGGCTCAG GGAAGGTGAC ACAGTGGTCT GGACCTTTCT CTGTCTGACC GTGCGACTGC CATGGCCATC CCCTGTGCTG GGGGCCATC	CACAMGANG COGMAGATCA COTCTTCTAC TATGOCOANG GCTCCACCOA COTCTGGAGG CATCATTCAC AACTCAATGA	CTCGGCTCG GAAGTGGCA GAGTTCGGAG ACGTTGGAAT ACGTTGAAT TCTTACCTGC TACAGTGGAC
		10	15	20		30	35	40	45	50	55		99			8 8
	PCT/USO2/12476	990 950 990 990 990 990	220 00 00 00 00 00 00 00 00 00 00 00 00	1550 1680 1170 1180 1180		20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	500 400 500 500	200 000 000 000		60 60 60	200 565 665 680 680 680 680 680 680 680 680 680 680	D00		120 140 160 160	442 440 650 650 650 650 650 650 650 650 650 65	
•	CCAGTTCCG CCTCGGAGGA CCTCTGGGG CCACCGGAC LACCCGGATGC	ICTETECTO CCAGGAGGC ITTCCAGA ATCCACCAA CCTATACOTO CCAAGCCCT CCACATCTA TCCAGAGCC GCATGA TCCAGAGCCA CCATGAGGAGAA AAACAAACA CAGAAAAAAAAAA	GAACGIAC TCTACTCAGT GAACGIATT NATICTICAC CGACCCCAC CATTCCCCC CCTGCCATGC AGCCTCTAAC GCACACACACACACACACACACACACACACACACAC	ACATICHAN CENTROCARCA 19/ ACATICACA TETERGOAN GETROCOMO 16/ GETROGROBO ANANDETE AGRETICOC 16/ ANANDES AGRETICOC 17/ ANGORAC TEMPETATE CANTOTICO 19/ ANGORAC CENTRATE CANTOTICOC 19/ ANGORAC CONTRATE CANTOTICOC 19/ ANGORAC CONTRATE CANTOTICOC 19/ ANGORAC CONTRATE CANTOTICOC 19/	CCCCCCCC TACCCATCC CCCCCACAGT TCTCTTATC TGTCTCTA CTTGCTACT ATCTGCAC TTCTCTGTACT ATCTGCAC TCTCTCTGTACT ATCTGCAC TCTCTCTGTACT ATCTGCAC TCTCTCTGTACT	CCAMBBAT TTACABAA VAAACCCA TETETACTAA TECCABITA CTCEGGAGGC	MANGAMANG AMANGANGAC ACTOTETS GAATTECOA COAGGACAA GENGAGAAA	CTCTACAG CANTIGATA CTCCCTATG TGGTGGCTCC ATATAGTTA TTGCACAGG		1. S1 PPNVAEGKE VLLLVINLPO YPNAELLIQ NIIQNDTOPY AVAPTCEPE TODATYLMNV	HEADTH OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T	NYBAN REDYTLDYL YODDIYISP HTOYL FIAKITENIN GTYACTVÖNL LYGVA LI	41 51         TTCA000CC TGCT0ATTTT	ICRANCIAL TETECTITOT ACANCIATO ACATETATOO GCCTOTETO TETAGOGAT ATTICATE TANTITAT CACANCIAG ACTITITOC	CAMACTICO MACANGOGO CICCANCAN (COMACCION) CHARACTICO MACANGOGO CICTGOCANA (COMENTARIO ACANTETINA (COMENTARIO ACANTETINA (COMENCO CONTINUATO CANTEGORO COMENCO CONTINUATO CANTEGORO CONTINUATO CONTINUATO (CONTINUATO CONTINUATO CONTINU	n_
	TOTAL OFFI PONG OFFI PONG TAC BANT OFFI	SE TANK	TCC AND COTO TCT COTO TAX TO COTO	CAGC GGA CAAG ACA CTAC GTG TGGA ATC	A TANK	2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	20 C C C C C C C C C C C C C C C C C C C	ST TATE	54.1	THE POTE THE BOX	AQYS WPV TEN NSN TEN NSN TEN LDG TENL LDG	RAYY COLON REIN GIPOO ATVG IMIGY 1_006952.1	24C 23	MAT TO THE	7464 CG CG CG CG CG CG CG CG CG CG CG CG CG	nce 31.1

TOTOLANDOS NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL NO CONTROL

33

4

NM\_006952.

Seq ID NO: 534 DNA sequence Nucleic Acid Accession #: N Coding Requence: 11..793

65

ATTACTORY

ATTACTORY

CACAGCTCT

ATCOCCATAT

ANTECEGACA A TOOMANDO A ATETGACEAA C GOCTOCETOO A

2

75

R ITVITITYA EPPKPITEN NS ELENGRILLI. LEVTRANDOP YS O VILGIGERIAA. SUPPRIJENS KG T VKITIVBAEL PKPBISENS KG MERIFILIM YERINGAYV K LILGCHRAN PEPVERRIN KI S SITVBAGGIS PGLANGATVG IN

25

8

င္တ

391

39

Beg ID NO: 515 Pro Protein Accession

88

8

WO 02/086443 сессемвая акатавска вывассамат воспосская вамасатас

Sag ID NO: 543 Protein sequence Protein Accession #: XP\_015292.2

S

PCT/US02/12476

PCT/US02/12476						•		-					
3000 3060 3120 3180		77000000000000000000000000000000000000			8 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		60 120 180			4 4 4 6 6	9 6 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		
CUMANTICA GCCCAAGCT CCCMATGCT CCCMATGGA CCTMATTIT RATTITCCT ATGTACTAGA ACTITITAT	41 51 COARQEROIA LAINPAGED CLEARAGON VAPESPENG EKETONILLA KROESELAK RESTLEGULE KROESELAK	AUGHENARIA YELLINA AUGHELIVEY HEAPPLIL VITADENER ROLLEGHERIA AUTEDENI WTAEVNEED AUTEDENI WTAEVNEED AUTEDENI WTAEVNEED SENVETCORE ONTO TULVE MILAANTOPT APPIDILUN	TOGGEDO	1 51   1   1   1   1   1   1   1   1   1	ACCOLOGIA DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE		41 51 CHOCERAND PHYADIOTHA CHYCERANT ECUNPRECIN LLESPHPFF LKCKIRYCH S18		11 51 	TACACCTACA TACTOSAGGT CTGCTCATCA TCCOGCCTC CTCAGGCGC TCTTCCCCAC CTCTGCGTGC TGTTCCCCAC CTCTGCGTGC TGTTCCCCAC CTCTGGGTGCT TTGCCGCCCC CAGGATGCCT TTGCCGCCCC	GTCCAGATCO GAAGGGTGA AACTGCATO TGGGGACAT TGGAATTACT TGAATTTCOT GCCATCATCA TGTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCTCC	ACATCACE TOGOSTICAL GOCTOCOTOA ATGGGTCCT GOCTOCOTOC CITGOTOCO GOTOTOCA CITGOTOCO GOTOTOCA CITGOTOCO GOTOTOCA CITGOTOCO GOTOTOCA CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOCO CITGOTOC	TOCTOGOCA CAGANGO GOTTCTCA TCCTGGCTG GANTOGA TCGGCTTCAC TGTGGANA ACAGCCGA CAGAGCTCA TGCAGTTGT
SANGTICT STITCCAGAC CINGGITGC NICGIUTAT	31     FREAEVTLEA   NPLK I PPSKR   DSPPECVPAV   HKPKPTQDT P	OKYBANYEN TTRKGLOPEA EGIPTGEPVC INIYEVHOLA DLSPHTSPPO TVIRATVCDC EDDTRDNVFY	padekerku.	31 5000000000 AAGGCCCC CCCCCTOOG	NAATATTC SAGAGCCAA SAGAGCCAA STCAAGAAT STCAAGAAT		11 IQARRURRO TOBGONRVW SRPKPBEKRP	292.2	Maccodocc accododoc cocredos chacodomo chacodomo caterrere	DOGCOOCCAC CTCCATCCAO CACCTACCTO COTOCCTOC	GCTGGGCTTC TGAAGGCACC CTATGGAGGA	GCACTTCGGG GTCCTGCTTC GTCCCGGGAA CGTGCCGTCC	COCCTOCT GACACCOSTO CTTCGGGGT CGTCCTGTGT
AACGTTAGA TOCATTCTO CTUAGTOTOC GOOTGAGGAC AAAAA	P_001784.2 21 CASEPCRAV VOERSEINER IPYSITOPOL	ANDNAPHEDA THPESHOGIC VPPSKVVBVQ LDREDEQPVR VRQVLAITDX LSDHCWKEQL RXIKEPLLLP	3 6	88548	MACACTTTC MACAGCATA TOCAGCATA CITCLITIAC CITCLITIAC CICATCATC	Seq ID NO: 541 Protein sequence Protein Accession #: Eos sequence	11 KOSPYRPDPO KOCBACKAN KOCBACKAN	quence n t: XM_035292 1576	21 	TCCTCAAATC TCCTCAAGCT TGGTCTTCGC CAGCCAAGCT TGAAGGCCGC	ACTICACATO ACTICACATI GCCTCTTTGC CCTACAGAAA	CCOTGGCCOT TCTTCOTGGC TCTTCOTGGC	TOTOCACACA AGOTCACACA COTTCTOGAA COSTCTACAT TCTCCACGAC
086443 actatett croccor cottita tatagard troccad	ession # 11	TAVANYELLD GDOCONFELLD GDOCONFELLD SDOCONFORT SOTTONOSP KQDTYDVHLS LVLLLURKK RNDVAPTIP	DIEGGSDAA BLOSGIJSSAB DQDQDIDI Beq ID NO: 540 DNA sequence Nucleia Acid Accession #: Eos Coding sequence: 1672	11 	GTONGAGAGA GTONGAGAGA ACCCATGC CACCTATCA GOCTOTGGCT GA	541 Protei	11   AGGRRAPROC PRVWTDANLI KIPPRPFWVI	NO: 542 DNA sequence : Acid Accession %: 2 sequence: 531576	11 CCBCGGCGCG AAGCGGCGCGC CTGGCGCGC CAGCGGAACA GGCATCTTCG GTGGTGTGGG	OGCACCACCA CTGCCCGCCT ATCGTGGCCC CCCGAGGAGG	GCCTGGCCC CTAGATCCCA TTATACAGCG ATGATCAACC	ATCCCGAGO ATCCCGATCT TCCAGGCTCT CACCCACAGC	
246486 8	. U . W . U W .	TOMOGRATI ANKATYLING PTSTATIVN PSACLAND VADHOPVER TVVLGLKKFL GAVLALLFUL GLEARPEVUL	DYECKSDAM . Seq ID NO: Nucleic Act Coding sequ	ATGAGGCTCC COGGGCTCC COGGGCTCCC AAGGCCGGG	TOTOGRAPH ANGRADIST CTCCTSSAAS TTAGGGGGC AGCTGTGTT AGCCTGTGTT AGCCTGTT AGCCTGTGTT AGCCTG	Seq ID NO: Protein Acc	1 	Seq ID NO: 542   Nucleic Acid Ac Coding sequence		CECCOCAGETC CTACCOCTCC ATCCCACTAC CTCCCCOTTAC GOCCOTTOAC	CAAGCTCCTO TOTOTCCAAT TOTOCTGCA CACAGAGGAA	GCCCGCATCCTO GTCCTGCATC GTTCACATCC CTCCATGATC	CCTCTTCCTG CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC CATCATCCTC
'n	10	5 50	3 3	35	04	<del>.</del>	20	6	09	02	75	80	88

•	1		21	=	=	31	
01	HAGAGPIGRA GTIIGSGIPV LEVYGSLPAP ILTAVNCYSV GNIVLALYSG	LAAPAAEEKS TPTGVLKBAG LKLMIELLI I KAATRVQDAP LFAYGGMYTL	EAREIGILAAK BPGLALVWA RPSEQYIVAL AAAKLIALAL WPVTSEAINP	 BADGSAPAGB ACGVPSIVGA VPATYLLKPL IILLGFVOIG YRYLPLAIII	 GEOVTLORNI LCYAELOTT I PPTCPVPERA KGDVSNLDPN SLP IVTLVTV	TLLMQVAIIV BKEGGDYAYM AKLVACLCVL PSFEGTKLDV LTNLAYPTTL	. 9 2 2 2 0
15	Stemisera Silsmihpol Reperentik Kprmilogip	Vavdegnyhl Litpvpglvpt Vallalpvppi Sttvlægkla	Gumeni i Pup Cuntliyaps Laclpliaus Quupqet	volscposyn XDIPSVINPP PWXTPVECGI	gslpt8brip Bppnmlcval Gpt11leglp	pvgsredhlp alighinlrh Vypfgvmkn	223
70	Seq ID NO: Nucleic Acto Coding seque	1 Access	sequence ion #: NM_00S: 8989	268.1			
25	TAMANAGOA TOTGATATO AGCCCTANGO	AAGAATTCGC AAATTCAGC AAATTCAGC	21.  - GOCCGCOTCO TOCTTOCTOA CAGTAGCAGC	ACACGGGCTT GTCCTATTGC TGACGCGTGG	41 CCCCGAAAC CGCCTGCTGG OTCCACCATG		120
30		CTTCATCTTC CANGGACTTC CTTCCCTOTG ACTCCTCOTG ACTCCTCOTG CCATGGGGAA	CACATOTA CACATOTA ACATOTACA AACAGTGGGC	TOTACCTOOT CTCGCCTGGGC GCCTCTGGGC TGGCCTACCG	OACOCCOAG COOCTOCTC CCTGCAGCTT GOAGOTTCAG GAAGOTTCAG	COTOTOTOGA ANCOTOTOGA ATCCTOOTOGA GAGANGAGGC ANGAAGCGGG	
35	TCCCAATCC ACGCAATCC TTTTCACCCT TCATCTACCT	OTTCCACTCA ATOTCCCAAT CTTCATOOTO	TTCTACCCCA ATACTOCACT GCCACAGCTG AGATGCCACG	AATATATCCT GCTTCATCTC CCATCTGCAT AGTGCCTGGC	CCCCCCTCA CAAGCCTCA CCTGCTCAAC	GTCAAGCCA GTCAAGAACA CTCGTGAAGC GCTCAAGCCA	20725
. 4	CONTRACTA CANAGED TO CANAGED TO C	TCATCACCCC CATCTTTCTO GAAGATACC GAGGTCTAG GGGCAGGCAA CCACCTGCCC	OCCICACA ATCTTGTGAG CATCTCTCAT CAGCTCGAGA CAGCTCGAC CAGCTCGAC	OTCATOCTOC GGGCTGCTG AOOTGCAACC TCAAACGCTC GCACTGGGCC	TCTCTTACCA GACTGGTCTG TGAGAGTGGG TGAGAGTGGGA AGTTCCCCCT	GACGECCEC GCAGGTTGGG GCAGGTAAGC TTCCTAGTCC	110000
45	Seq ID NO: 545 Pro Protein Accession	CIIIICIAGA 545 Protei ession B:	ATGGAATAG	TOAGGGCCAA	Ę		
50	MANGIFEGILL GANCEDEFF GANCEDIANT SEICHIFTLEN DDILEGDLIF	11 GGVNKYSTAP VSEVNEMALQ YVCSLVPKAS VATAAICILE LGSDSHPPLL	21 CHINTELVET CHINTCPBLL CHINTCPBLL CHINTELITYON PORPEDIVE	11 PRULVTLVTA VVMIVATREV VPMIVATER RECHECLARA TIL	41 	S1   PDCMTRQPGC ENSCRLYLMP NIVDCP18KP PHGTTSSCRQ	120
Ş	Seq ID NO: Nucleic Act Coding sequ	NO: 546 DNA sequence Acid Accession H: sequence: 26457	F. 703	391.1			
8 8	1 coaccavac coccacaca cccacacac coaccacacacacacac	11 AGCGCGGGCA AGCGCCCCCT AGGAGCGCTG TTCCGCGAAGG	21 GCGAGATGCA CCGCGGTCGC AGTGGCCTG GCACCTGCGG	acaccaage caaaagaaa gaggeettac gageecaage	41 TTCCTCCTCC GATAAGTGA ACCCCAGCA CAGGGCATCC	S1 	120
57 57	NASA COCC	GEGLAGANG TECCAGGANG TECCATEGGG TECTGTETGE CCCAGGCAT AACACATCA	OCACCAMOT CCATCOGCA GAMGGGMA CCTGGCCACO TGTTAGCTT AGTGCCCAA ATMACTGAC	COCCANGOC CACCANGOC CACCACATA TATCATCA TRACATCA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRACACA TRAC	ACCETAMAA TACACCCCA CCAAGCCTGG CCCAGGCCCG TACAGGATT TTATTCTTCC CAATAAAAGC	AGGGGGGTA AGACCAAGC ATGCCACGA AGATGACC TOTCCTCTC CTOGGAAGCT CCACAATTCC TCTTTTTTTTTTTTTTTTTTT	24 4 8 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
8	Seq ID NO.	547 Protein	in sequence NP_002382.1				
8 8	1     MOHRGFLLLT   COACTORING   RVTKPCTFRT	11  - LLALLALTBA RVPCSPKKEP KAKAKKKEP	21  - VARGEDKVKK GADCKYKFEN GKED	31  - GOPOSECAEM HOACOGOTOT	41   AWGPCTPBBK KVRQGTLKKA	51   DCGVGFREGT RYMQCQET1	120
	Beq ID NO.	548 DNA 880	fuence				

:

PCT/US02/12476						·	•								v							
	120 120	240 300 360	420 480 540 600	720	.a.	9	110 · :: 240 · ::			120 180 240	000	0 0 0 0	720		120		. 60	7 4 0 7 4 0 7 0 0	6 6 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	666 720 780	900 900 960 1020	1080 1140 1200
	S1   CACCAGCATC GOTGGCTGCC	ACCEGGATGC GGCCCTCCAG CTACAGGCAC CATAGAGGAC	TACATOO TOTTOACTOC TOCATCTOC	GGAGAGTAAG		51    -   PVOYTLOPGC	MANDY KOLEO IDPCPNILVDC HPWHALKESK			TGCCTCCTGC CAGACCAAGC GCGACCAACA TCACTGTTGC	AACTATACOG CTCTGCCTAC	AGGACCTAT	AGASTETES		S1     BDNLEIVLHR   TTPIQEMCQ		91    -  -  - 	AAGCOGACGC AAGCOGACGC GAGCAGCGGC	CANGACCAGC CAGCTCCGCG CCTGTGAACA ATTCCTCAAG	CACATTCAGT AAGGCACAGC CTGCCCAGTG ACAGAAAAA	GAAATCAGT CCCAGCACCA CCTGCCCGGA ATATCGCTGC	AGTACCGGCAG AGTAGCCAGG GGGCCTGTGC
-	41   ACMACACTC TGATCCTAGT	ACACACTOCA TCCCGCTOTO ATOTOGCCTA ATTTCAAAGA	GGAGGTACK TTTACTTCCT GCCCCAACCT TTATGATTTC	ATGCCCTAAA		41   OEVMODEQED	ettraprus Yhldmylkoo Rekraotokn		<b>\$</b> _	AOCCATGCTO GGACATCCCC CATGGCCATO CCACATCACC	GENERACIAC GETCAAGATC TETCCHGETT	DCCCTGCCC TTTCTAGCTC	CATCTOTOTO		41   VHITGLLPTP NPLPLCLQDT RP		41     OCTOSTCTOC   COGAGAGGCT	CCACAAGGAG CCACAAGGAG TGGGGAGTAC	AGTCACCCCC  GTACCGCATC  CCTGGGCATC	GAACCOOSTC GAACTACCOS CAACTACCOS TTTCTACCOS	CUACCACAGA CUACCACACA COTOCTOCAGA COTOCTOCAGA	TONOGONANG TONOGONANG COTGGAMAGG
006783.1	11 	Trootcocka Oroccaro Aagaggaato	ATTRACCATT	CACCCCATC		31       PRUMILUVAA	MYVPYPLYNG MYVPYPLYNG CYLLLKVCPR	2571.1	11 -	CCACAGCCGC TCCCGGCCAT CCTGGCACTC	ATCCAAGAA ACTACGACAA	OGGCTTTCAG AGCCGTGCGG	ATGAGGCTGCT GGAGGCTGCT		11 11 11 11 11 11 11 11 11 11 11 11 11	NF 006500.1		A GCACAGCCCT F GGTTTTCTGT S AGAGCGAACC	CCCTGACTCA GOTCCCAGGA AGGTCAACCC TAGGGAGGAA	A AGCAGGAGAA F ACACCTTGCA F ACTGTGAGCT	TCAGCATCAGA ACGGGGCCT ACGGGACTT	A CCCTGACCTGA A CACACCAGGT
Ē	CACTITCATC	CTTTTTCCCS CTTTTTCCCS AGCGCTGCTG	A AGCACCTTT A AGCACCTTT A AAAATOTOOG A GAAAATOTOOG	CCANANAT C GATTTCAGAT	40: 549 Protain sequence Accession #: NP_065774.1	21     OXCWITVIPI	VENTRUMALO LIPVETPALLO I ELMATYTESI PPRITPRAMP PTITPHIBASV ICHLINVAEL CONDUNATIOPP 8	squence on #1 NM_002571 587	<b>-</b>	TCAGAGCCAC B GTCTGTGGTG TTGGCAGGGA	AAGACTGGAA CTCGATACTG	GCATTCATCA	TCAGAAGAGG ATTRCCATGG	ein sequence . NP_002562.1	21     BHANATHINIE   KPKINYTVAK   RPLPRHLWYE	nquence 11967	21     CCAAGCATGG T CCTCAGGTCG		d detactered c Angedetere d ceanacate	C COOCCTCTOR O ACTOCTTTOT T OCCCACTTTT C AGGGAAGTCA	C GTGGGAATGC T CCACCACACT A ACCAAGACA T GAATGTCAGG	C AGCAGCTCA C AGCAGCTCA G AGAGAAGAGA
WO 02/086443 Netc Acid Accession \$1 ling sequence: 1786	11     GGACGCTGCA   GGATCACAGT	T OCCUPACCA T OCTATOACCA T OCTATOACCA OCAAOTICAG	ACAMOGITICA TCATCTTTOA CCTOOOTOTT	A DANTOAGET	S49 Protes	11     GGVNKHST8	SCONAITOR	NO: 550 DNA sequence : Acid Accession 8: Needuance: 99587	=_	derecadade corocecto a cerecada r estecada	T CCTTGGAGGG	A GATCATGCAG F GGACTTGAAA	A TANCACACACC	551 Prote	11 	8eq ID NO: 552 DNA mequence Nucleic Acid Accemsion #: 2 Coding mequence: 271967	11   	T COTCOAGOTO O CACCTCAOC C TOTGOSCCAO	A GGACAGAGOG T GTGCCAGGOC C TCCGGAGGAG	C TOTOGRATOGC A AGACAAGAT T GAAGGAACC	A AUTOGAGCCC A TOGCAACCCT A GGAAGAGACA G TOGCGCTAT	C ACAGGAACTA O ACAGGAAGGC T CCAGTGGCTG
WO 02 Fueletc Ac	TOGATICOG BOGAAGGTGT	CAGGAAGTGT AAAAATGTGT CTGATCTTCG GAAACCACTC	TTTTCGAN TACCACCTGC TTTATTTCTA	AGCTAN	Seg ID No. Protein Ace	1     MDMGTLHTF	KKHKVRIEG IKKHKVRIEG FISRPTEKTV QNEMORLISD	Beq ID NO: 550 E Mucleic Acid Acc Coding sequence		CATCCCTCTG TCACCCTGGG AGGACCTGGA	AGAGGGCCGA AGAAGAAGGT TGGCGAACGA	AGACCATACA	TTCANANA TCCTGCTGCA GCAGAGGTTA	Seq ID NO Protein A	1 	Seq ID NO: Nucleic Aci Coding sequ	ACTTGCGTCT TCGCCGCCTG	AGTCCCAAGG AGTCCCAAGG	TCACCTICA CCATCTTCTT TCTACAAAGC GTAAGGAGCC	COTCCCAGAC TOOTTAAAGA GGAACCACAT	TOTOGCTODA GTTTGGCTODA GOGAOGGCAGA AGGAACACAG	TGAGTGAACC CCCCTGAGAG ACCTCGAGTT
	<b>د</b> م .	10	15	Ę	2	25	. %	ž	3	40	45	?	20	55	09	3	3 8	?	75	8	;	<b>2</b>

	GGATGGCATT	CAAGGAGAGG	AAGOTOTOGO	TOAAAAAAA	TATOOTOTTO	ATCTOTOTT	: 3
S	AACMAGACCA		CONCERCEN	TCTCCTGGAA	COTCAACCCC	ACCCCGGAGC	132
	TOTTCOAGAC	ANGITUTIONA	TGCAGGGCT	CCAACGACCT	COCCAACACA	ACCACTOOC	156
	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCACAG	CACCTCCACA	ATCCTAGTOC	3.5
2	TOGCOOTGCT		CTCTATTICC	TCTATAGGA	GOCCAGCTG	CCOTOCAGGC	91
	TTAGTCAGA		GANGAGATGG			GOTGACAAGA	192
;	CAGCTCCCTT		ACCATTCCCA		CACTUTATION	TCAGCCAAAG	2 5
ე.	GGCCACTGGG	DACTAGAGAG	AGGACCTCAC	CTCCCCTCAC TTGGCCCTGC	Maccacatt	TCAGGGACCA	2 2
	GTCCACCACC	~ ~ ~		ADCTEATECC	AAGCAAGAG	CCCCAGTCTC	222
20	AAATACCTOO			CACTORACCTC	TCTGAGCTGG	TTTCCTOCCC	22
3	GCCTGCTCAT	отталлатас	acterto CA		AGAGCACCCC	AGCGGCATCC	2 2
	ACATTTTTC	THOSTCAGA	AGCCAGGAAC		CCTTAMAGA	TACGTGCCOO	238
25	TCACAAAGTC	AGONCANANC AGONCANANC		ACACCOCTT	AACCCTOTCT	CTACTALANA	2 2
	CTGAAGCAGG	AGALTGGTAG	GCGTAGTGGT	TEGCACCTAT	AGTOCCAGCT	ACTCOGNAGO	2 2
	ACCOUNTACT		AACACABCGA		COAGGAAAAA	TAGGCTCAA	3 5
<u>.</u> چ	TCCCCOTOTT	CAAAGATGAG	CATAGOCCTC	TECHTCATOO	ACOTAMACT GGATTAAAGC		2 2
	TTAGCACCAA	ACTICIACA		CTOCCCCAAC	CTTCOOTOT	CCCAAATGAG	3 5
35	CTOTOTOTAL	GCATACATAT		TATATOATATOT	CAGGROSTOTA		2 2
3	AAAGCTTAAT	TOTCCCAGAA		TOCTATATA	TTCTACATOO		22
	AGAGATCAGG			MATGGTCA	AGCTCTACCA	GAGCAGACAG	
<del>6</del>	TGTTAGCCTACT	AGCTA TOTOC	CTTCCTATO	TTTCCOTCCA	GCACGAAGGA	כבומתתתחו	Š
	Seq ID NO: Protein Ac	O: 553 Protein Accession #: N	n sequence NP_006491.1				
45	<b>-</b>	=	12.	11-	<b>\$</b> -	12	
	GLPRLVCAFL	LAACCCCPRV	AGVPGEAEQP	APELVEVEVO	STALLKOGLS STROKTOODS		9 5
9	REGEVRIQLE	VYKAPESPNI	OVAPLOI PVN	SKEPEEVATC	VGRNGYP I PO	VINYKNGRPL	: = :
3	TVPVPYPTBK	WLEVEPVON	LKEGDRVEIR	CLADGAPPPH CLADGAPPPH CLADGAPPPH	FEISTONPET		225
	TLTCEASSSO	DIEPONIAES	TDOVLERGEV	LOLHDLKREA	COOYRCVASV	PRIPALMETO	: ;
55	LVKLAIFGPP STLAVLVTPE RANSTSTERK	LLETOVECTA LPEPESROVV	SWDLGKWISI SWDLGKWISI IVAVIVCILV	LPLELWHLTT LAVLGAVLYF LAVLGAVLYF	LIPDSHITTO	LETSTABPHT REDKOBITLE	2 %
	PERKTELVVE		QLIQGSSGDX	RAPGDQGERY	IDLRH		
99	Seq ID NO: 3 Nucleic Acts Coding seque	554 DNA sequence id Accession #: M uence: 1652639	- '-	003183,3			
;	<b>-</b> -	<b>=</b> _	<b>z</b> _	<b>=</b> _	<b>5</b>	<b>15</b> —	
8	TOGAGCCTOO			ATGTGAGGGAG	TTTTCCAAA	CCCCOTCAGG	- 2 :
	TATTCCTGAC	CAGCGTGGTT	CCTTTCGTGC	Todogoogo	ACCTCCCGAT	GACCCGGGCT	1 7 7
2	CTTTATCTAA			DAMANGA	TCTACAGACT		2 2
	GTACTGAACG			TCGTGGTGGT CTGGACACGT	GGATGCTAAA GGTTGOTGAG		7 5
75	AATATAACAT	AGAGCACTT	TOGAGATTTO	TTATATOR	CANGACAA	AGAATGTTAG	9 6 6
	ATTTAAAAGT	GGATAATGAA TCATCGAGTG				AACACOTOTA AACACOTOTA	2.2
8	CAACTACAAA				TOACATCTAT	COGAACACT	2 2 3
	AGTOTOCACA				CATOCCAAA	AOTTACCOA	
82	CTGAGGAAGC	ATCTARAGET	TOCTTOOCNC	COMMENA	CAGCCATOGA	DOTOTTOOC CONSTITUTE	222
	GCACAAAGAA	TTATGGTAA	ACCATCCTTA	CAAAGGAAGC	TOACCTOOT	ACAACTCATG	13

PCT/US02/12476

	WO 02/086443	_						
	AATTGGGACA TAATTTTGGA ATGAGGACCA GGGAGGGAAA		GCAGAACATG	ATCCCATAGG	TCTAGCAGAA	TOTGCCCOOA	1440	_
		-	TOCHOTANC	MICMICTA	TANDACCATT	GANACTAAGG	1560	
ç	CCCACCAGTO TTTTCAGAA	-	COCACCAATA	AAGTTTOTO	CAACTCGAGG	OTOGATGAAG	1620	
,	-	į	Agracyana	ACAGGAACAG	TOTAL STATE	AAAAACTOTC	1740	
			AAGTGCCAGG	AGGCGATTAA	TGCTACTTOC	AAAGGCGTGT	1800	
		-	AGTGAGTGCC	ממכנונטים	AAATGCTGAA	AATGACACTG	1960	
=			TOTANGGATG	GGAAATGCAT	CCCTTTCTGC	GAGAGGGAAC	1920	
2	ACCAGCINGA GICCININGA ACCITICATA CIRCININGAS		TOTANTON	ATOMETICA ACT	CTOCAROGIC	TOCTGCAGGG	1980	
	_	_	CONTITIONS	ACATGAATOG	CAATGTGAG	AAACGAGTAC	2100	
	•		TOGGATTICA	TTGACCAGCT	GAGCATCAAT	ACTITIOGAA	2160	
3.			gradootra	recroarity	CTCCTTGATA	TTTTGGATTC	2220	
3		-	TOTOTOGATA	ACANATTOCA	TAMACAGTAT	GAATCTCTGT	2280	
	CICIOTITICA COCCAGIANO		GTCGAAATGC	TOAGCAGCAT	GOATTCTOCA	TCGGTTCGCA	2360	
			AAA CTOOR OF	ACCAGAGA	CONCESSOR OF THE	CALGORAGE		
6	_		GACGAGGATG	COTTTOACAA	GGACCCCTTC	CCANTAGCA	2520	
2		-	GAGGATCTCA	COGACCATCC	COTCGCCACA	AGTOAAAAGG	2580	
	-		COTCAGAATC	GTOTTAACAO	CANADANACA	CAGTGCTAAT	2640	
	_	- '	CTTANGTGTG	CAMATATT	TTATAGATT	GACCTACAAA	2700	
	TTTGAACTIC CTGCAGGTAA		ACADATICATIO	TOTAL TOTAL	TAGGAGATG	THEADAGO	2820	
52	_		TATTTOAG	GCTTTCAGGT	TITAGITITE	AAATATCTT	2880	
		_	AGAMATACA	OCTOOR/TTOO	OTTATOAATA	TITACGITIT	1940	
	TOTANATIAN TCTTTTATAT	-	TOATAACAGC	ACTOACTAGG	GAAATGATCA	mmmm	3000	
	-	-	GAATATGAAG	CATTTOOCAT	TTATTTGTCA	DAMAGEGGA.	3060	
ç	-		TTTTTTTGC	CTTCAACTAA	AAACAAAGGA	GATAAATTTA	3120	
2	٠.		GTGGGTCTAT	TECTAGETAL	TACCCAGAGE	TITTA TOTAG	3180	
			ATTTAGAAAT	CATTTOGGTT	AATATGGCTC	TTCATAATTC	3240	
	_		TAACCACTAC	CTTACAGTGA	GOOCTATACA	TOGTADCCAG	8 3	
	Τ.		ACTOTATA	GOCCETGATE	TUCTUGGCAG	TITITCIUIA	3360	
35	CTATTOGEN GOADTONED		ALCCIOLIA	TRATAGGGA	MANGETT	AGAMATICA	2430	
;		_	GOTGACAGAG	TOAGATCTOC		211000000		
					;			
	Saq 1D NO: 555 Pro	ntein	555 Protein sequence					
40	Protein Accession #1 NP_003174.2	ž.	003174.2					
2	=	٠		.;	,	;		
	:_	_	•	:_	: -	<b>.</b> –		
	MROSLLFLTS VVPFVLAPRP		PDDPGPGPHO	RLEKLOSLIS	DYDILSLSNI	COHSVRKEDL	9	
77	<b><i>QTSTHVETLL TPSALKRHPK</i></b>	REF L	LYLTESTERY		CHUESEYTAK	WODPFICHVV	120	
3		181	NTDGAETHIE	PLWRFVNDTK	DKRMLVYK6B	DIXMARLOS	180	
	PRVCGYLKVD NEELLPRGLV		DREPPEELVH	RVKRRADPOP	MOSTCKLLVV	ADHREYRYNG	2 5	
			PETDIABEAS	KVCLAHLPTY	ODPOWOTIGE	AYVGEPRANS	360	
5			NEGLIBTION	GKTILTKEAD		PGAEHDPDGL	420	
2	-		SCHEWNAM	BNCSKQSIYK		QERSYKVOON	68	
	SRVDEGEED POINTLANDS		CONSDICTIONS	GVOCEDRANSP		OKKCOBAINA	9 5	
			AENOIVCIOS M. W. W. DYCKOL		PCEKEDONA P	CACHETUNIC	0 9	
;			LIFWIPPBIL			SNVENLASHO	720	
55			PAPVIPSAPA		PETDS	HADEDGFEND	780.	
	PPPNSSTAAK SPEDLTDHPV		ARBEKAABPK	LOROMRYNSK	STEC			
	Seq ID NO: 556 DNA sequence	000	ence					
9	Nucleic Acid Accession #:	ion 1	#: NM_021832.1 248 .	112.1				
	:_ 	. –	-	<b>=</b> -	<b>:</b> _	ĭ		

					!			
99	Seq ID NO: Nucleic Ac. Coding seq	Seq ID NO: 556 DNA sequence Nucleic Acid Accession \$: NM_021832.1 Coding sequence: 1642348	Tuence 1 8: KM 021 .2248	.012.1				
		=-	<b>z</b> _	<b>1</b> -	<b>=</b> _			
3	TOGAGOCTOG	CCCTAGAATC	TTCCCAGTAG	00000000000	ACCRAMACAG	GATTGAGGGC	9	
3	CTAGGCCCGG	•	CCTCCCCCGA	TOTOAGCAGT	TTTCCGAAAC	ccontagge	120	
	ATTCCTOACC	AGCOTOGITC	CTTTCGTGCT	CAGGGCCGGG	CCTCCGGATG	ACCCCCCCTT	2 2	
	COGCCCCCCAC	_	AGAAGCTTGA	TICHTIOCIC	TCAGACTACO	ATATTCTCTC	300	
ç	TITATICIAAT	-	ATTCOOTAG	AAAAAAAA	CTACABACT	CACACATOT	360	
2	AGAMACACTA	CHARCTETT	CAGCTTTGAA	AAGGCATTIT	MATTATACC	TOACATCAAG	420	
	TACTGRACOT	1300 EE	ATTTCAGGT	cornandara	GATGGTAMA	ACCIMAGOGA	9	
	<b>OTACACTUTA</b>	_	ACTICITICAC	TOCACACOTO	OTTOGTOAGC	CTGACTCTAG	240	
	OGITCTAGCC	_	ATCATCATOT	TATAATCAGA	ATCAACACAG	ATGGGGGCGA	9	
7	ATATAACATA	_	GOAGATITGE	TAATGATACC	AAAGACAAA	GAATGTTAGT	9	
c	TTATAAATCT	GANGATATCA	AGAATOTTIC	ACCTITICCAG	TCTCCNANG	TOTOTOTA	720	
	TTTAMMOTO	CATAATGAAG	AGTTOCTCCC	AAAAGGGTTA	<b>OTAGACAGAG</b>	AACCACCTGA	280	
	AGAGCTTGTT	CATCGAGTGA	AAAGAAGAGC	TOACCCADAT	CCCATGAAGA	ACACATOTAA	940	
	ATTATTOOTO	GTAGCAGATC	ATCOCTTCTA	CAGATACATO	GGCAGAGGGG	AAGAGAGTAC	906	
ç	AACTACAAAT	TACTTAATAG	AGCTAATTGA	CAGAGITICAT	GACATCTATC	GOLACACTTC	960	
2	ATCCCATANT	<b>GCACOTTTTA</b>	AAGGCTATGG	AATACAGATA	GAGCAGATTC	OCATTOTOM	1020	
	STCTCCACE.	CAGOTALAC	CTGGTGAAAA	OCACTACAAC	ATOGCANANA	<b>STTACCCAM</b>	1080	
	TGAAGAAAAG	GATGCTTGGG	ATGEGAAGAT	<b>OTTGCTAGAG</b>	CATTIAGGE	TTGATATAGC	1140	
	TOAGGAAGCA	TCTANAGETE	OCTTOGCACA	STITIOS	TACCARANT	TTGATATOGG	1200	
90	ACCICITION	TTACCTTATO	TTGGCTCTCC	CAGAGCAAAC	AGCCATOCAG	<b>OTOTITOTO</b>	1260	
2	AAAOGCTTAT	TATABOCCA	TTCGGAAGAA	MATATCTAT	TTGAATAGTG	GTTTGACGAG	1320	
	CACAMBAAT		CCATCCTTAC	ANAGGAAGCE	GACCTOOTTA	CACTCATGA	1380	
	ATTGGGACAT	AATTTTOGAG	CACAACATGA	TCCGGATGGT	CTAGCAGNAT	GTGCCCCGAA	146	

HOGGLELE WVPVLARE DEDGTORIO REGLEGELE DITLELERI COGGVEREUL
OFFINENTEL TPEALMENT LITEGERE DESFENANCIO CORESENEUL
OFFINENTEL TPEALMENT LITEGERE DESFENANCIO CORESENEUL
RECOGNICALI TREDDULIEI MTGARMI E PARRIMONTO RESERVATES DITAMENCIO
RECOGNICALO REGLEGERO DESPETARE MYRIGARDORI PROTECLULA VAGRENDO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO ANGRENDO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO REGLEGERO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO REGLEGERO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO REGLEGERO
ARTHERICA DESPETARE MYRIGARDORI ANGREDIA PARRIMONI
ARTHERICA DESPETARE MYRIGARDORI CHERICALO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO
ARTHERICA DESPETARE MYRIGARDORI CHERICALO
ARTHERICA DESPETARE MYRIGARDORI CHERICALO
ARTHERICA DESPETARE MYRIGARDORI CHERICALO
ARTHERICA DESPETARE MYRIGARDORI PRITICALO
ARTHERICA DESPETARE MYRIGARDORI PROFEDELIA
ARTHERICA DESPETARE MYRIGARDORI PROFEDELIA
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REGRESANCIA
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI REPORTIGALO
ARTHERICA DESPETARE MYRIGARDORI ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINUE ARTIMETE DEL CONTINUE ARTHERICA DEL CONTINUE ARTHERICA DEL CONTINU GTTTTTTT ATACACTAT ATOMACGET GARATOMO CONTROLLO E GARANTTA GARACTAT ATTACACTA TOTACACTA ATTACACTA ATTACACTA ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ATTACACT ACCUSANCE TACCACTAC ATTACACT ATTACACT ATTACACT ACCUSACT ATTACACT ACCUSACT ATTACACT ACCUSACT ATTACACT ACCUSACT ACCUSACT ATTACACT GARACTAC ATCACT ACCUSACT ACC Beg ID NO: 558 DNA sequence Nucleic Acid Accession B: NM\_004994,1 Coding sequence: 20..2143 Seq ID NO: 557 Protein sequence Protein Accession #: NP\_068604. TROCKCOME ATTACANCE OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF GCCCTCACCA TTTGCTGCCC Ś 33. 

<u></u>
1140 11800 11800 11800 11800 11800 1160 116
22222222
SEARERSEEE
TTRAGAGGC COCHOGNON CCCHOGNON OCCUTIONA ACCOUNTITION TO TO
CCCV CCCV CCCV CCCV CCCV CCCV CCCV CCC
10002016100
ACTORITC TRUGUAGO MOSTORICA ACOSTORIO COCAGODOS MOSTORIOS COCAGODOS MOSTORIOS COCAGODOS MOSTORIOS COCAGODOS MOSTORIOS COCAGODOS MOSTORIOS COCAGODOS MOSTORIOS
25 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
ACCORDED OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORDING OF ACCORD
CCCCCTCC CCCLACTO ACCOSTCT TUAGAGAC INTERCENTAL CCCCCAGATO TOCOCCTORA GEOGRAPHIC CCCCAGATOS CCCCCTAGA GEOGRAPHIC CCCCAGATOS CCCAGATOS GEOGRAPHIC CCCCAGATOS CCCAGATOS GEOGRAPHIC CCCCAGATOS CCCAGATOS GEOGRAPHIC CCCCAGATOS TRANCOSO TRANCOSO GEOGRAPHIC CCCAGATOS TRANCOSO TRANCOSO CCCTAGATOS CCCCAGATOS AGRACIANOS ACTAGANICOS AGRACIANOS AGRACIAN
32553555555
9994949494
288888888888
TETTECTOR TOURCAMET TOURCAMET TOURCAMET TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME TOURCAME
8758888888888
86443 AMACTITET INTERCENCE COMMOTITET INTERCENCE COMMOTITET INTERCENCE COMMOTITET INTERCENCE COMMOTITET INTERCENCE COMMOTITET INTERCENCE CONTINUENCE C
186413 AACTTITCT CCUAGGCTC CCUAGGCTC CCUAGGCTC CCTTGACA TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC TTCTACTGC
336888EEEEEEE
\$ 22882848E
WO 02/086443 ccrtacoda descripción concuerto accreator accreator of control control concuerto accreator of control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control con
O E E E E E E E E E E E E E E E E E E E
> E E E E E E E E E E E E E E E E E E E

Seq ID NO: 559 Protein sequence Protein Accession #: NP\_004985.1

2

15	Protein Ac	Protein Accession #: NP 004985.1	NP_004985.1				
		::	21	31	1	31	
	_	_		_	-	!_	
	MSLWQPLVLV	LLVIGCCPAA	PROROSTLVL	MSLWOPLVLV LLVLGCCPAA PROROSTLVL PPGDLRTNLT DROLAREYLY RYGYTRVAEM	DROLAREYLY	RYCYTRVAEM	9
ć	RDRSKSLOPA	LLLLQKQL9L	PETGELDSAT	ROBEKSLOPA LLLLQKQLSL PSTGELDSAT LKAMRTPRCG VPDLGRPGTF	VPDLGRPQTF	ECDLICHERRY	120
3	ITYMIONYBE	DEPRAVIDDA	PARAPALMSA	ITYMIGNYBE DLPRAVIDDA FARAFALMSA VTPLIFFRVY	SRDADIVIOF	GVAEHGDGYP	180
	PDGKDGLLAS	APPROPRIOR	DAHPODDELM	BLCKOWVPT	RECHADGAAC HPPFIPEGRS		240
	YEACTTOORS		NYDTODREGP	DOLPMCSTTA NYDTODREGP CPSERLYTRD GNADGKPCQP	<b>GNADGXPCQP</b>	PPIPOCOSYS	300
	ACTIDGRSDG		DRDKLPGFCP	DRDKLPGFCP TRADSTVAGG	NBAGBLCVPP	FTFLOKEYST	360
ď	CTSEGREDOR		<b>SDKKMGPCPD</b>	LMCATTSNPD SDKKWGPCPD QQYSLFLVAA	HEFOHALGLD	HSBVPEALMY	420
3	PMYRETEGPP		HLYGPRPRPB	CANDOVNGIR HLYGPRPEPB PRPPITITING	PTAPPTVCPT GPPTVHPSER	GPPTVHPSER	480
	PTACPTCPPS	ACPTOPPTAG	PETATTVPLS	PVDDACHVNI	PDAIABIONO LYLPHODINYN	W.Y.DOWATAT	540
	RPSECRESRP	QGPFLIADKW	PALPRKLDSV	PALPRKLDSV PEEPLSKKLP	PPEGROVAVY TGASVLGPRR	TGASVLOPER	900
	LDKLGLCADV	ADVTGALREG	RCKMLLPBGR	AUVTGALREG RCKKLLFEGR RLARFDVKAQ MVDPRBABEV DRMFPGVPLD	MVDPRBABBV	DRMPPGVPLD	999
30	THEVPOYREK	AYPOODREYW	RVSSRSBLNQ	THEVFOYREK AYPCODRFYW RVSSRSELMG VEGVOTVTYE ILOCPED	11QCPED		
3							

8eq ID ND: 560 DNA mequence Nucleic Acid Accession #: NM 000213.1 Coding sequence: 127,.5385

35	,	=	12	11	=	15	
	_		_	_		-	
	CCCCOAGGTA	GTCCAGGAC	GOCCICACAG	CAGCAGCCCAG	GCGCGGAGGG	AGCGAGTCCG	9 5
5	AAGAGGATGG		CCCCAGCCCA	TOGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
9	AGCOTCAGCC	•	CTTCGCAAC	COCTOCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
	COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACACCCAGGC	GOAGCTGCTB	OCCTACTOCA OCCOSCINOLI	CACACCACAT	OTTCAGGGAC	200
	GTCATOGAGA	_	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC	750
31	AGCCAGATGT	CECCEAAGO	ccracaanc	COTCTGCGGC	CCCCTGAGGA	<b>GCGGCATTT</b>	480
?	GAGCTGGAGG	TOTTTGAGGC	ACTOGAGAGC	CCCOTGGACC	TOTACATECT	CATGGACTIC	540
	GTCCTGAGCC		COACTACACT	ATTOCATED	CANOTAGE GCANOTAGE	CCTGGCTCGG	009
	AGCOTCCCOC	_	GAGGCCTGAG	AAGCTGAAGG	Agecerage	CACAGAGAG	120
Ş	CCCCCCTTCT	CCTTCAAGAA	COTCATCAGE	CTGACAGAAG	ATCTCCATCA	OTTCCGGAAT	280
?	AAACTOCAGO	GAGAGCGGAT	CTCAGGCAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATOCC	840
	ALC: COLORER	CAUCHOLOGIC	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCCACCTG	96
	OCCATCATOA	GCCCCAACTA	TOPACHOON	TATOMOST IS	ATORCACION	Corderader	96
;	TACAGGACAC	-	gregorance	ACCCTOUTOC	OCCIOCICO	CAAGCACAAC	1080
S	ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
	TATTTCCCTO	TOTOCTORU	ававаласта	CAGGAGGACT	COTOCOACAT	COTGGAGCTG	1200
	CTGGAGGAGG	CCTTCAATCO	<b>GATCCGCTCC</b>	AACCTOGACA	TCCGCCCCT	NONCHOCCCC	1260
	CCAGGCCTTC	GOACAGAGGT	CACCTCCAAG	ATGITCCAGA	AGACCAAGGAC	TOGGTCCTTT	1320
6		GOOGGAAGI	GGGTATATAC	CAGGTGCAGC	TOCOGOCCCT	TOAGCACOTO	1380
3	TOTAL DOCUMENTS	ACCIONAL PROPERTY OF THE PARTY	CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOMA CIOCOM	GACCAGAGG	GCAACATCCA.	TCTGAAACCT	1440
	COLUMN	ACCURATION	DATE CALCAC	SCATCHES.	Groandro	CACCTGCGAG	1500
	TOTOTOTOCA	GCCAGGGCTG	GAGTGGCCAG	ACCTOCAACT	GOODACE	Gracional	1550
,	GACATTCAGC	CCTOCCTOCO	GGAGGGCGAG	GACAAGCCGT	GCTCCGGCCG	TOGGGAGTIGE	1680
65	CACTGGGGGC	ACTOTOTOR	CTACOGCGAA	OCCUCTACO	AGGICAGIT	CTGCGAGTAT	1740
	GACAACTTCC	AGTOTOCOCOS	CACTTCCOGG	TTCCTCTOCA	ATGACCCAGG	ACCIOCITOC	1000
	ATGGGCCAGT	<b>OTOTOTOTO</b>	accreamag	ACAGGCCCAA	OCTORORCTO	TCCCCTCAGC	1860
	AATOCCACCT	GCATCGACAG	CAATGOOGG	ATCTGTAATO	<b>GACOTOOCCA</b>	CTGTGAGTGT	1920
5	GGCGCTGCC	ACTRICCACCA	<b>GCAGTCGCTC</b>	TACACCOLACA	CCATCTOCGA	GATCAACTAC	1980
2	TOTAL CONTROL	ACCOMMOCE	CTGCGAGGAC	CTACGCTCCT	GCOTGCAGTG	CCAGGCGTGG	2040
	Caccancera	AGAGAGGGGG	COCACOTOR	GAGGAATGCA	ACTICAGOT	CARGATGGTG	2100
	GACTGCACCT	ACAGCTACAC	CATOGAAGGT	ON CONTRACTOR OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF	COLUMN	CLANGUAZUAC	2790
è	CTGGTGCACA	AGANGANGA	CTOCCCTCCO	COCTOCTTCT	COTOCCTCAT		2280
C	CTCCTCCTCC	TGCCGCTCCT	<b>ATCCTTOCTA</b>	CTGCTGCTAT	GCTCGAAGTA	CTOTGCCTOC	2340
	TOCKOGO	OCCIOOCACT	тетесеолос	TOCMCCGAG	OTCACATGOT.	GOOCTITAAG	2400
	CANCACCACT	ACATOCTOCO	DONGARCETO	ATGGCCTCTG		CACGCCCATG	3460
		OCCUPANT OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PA	GOCCUTUNC	DIGITATION		CACACATO	2520
8	GGGTOTOT	TOTAL COLUMN	TOTAL COLUMN	ACCATOMACC	COCOGAGCT	GUGCCTAC	2580
;	CACTGOTOCOC	Agrandan	SCHOOL STORY	A COMPANY		TURCACTOO	2640
	TCCGGTGTAC	ACAACCTCCA	GCAGACCAAG	TO COUNTY OF		COCCURATE	2700
	CAGACCACA	CCATTOTGGA	CACAGTOCTO	ATOGGGGGG		S S S S S S S S S S S S S S S S S S S	2870
,	CTGAAGCTTA	CACACAAACCA	GOTOGAACAG	AGGGCCTTCC	ACCIOCATION	OCTOCCCC	2880
S	OCCTACTACA	CCCTCACTGC	AGACCAGGAC	<b>DCCCGGGGCA</b>	-	CCAGGAGGGC	2940
•	GTGGAGCTGG	TOGACOTACG	<b>agracecete</b>	TTTATCCOOC	Ξ.	CGACGAGAAG	3000
	CAGCTGCTGG	TOGAGGCCAT	carcoracoc	acadacaetra	CCACCCTCGG	ОСОСОССТО	3060

	2000					5
	Codecacacac	ACACCCAGGC	COACCTOCTO	OCCCCCCCCCT	OCCAGCOGA	CAGCATCOTO
	GTCATOGAGA	<b>OCADCTTCCA</b>	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC
2	AGCCAGATGT	CCCCCCAAGG	ccracagana	COTCTGCGGC	CCCCTGAGGA	GCGGCATTT
2	GAGCTOGADG	TOTTTGAGGC	ACTOGAGAGC	CCCOTOGACC	TOTACATOCT	CATGGACTIC
	TCCAACTCCA	TOTOCOATCA	TCTGGACAAC	CTCAAGAAGA	TOGGGCAQAA	CCTGGCTCGG
	<b>GTCCTGAGCC</b>	AGCTCACCAG	COACTACACT	ATTOCATTO	OCAMOTITION	GOACALAGTC
	AGCOTCCCCC	AGACOGGACAT	GAGGCCTGAG	AAGCTGAAGG	AGCCCTGGCC	CACAGTGAC
9	CCCCCCTTCT	CCTTCAAGAA	COTCATCAGO	CTGACAGAAG	ATCTOCATOR	OTTCCGGAAT
Ž	AVACTOCAGO	GAGAGCGGAT	CTCAGGCAC	CTGGATOCTC	CTGAGGGCGG	CTTCGATOCC
	ATCCTGCAGA	CAGCTOTOTO	CACGAGGGAC	ATTOCCTOC	GCCCGGACAG	CACCCACCTG
	CHESTICATION	CCACCGAGTC	AGCCTTCCAC	TATOMOGILO	ATOGCGCCAA	COTOCTOOCT
	<b>GGCATCATGA</b>	GCCGCAACGA	TGAACOCTGC	CACCTOCACA	CCACGGGCAC	CTACACCCAG
	TACAGGACAC	AGGACTACCC	OTCOOTOCCC	ACCCTOUTOC	ОССТОСТСОС	CARCACAC
2	ATCATCCCCA	TCTTTGCTGI	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC
	TATTTCCCTO	けつけつけつけ	одоволяста	CAGGAGGACT	COTCCAACAT	COTGGAGCTG
	CTOGAGGAGG	CCTTCAATCG	<b>GATCCOCTCC</b>	AACCTOGACA	TOCOGGCCT	AGACAGCCCC
	CCACCCCTTC	GGACAGAGGT	CACCTCCANG	ATGITCCAGA	AGACCAGGAC	TOOOTCOTT
5	CACATCODGC	GGGGGGAAGT	<b>OGGTATATAC</b>	CAGGTGCAGC	TOCOCCCT	TOAGCACOTO
2	<b>GATGGGACGC</b>	ACOTOTOCCA	астоссавла	GACCAGAAGG	<b>GCAACATOCA</b>	TCTGAAACCT
	recriences	ACCIGCTCAA	GATOGACCCO	<b>OCCUTCATCS</b>	OTOATOTOR	CACCTGCAAG
	CTGCWWAG	Адотосаотс	AGCTCCCTOC	AGCTTCAACG	GAGACTTCOT	OTGCGGACAG
	TOTOTOTOCA	GCCAGGGCTG	GAGTGGCCAG	ACCTOCAACT	GCTCCACCGG	CTCTCTCAGT
ų	GACATTCAGC	CCTGCCTGCG	<b>OGAGGGCGAG</b>	GACAACCCOT	<b>GCTCCGGCCG</b>	TOGGGAGTGC
2	CACHGGGGGG	ACTOTOTOTO	CTACOGCGAA	OCCCOCTACO	AGGGTCAGTT	CTGCGAOTAT
	GACAACTTOC	AGTOTOCCCCG	CACTTCCOGG	TTCCTCTOCA	ATGACCCAGG	ACCIOCACC
	ATGGGCCAGT	grandrarda	accreerred	ACAGGCCCAA	<b>ACTIONALIS</b>	TOCOCTORGO
	AATOCCACCT	GCATCGACAG	CANTOCOCC	ATCTCTAATO	<b>GACOTOOCCA</b>	CTGTGAGTOT
_	GOCCOCTGCC	ACTRICACCA	SCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC
>	TCGGCGATCC	ACCCGGGCCT	CTGCGAGGAC	typedicti	GCGTGCAGTG	CCAGGCGTGG
	000000000000000000000000000000000000000	AGAAGAAGGO GCGCACTTGT	TOTAL COLOR	GAGGAATGCA	ACTUAL VALUE OF	Change and a second

TRYONORY COLTRICATOR GUAGALOC MANAGEM TOTAL TRYONORY TOTAL ORGANICAL STATEMANTS COLORARIA CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT AND CONSTRUCT ဓ္က 2 13 8 23 <del>수</del> 33

Seq ID NO: S41 Protein sequence Protein Accession #: NP\_000204.1

5

20		=-	<b>11</b> –	<b>:</b> :	<b>=</b> _	11.	
·	MAGPRESPHA	RLLLAALISV	BLEGTLANRC	KKAPVKBCTB	CVRVDIDCAY	CTOEMFRORR	
	COTTOABLLAA	GCGRESIVVA	ESSPOITEET	OIDTTLARGO	HSPOGLRVRL	RPOSERMFEL	_
	EVPEPLESPV	NS40W11ATO	ALINGLIGGSM3	RHOGHTARVE	SQLTSDYTIG	VEVXCVVXX	_
;	POTDMRPEKL	<b>ddds</b> Ndaday	PSPIONISLT	KOVDEPRNKL	QUER I BONILD	APECGFDAIL	•••
S	<b>OTAVCTRDIG</b>	WRPDSTHLLV	PSTEBAPHYB	ADGANVLAGI	MSRNDERCHL	PTTGTYTQYR	
	TODYPSVPTL	VRLLAKHNII	PIPAVTVRY	<b>SYYEKLHTYP</b>	<b>BV88LGVLQB</b>	DSSNIVELLE	-,
	EAPWRIRSKL	DIRALDSPRO	LATEVTSKMP	OKTRIGSPHI	RRDEVOIYOV	QLEALERVDG	•
	THVCQLPEDQ	KGNIHLKPBF	<b>BDGLftytDAG1</b>	1COVCTCELO	KEVRBARCSP	NGDINGGGG	-
,	CSEGWSGOTC	NCBTOBLEDI	OPCLREGEDK	PCSGRGBCQC	CHEVEYOECH	YECGPCEYDN	
3	POCPRISGFL	CHERCISMO	<b>OCVCRPONTO</b>	PSCDCPLENA	TCIDSNOGIC	MURGHOECGR	•
	CHCHOOSLYT	DTICBINYSA	THPOLCEDLR	<b>GCVQCQANGT</b>	<b>GEXTAGRAPCES</b>	CAPRATONIDE	_
	LICRAEEVVVR	CSFRDZDDDC	TYBYTWEGDG	APGPNBTVI,V	никиосерав	PHALIPLLL	•-
	LLPLLALLL	LCHIKYCACCK	ACLALLPCON	RCHDWGPKED	HYPICRENIALA	SDHLDTPMLA	•
;	BONLKGRDVV	RWKVTNINGR	POPATHAABI	NPTELVPYGL	BLRLARLCTB	NLLKPDTRBC	_
3	AQLRQEVEEN	LNEVYROIGO	VHICLOOTKPR	COPNACIKO	HILVDIVIAL	PRSAKPALLK	-
	LTEKOVEORA	PLIDLKVAPOY	YTLTADODAR	CHVEPQEOVE	LVDVRVPLFI	RPEDODEXQL	_
	LVBAIDVPAG	TATLGRRLVN	TTIKEGARD	VVSFEQPEPS	VERCEDOVARI	PVIRRVLDOG	=
	KSQVSYRTQD	GTAGGNRDYI	PVEGBLLFOP	GRANKELOVK	LLELOEVDBL	LRGROVERPH	×
í	VOLSHPKFGA	HLOOPHSTTI	LINDPORTOR	BPTEOMLESO	PPPHODLOAP	ONTINAKAAGB	=
2	RKIHPNWLPP	SCHMOYRVK	YWIQCDSESS	AHLLDSKVPS	VELTHLYPYC	DYEMKVCAYO	=
	AQGEGPY89L	VSCRTHOZVP	BEPCRLAFIV	VBSTVTQLBW	ABPARTNORI	TAYEVCYGLV	Ξ
	MODINADIOPM	KKVLVDNPRN	RMLLIENLRE	BOPYRYTVKA	RNGAGNGPER	BAIINLATOP	=
	KRPMBIPLIP	DIPINDAGED	EDYDSFLAYS	DDVLRSP8GB	ORPBVSDDTE	HLVNGRMDPA	=
	PPGBTNSLHR	HTTTSMAYO	THLEPHVPHR	VLBTBSTLTR	DYNBLTRBEH	SHSTTLPRDY	Ä
2	STLTSV9SHD	GRLTAGVPDT	PTRLVPBALG	PTELRVSWOR	PRCERPLOGY	<b>BVBYQLL#100</b>	=
	ELHRLMI PWP	AOTEVVVEDL	LPWHBYVPRV	RAOSOBGWGR	ERECVITIES	<b>GVHPOSPLCP</b>	=
	LPGSAFTL8T	PBAPGPLVPT	ALSPDSLQLS	WERPRRPHOD	INDYLUTCEN	AQGOODATAP	=
	RVDCDSPRSR	LTVPGL6BNV	PYKPKVQART	TEGPOPEREG	ITTERODOG	PPPQLGBRAG	Ξ
6	LPOHPLOSBY	SSITTTHES	TEPPLADGPT	LONGHIENGO	SLTRINTORF	VSRTLTTSOT	-
2	LETHINDOOPP	៩					

Seq ID NO: 562 DNA sequence Nucleic Acid Accession #: NM\_01333.1 Coding sequence: 1..63

8

**5**—

PCT/US02/12476						
1120 1120 1120 120 120 120 120 120 120 1		900	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	900 900 1020 1100 11140 11300 11300	200 200 300 300 300	1120 120 120 120 120
ECUSARIOCTE ANTOCATO TOTALOGORY CONTENTION TOTALOGORY CONTENTION TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY TOTALOGORY	\$1    -   PTKGLPDHP8	S1 DACCTIAGTE	CATALOGUE STOCKTOC SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL S	ACTIVALAGE STANTEGAGE STANTEGAGE FITTACTITI TITACANGAN TITITICATO TACTOMAGE TACTOMAGE TACTOMAGE TACTOMAGE TACTOMAGE TACTOMAGE TACTOMAGE	51   	S1   Accession archecter recentain ccantrean Activation Trecessere
MAGTICTOC NAGOGOCOC CONTROL NAGOGOCOC CONTROL NAGOGOCOC CONTROL NAGOGOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOC NAGOGOCOCOC NA	41      TRSQLANTE	41 41 CTTCCCTGC CTTCCCTGC	CONTRACTAC CONTRACTAC CONTRACTAC TATATATATA COCTUNANC COCTUNANC COCTUNANC COCTUNANC COCTUNANC COCTUNANC COCTUNANC COCTUNANC	ACTOCTOMA ACAGCTOCT ACCAGACT SCAGATTC SCATATTA SCATATTA COMPATTA COMPACCA ACTOTAMA	41	41 MAACCTTGA MAACCTTGA MAACCTTGA CTTATOGAG COGTCGACCC
TETTGGGGG ACCTTGGCGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGTATGG ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATTGT ACATT	31 41 Lespepgish ttrsqlante	915.1 31 	CACACATTA CAMATTAC INCOCOCCA TTTATCTCA TCCACATTA TCATAATGA CACATCAGT CACATCAGT	ATATECATO CCTATOTO CCTATOTO CCTATOTO ATCACTOT TCCCTOTO ATCACATA AATCACA	TLENE PRIVE PRIVE TTTT PORTA PRESING	CTOATO CAGGGG CTGGGT ACTACA ACTACA ACTACA TGGCTG
COCTOLAGE CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO CATCOTORIO C	n sequence P_037464.1 21   VRVMESLEGL	Los Los	MOTOTITICA TITOCCOTO STCCATCTTC GOTTGCAGAC STCCATCTTC GOTTGCAGAC	MAGGGAG TACTACATA MACCGAAAC CTTCTACCA CAATGATCT TATATATCT TATATATCT TATATATCT TATATATCT TATATATCT TATATATCT TATATATCT	P_016404 P_016404 21	21 TCCGCACTGC TCCACAGGAA GGAGGTGTCC CTCCATTCC AGAGGAAGAG
086413 detrituter crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocce crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc crecescocc cre	NO: 563 Proteil Accesson B: NI 11 YEL GVVLTELSIF	S64 DNA end Accession ance: 250.  11  TTCCTTAATTA	MATCHCCC TOOGRAFTCAO ACACATTOT OTT ACCAOT ALACATOT TITATOCAAT TITATOCAAT	NTOTCAGE TECTATEGE INVOTCATEGE INVOTCATE TECTATEGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TECTAGE TEC	S65 P MANECH MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP MATSP	111 
WO 02/086443 GOODAGO GETTTO GOODAGO GETTTO GOOTAGO C COGOA GOOTAGO C COGOA GOOTAGO C CACAC GOOTAGO C CACAC GOOTAGO C CACAC GOOTAGO C CACAC GOOTAGO C CACAC GOOTAGO C CACAC GOOTAGO C CACAC		Seq ID NO. 564 DNA sequence Nucleic Acid Accession B: No Coding sequence: 230-1126 011 11 21 010-02-030 programs Arcorr Archardta Arcorrants Arcorr	COCCOCCT AACTOMOGA CAAGAGACT CAAGAGACT TACTGAATO TTCTATCTCA ATACTCCATO CAAGACTTCA	ATCCTGACAA CCTTTGGGGG GTGCTGGTGA AGTCACTTAO ATTACACTTA ATTACACTT ATTACACTT ATTACACTT ATTACACTT ATTACACTT ATTACACTT ATTACACTT ATTACACTT	Beq ID NO.  AMENITAKI  GANAMETRI  PTANNETRI	2 883235
2 0 · 2 0	<b>v</b> ) 0	ν, o	ν O	رة و د	8 0 8	e sa .

13

2

23

ဓ္က

35

8

•		
PCT/US02/12476		
666 720 720 720 720 720 720 720 720 720 720	1120 1120 1140 1140 1240 1240 1240 1240	11 1 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
RACTOTACCO RATINGGOOD RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECTERING RECT	S1 ILGIHLLIQE ILGIHLLIQE ILGIHLLIQE ILBEDDVAD VLEEDPQVAD INGLOGETE ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES ILVOCTERSES	III   MASANCAN MASANCAN MASANCAN MASANCAN MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MITTERCATT MI
ASSOCIATED SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIA	11 HYLGFOLYDA HAYCLRBAGR BAYCLRBAGR PARTIENLAD POR GOFLDMY FYED THAI HYKSGMOT EG BYKNALLML	14   doubters   doubt
INCCLORED TO THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE CENTER OF THE	11 TOYOFIHTEK RANGEDPDY RANGEDPOY RANGESPTOL RANGESPTOL RANGESPTOL RANGESPTOL RANGESPTOL PELIATVIOL PELIATVIOL RELVSGAILY	11 11 11 11 11 11 11 11 11 11 11 11 11
darbakthe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Garbakhe Ga	n sequence P_005320.3 21 1 VLGGILAAY SGRRGGVAL GGTRGGVD RXWHARWE RRWLLGGR RRWLLGGR REGVYDGF LYBLLGR CGDLFSETEL	* 60586546584546506540646565648646546565656656
186443 Datestran Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcocan Marcoca	1.1 Prote siston #:  1.1  VOTSLFALA WLDTFHEYL CORRESWYTA CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFIES CORFI	1912 BM 486 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146- 1916: 146-
WO 01// TTCAAGGCC ONTECTAGGCC ONTECTAGGCC ONTECTAGGCC ONTECTAGGCC NOTIFICAGGCC   NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCC NOTIFICAGGCCCCC NOTIFICAGGCCCCCC NOTIFICAGGCCCCCCC NOTIFICAGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	23 5555584655	MUCHALG ACID RECORDS SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE ACID SEQUENCE

ATTCHART ATTCHART CONTRACT OF CANCELON CONTRACT OF CANCELON CONTRACT OF CANCELON ACCURATE TO CONTRACT AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY ACCURACY ACCURACY AND ACCURACY ACCURACY AND ACCURACY AND ACCURACY ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURACY AND ACCURA TCACCTCT CONTROL TECHNAMIC CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CON

\$

S

55

ଞ

જ

2

72

8

PCT/US02/12476 Seg ID NO: 573 Protein'sequence: Protein Accession 8: Bos sequence

WO 02/086443

MILKAPLAC II
POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POASTITEM OR POAST ENTITINE

PRINCECTOR

CONCESSIVE

BENESSIVE

PRESECTOR

 2 4 15 25 30 35 45

Seq ID NO: 574 DNA mequence Nucleic Acid Accession #: E Coding mequence: 148-4518

CACACATA OR ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO ORCONDO OR 20 55 8 65 2 73 စ္တ 85

THE AUTHORISTIC CHARGETIC AGACHAGO GOLOGICOS ANTITICAMA MATCHAGA ALA AGACHAGO 233
AGATTICTOR AGACHAGO CATROCAGO STOTINGO ANTITICAMA MATCHAGA ACCAGANA 233
AGATTICTOR AGACHAGO CATROCAGO STOTINGO STOTINGO ACCAGANCE GAANATCE 234
COTTANCANO CATROCAGO ANTITICATOR AGACHAGO 244
THE ALACACAGO STATINGO CTROCAGO CATROCAGO ACCAGO 244
THE ALACACAGO ANTITICATOR ATTAINANCE CTROCAGO ANTITICATOR AGACHAGO ATTAINANCE CTROCAGO ATTAINANCE ATTAINANCE CONCINCAGO ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINANCE ATTAINAN 52 35 တ္ထ 13 55

Seg ID NO: 575 Protein sequence: Protein Accession #: Eos sequence

8

HILDREAG (QLLCVCLLD N GERNIDEZ CONCUCLO O GERNIDEZ CONTACTOR O TOVORITY PROPERTIES ON TOVORITY PROPERTIES ON TOVORITY OF ALL METALICO CALLENILD NO TOVORITY OF ALL METALICO CALLENILD NO TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL TOVORITY OF ALL VERSRVOISB LEGEG HIPDOGNMAE DEFVY VLEVRHPOCP KMPNP MHQLEKENBV DVYQV/ AALPOGNIAB SLESL 8 જ 83

Ş

ı			۶
	7		

PCT/US02/12476

PC1/US02/124/6		WO 02
		AAACTACAGA
		AGGITTGCTA
	•	GATATTCAAC
		OTAMATACTO
	^	ATTITACTAC
181		CATTAGCTGG

8eq ID NO: 576 DNA sequence Nucleic Acid Accession F: 208 Coding sequence: 148-4494 WO 02/086443

2

2

HILDERIAC IQLICYCRID HANTYROR ILVERIONY YOLLOWY YOLLOWD KYPYCRIBY

1097 HIDDEL TOYNONIKEL KYGORDTEL BITTINTOR THEHIOTOP WEGOVSEN

11 KARITTEN GRONSELOE SYSTEMIC BETTINTOR THEHIOTOP WEGOVSEN

12 KARITTEN GRONSELOE SYSTEMIC BETTINTOR THEHIOTOP WEGOVSEN

13 KARITTEN GRONSELOE SYSTEMIC BETTINTOR THEHIOTOP WEGOVSEN

14 KARITTEN GESSERVOA BENEDORIO ENGINEMAN DESPRINTOR THEKENONI WEGOVSEN

15 KARITTEN GESSERVOA DESPRENCA METANIO GESTANIO GESTANIO GESTANIO GESTANIO GESTANIO GESTANIO METANIO ACTACIOM MATOTIFOT TITTAGNOTE MATTITAG CEG MOSTITOLA CATELIACIA CITTAGNAC TIGACENTA MA GIANTICAA CATELIACIA CEGNIZATE CALTAGNACA MATTIAGNA TITAGNAC CECNICATO CEGNIZACE CALTAGNATO ATTIAGNAC TITTAGNAC CALTAGNATO TITTAGNATO CALTAGNATO TIT CATEGOTACA CONTITAGNATO CALCAGNATO MA MATTITATA GOANTAKA CATAGNAC CATAGNACA MA TICAGNAMIA MATRIANIA CETAGOMA CATOTICOA MA Seq ID NO: 577 Protein sequence: Protein Accession 8: 508 sequenc 2 15 2 25 ဓ္က 35 <del>\$</del>

COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUTAGO
COCCUT

2

25

30

35

6

Seg ID NO: 578 DNA sequence Nucleic Acid Accession #: EDS sequence Coding sequence: 501-4514

45

 CACACATACO CAMAMANA COGGOGOGO CANTANANA CATTORNA ANTICANA ANTICANA ANTICANA CANTORNA ANTICANA CANTORNA ANTICANA CANTORNA	LI CACOCACAT ATTECTTCO COCTACACA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGECA ANTEGE	TEACTTCOM CTCACTTCOM CTCACTTCOM CTCACTTCOM CTCACTTCOM CTCACTTCOM CTCACTTCOM CTCACTTCOM ANACTTCAM	TETATACCT COTCOCATO CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTENANC CONTEN	41 GANGATINA TGAGANGCO AGROTICCE AGROTICCE AGROTIANAN TATTANANA GALTANANA GALTANANA GALTANANA GALTANANA TATTANGCA AGROCIANA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TTTTANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGANGCA TGAGAN	ACMACAM AGAGOCOCO COTTOCOTA AGAGAGAMA ACAGAGAMA ACAGAGAMA ACAGAGAMA ACAGAGAMA ACAGAGAMA ACAGACATA ACAGACATA ACAGACATA ACAGACATA ACAGACACA ACAGACACA ACAGACACA ACAGACACACAC	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 TTCAGAAC GGGAAAGAC AGTGGATCO GCACTATCO GCACTATGO AACAGGGAA AACAGGAAA AACAGGAAA	AGAMATOTT TCGAMCGTA AGAGGCAA CAATAATTGA CATAATTGA CTTATATGAA GAACATTGAA TGAACCTAGAA TGAACCTAGAA TGAAGCCAAGAA TGAAGCCAAGAA	ACCAGENTA TATGATACCA ACCAGENTA ACCAGENTA ANATACAGO OCTUANTTA GAAGGGGTA COCCAGNTTA ACTAGCONT	COAGAINTA TEATTHEAN MITTITION TOACTATOT ACCIACTON THOSAACTON THOSAACTON COCCOACAN	TACCACCTT OTTTCCACTT AGATCACTA TCTCACATA TCTCACATO AGACTACACA AGACTACATA ACACTACANT AGACTACANT	TOTATACA TOTACCAGO ONAGCATAG OTAGCATAT CCTACTOATA ANGAGOAGO ANTGCTACAA	228228822
 CONTRACTOR ACTIVITATION OUTTATION OUTTATION OUTTATION ANACCOUR	TATTECETTO AGCCTCTTA AGCCTCTATA CACTTCAA TATCCATTC GACAATACA	ACTICIONA AUTATOCIA ACCTINATA CTTANTACTO ATCTCTONAN ATCTCTONAN	CTOTOSCTOR CAGTITCTAT CAGTITCTAT CAGTITCTAT CAGTITCTAT ACATATCCAGA	ACTOCACCE TCTTAGATCT AACAGAATAT TTCTTCAGGC AGGGTATATA	CACACTOTOS CCACATATOS ONOGRAGOS TCCACTCCOS TTTCCTCCO	RSSRRRRR
 TOTOGRAPHOC OCTITIONS CCTITIONS	TAGCTCTACA GACTAATTAC AGGCCCAGTG	ACTORANTAC ACTORANTAC ACTORANTAC	CACAGCCCAA OTOTTGATGA OTCCCTCAGT	TOTTGGATCA ATCTGAGANG TACAGATCTG	DAGGGAAATE GOCAGAGAAA ACAACCAAGT GAAATGCCAC	3560

MACCAMITIC A MACGARIATIC A MACGARIATIC A MACGARIATIC A MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATICA O MACGARIATIC

ප

55

2

65

Š

င္ထ

82

တ္တ

s
~
₹
-
ñ
•
S
=
5
_
C
ã.
_

Č	27.7007						,
? •							۲
ATTATTCTAC	CTTTGCCTAC	TTCCCAACTO	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340	
CCAUACACA CA			ACCIONIAL	CICCOCACA	ALCOACEG	2460	
ATACAMICA		-	MOTORIAL	TOOLCI MOC	CALCOLO I LOS	2530	
A COLORAGO	-		CONCORATO			2480	
ACTINGACOR	_	_	TATCCACACC	TOCANCACC	ATCTTTCCAA	2640	
TTCAGATGA	-	-	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700	
ATGCAAGTAG	-	_	AGACACTGAA	AGAGITITIAC	CAGGAAGTCC	2760	
AGAGCTGTAC	TOTTOACTTA	_	CAGACAGCTC	CARCACCO	GACIACAGC	2820	
CARAMICO	_		ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880	
PTGCTGAAAA	_	_	ATATCAATGC	CAATTATOTT	GATGGCTACA	2940	
ACAGACCANA		_	OCCCACTONA	ATCCACAGCT	GAAGATTTCT	3000	
DGAGAATGAT			TTATTOTCAT	CATAACAAC	CTCGTGGAGA	3060	
NAGGNAGGNG	AMANIGIDAT	_	CTGCCGATGG	CACTOAGGAG	TACGGGAACT	3120	
TCTGGTCAC	-	_	TTCCCTATTA	TACTOTOAGO	AATTTTACTC	3180	
IAAGAAACAC	. AAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGA	COTOTOTOA	3240	
CACAGTATCA	CTACACGCAG	_	TOGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300	
<b>TOACCTITIOT</b>	GAGAMAGGCA	OCCTATOCCA	AGCGCCATGC	AGTODOGCCT	GTTGTCGTCC	3360	
ACTECABTEC	-	AGAACAGGGA	CATATATTOT	<b>GCTAGACAGT</b>	ATOTTOCAGO	3420	
AGATTCAACA		STCACATAT	TEGGETTETT	<b>MACCOTC</b>	COTTCACAA	3480	
DAAATTATT	COTACAMCT	CAGGAGCAAT	ATGICTICAT	TCATGATACA	CTGGTTGAGG	3540	
CCATACITAG	TAMBANACT	_	ACAGTCATAT	TCATGCCTAT	GITAATGCAC	3600	
TOCTICATTOC	TCCACCAGCA	GGCANACAA	ACCTAGAGAA	ACMATTCCAG	CTCCTGAGCC	3660	
NOTCHARTAT	_	_	CAGCCCTANA	GCATGCAC	AGGGAAAAA	3720	
ATCGAACTIC	TTCTATCATC	CCTCTGGAAA	GATCAGGGT	TOCCATTICA	recerdadro	3780	
GAGAAGGCAC	: AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840	
TCATCATTAC	CCAGCACCCT	CTCCTTCATA	CCATCAAGGA	TTTCTOGAGG	<b>ATGATATGGG</b>	3900	
ACCATAATGC	: CCAACTOGTO	OTTATIGATIC	CTGATGGCCCA	AACATGGCA	GAAGATGAAT	3960	
ITGITITACTO		-	TAMATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020	
<b>POCCTORAGA</b>	_	-	AGGAAAAACT	TATAATTCAG	GACTITATO	4080	
TAGAAGCTAC	: ACAGGATGAT	TATOTACTTO	AAGTGAGGCA	CTTTCAOTOT	CCTANATOOC	4140	
CAAATCCAGA			TYDAACTTAT	AAGTGTTATA	MANGANGANG	4200	
CTGCCAATAG	_	-	ATGATGAGCA	TOGAGGAGTG	ACCIOCACCAA	4260	
2111010100		_	MCTAGNAM	AGAMMATTCC	OTGGATGTT	4320	
ACCAGGTAGC	_	-	OCCAGGAOT	CTTTGCTGAC	ATTGAGGAGT	4380	
ATCASTACT			TTGTGAGCAC	MGGCAGGNA	CAGAATCCAT	9	
CACCTCTCT	-	_	TOCCTGATOO	MATATAGET	GAGAGCTTAG	4500	
AGT CT TT A 0 T		-	GOODLICACA	TCTGAGCATT	Grincerer	4560	
TCCTAMATT			TICIGITATE	TOTTOATTE	CLATCACCTO	0790	
ACAGI AACTT		CONTICTOC	SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCAMILLA SCA	TAIL AT LANGE	AATOTOTOTO	000	
	ACTIVIANT	IACLIALIA!	TOWNER OF THE PERSON	MATICALICA	ALL LACOUR	900	
TEATAGAGG			AAATOTTOT	TTTAGTOTE	AAATTTTAG	4860	
TOTATOT			GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920	
MINAMOR	-	_	ATTITACASC	TOCAGTATTC	ACCTANAGTA	4980	
DAAATAATCT	_	GTANATACTG	CCCTAGTGTC	TCCATOGACC	AATTTATA	5040	
TATAATTOT	-		TOAOTCAAGT	TETCTAGETC	TOTOTAATTO	5100	
AXTITO TITA	٠.	_	TCTTACTCTA	CCASTTTCT	GACATTOTAL	2160	
<b>TOTOTTACCT</b>			GCATGTAATT	TTAACTTTTO	TOGANAATAG	5220	
WATACCTTC			GAGAATAACA	CCTTACCAM	CATTOTTCAA	5280	
ATTENTAL	-	TGCAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAAA	3340	
WWWWW	AMMANAA	₹					

Bog ID NO: 579 Protein sequence: Protein Accession #: 508 sequence 55

	9	120	180	240	300	360	\$20	480	540	600	660	25	380	940	900	960	1020	1080	1140	1200	1260	1320		
151	AVKGKGKLRA	YIYNGBLISP	<b>QYKFSRQVFS</b>	LYGOLDGEDO	PTDNPBLDLP	RIGTKYNEAK	HTVEGTSASL	BEPATEAIPP	ECHVWPDBST	EMPHYSTPAY	EGLESEKKAV	ADVOCE 1441	DATCHOURY IN	EDFICKMINEH	NUTLENTRIK	VVVHCSAGVG	LVEAILSKET	REKNRTSBII	MINDHNAGLV	DPILEATODD	TAGTFCALTT	ENPSTRIDEN		
<b>3</b> _	DADRPSSFEE	NLLPNSTORY	DYLONNFREQ	YDTHIEKFAV	KYEDOLIVDA	POISTITHYN	TEGTIVIELPP	LOTGAEDSSG	BEESLKDPSM	MSQGPSVTDL	BSHESRIGIA	PRVIBTPPTP	<b>OITADBBNHP</b>	AAQGPLKSTA	VOVLAYYTVR	AYAXRHAVGP	EBOYVF LKDT	DYBAALKOON	LLHTIKDPWR	LENEEKLI 1Q	MIVHDEROGV	<b>ILSLVSTRQB</b>		
<b>:</b> -	PPLEMOIYCP	OMLOPFILL	MOOSGYVMLM	LUTWERPRUV	VAICTNGLYD	SATHUIRKKE	RLATERDIBL	REBSLLTBFK	NAGEDBTESG	TTKBPSAGPV	TOPVYNEASH	AHPYLEDSTB	OBVOSCTVDL	DOYNRPKAYI	YOMPLYTOKS	LPVLTFVRKA	REGRATIVOT	LLSQSNIQQS	BNBPILTOHP	VILMAREHKC	KEBAANRDGP	<b>IEDYOPLYKY</b>		
21	CSENSLEGOR	GVEBVBRPGK	QLAVFCEVLT	QADPENYTSL	LPRIMBYVLQI	EGAIVNPGRD	SLASTSOPVT	BLATVBITEY	YDVLIPESAR	TRIRVDESER	BTVNVVKBQT	LIYWRKCPQT	REPETLKETY	LTDYINANYV	<b>QYMPADGSER</b>	WPDMGVPBYB	VALFOPLIGHT	GKTKLEKQP0	NABYIMOYYO	DEPINCESFK	SKTPELIBVI	NLMRPGVPAD		
=-	HWGKCNINSSD	ENLOPKAIID	PKDTV91859	AVCSSEPENV	ODLGATLANL	KEESEGKOIE	PSCKCDVPNT	PHYNLEGTAE	PREENPETIT	GRESPLOTIVY	TPBBRQQDLV	PICLWLVGI	ADLHABSOTT	LAQLAEKDOK	LVEKGRRKCD	RVVTQYHYTQ	MLCOLOHEGT	VNALL, I PGPA	BLEGROTOYI	EDEPVYMPNK	I dBGdNdNAd	VDVYQVAXMI	ESTEBLY	
	NVPXABKITE	LOILPEVOTE	PCTDTVDWIV	BYTCKBEIHE	THRIBPLADOY	PELIGTERII	TARSPIRGSB	NDGSKTVLRB	IBENISOGYI	DITAOPDVOS	PPTEVTPHAP	IPLVIVSALT	1 P I KHP P KHV	IVAYDHSRVK	NVEVIVNITN	KGSOKORPSO	RTGTYIVLDS	EVLOSHIRAY	PVERSRVGIS	VMI PDOGNWA	YALEVRHIDG	LAGICIENENS	GAALPDGNIA	
	;	09				;	3				•	2					2				;	Š		

<sup>85</sup> 

	22222			2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3			
ARCANCHA ARGAGCECE GOCTECATA ACAGGAMA THOOGHAM AGATTACA ATCATEGA ATCACCA ATCACCA ATCACCA ATCACCA ATCACCA ATCACCA ATCACCA ATCACCA ATTACCACA ATTACCACA ATTACCACA ATTACCACA ATTACCACA ATTACCACA	AGAMATTE GCAGGCTOCT TTTALAGAT ANTICACA ACAGTTEA AGCAGTTEA TCTTOTACA TCTAGACA TCAAGACTEG	AGTAGECATA OCCTACTOAT CAAGGAGAA CAAGGAGAA TOGATGETAGA ATTECTOAG ATTECTOAG TAAATTAGC TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TCACACTOT TC		TTANGORDA TTANGORTA TOCACATT TOCACATTA CCACAAATA ACACACAA	TOANDGENC TOANGENTE CETCETORON OTACHENCE ACTIVECTOR TATOTTCA TATOTTCACA COSTICACA ACTICACA ACTICACA ACTICATANC	CCTGAGCCA CCTGAGCCAG CCTGAGTGA CCTGAGTGGA CATGAGTT AGATGAGTT CACTCTTATC	
GGGGGATTAA GGGGGATTAA ACTACAGACA ATATTGATGA ATATTGATGA ATATTGATGA ATATTGATGA ATATTGATGA ATATTGATGA ATATTGATGA ATATTGATGA		TTCTTCAGAT TTGTCGACAT CAGGAGAGAGA GAGGAGTCACA AACCAGTCACA AACCAGTCACA AACTACACACACACACACACACACACACACACAC		TTGGCCTGAC CAGCCTGAC GCTTCCAGAC CTCCAGAC CGAGCATTTA AAAAGTTTA CCCACCACCC GCAGGGTTAA	CCMTATOT  ANTECIOLO  TOTALO  ODAGTICO  ODAGTICO  OCTORO  TOTALO  TOTALO  TECHOOTICO  ANTECO  A		MANTICOTI TTCTACACA OCCURACA ATATACTA ATATACTA TTATACACA TTATACACA ATATACACA ATATACACA ATATACACA ATATACACA TTATACACA TTATACACA ATATACACA TTATACACA ATATACACA TTATACACA ATATACACA TTATACACA TTATACACA ATATACACA TTATACACA
		ATGGGTTATG GACCACTGA ATTGGAACT ACTACCACACA TCCCCACACA TCCCCACACACA	MACATACCA CTTATACCA TCACTAMOS GCACAGCCO COTOTTATO GGTCCCTCAG GAOGTACAC MACATOGTAT	GAGCTOTA GTGATCOTOT TGGACGAMT ATATCCACA ANGCATTC GAGACACTOA GCGACACTOA GCGACACTOA	TATACANO GOCCACTOR COTTACTORO COTTACTOR COTACCONT COMMODIA ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN ANGOCCAN	ATCHCGGCTC CGAGGTGGCTG CCCTAAGC TCAGGGTTG ATCAGGGTTG ATCAGGATT GATGGCAAA ANTEGTGGAA GAAAACTTA	GANGGONG CENGANNG CENGANNG CENGAGE CENGAGE CENGAGE CONTTACH TOACTAN TTACACT TTACACTAN TTACACTAN TTACACTAN TTACACTAN TTACACTAN TTACACTAN TTACACTAN
CCCACTICAL CTCCCCCCC CTCCCCATACA CCCGATTCA CCCATACA CCCATACA CCCATACA CCCATACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACA CATACTACTACA CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTAC CATACTACTACTAC CATACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTAC CATACTACTACTACTAC CATACTACTACTACTAC CATACTACTACTACTACTACTAC CATACTACTACTACTACTACTACTACTACTACTACTACTA	TTATCCATT TGGAGCCTTCTG TCCCTGGAC CCAGTTGGCT GGACTACTTA TCCCTGACCTTA TCTCTGGCACCT TTATGGCTACCT TATGGCTACCT TATGGCTACCT TATGGCTACCT ACCCAGCACCT ACCCACCT ACCCACCCACCT ACCCACCACCT CT ACCCACCACCACCACCT ACCCACCACCACCACCACCACCACCACCACCACCACCAC	GCTACCCAT ANATACAG CCCTGAATTA ACCCCAGATT ACCCCAGATT GACTTTAAAT GACTTCTCAG ANATGATGGC ANATGATGGC ANATGATGGC ANATGATGGC ANATGATGATAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACTAAAT ACCCTACAAAT ACCCTACAAAT ACCCTACAAAT		TANTACCCTT TOTCATCTAC CCCTAGAGIT AATTCCAAT TOTAGAGIT AATTCCAAT TOTAGAGIT TOTAGAT TOTAGAGIT TOTAG	ACTGACTGAT TOCTGCCCAA TOAGTACTOOA TOAGTACTOOA TOAGTACTOO AAAGGGTCC GOTGGCCTAAC AAGACAGGC AAGACAGGC TOTGACATA TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO TOAGATACTO	CAGAGGCAC CTCAGCCTCC CTGATCCTCC TGTGGAMAN TGCCTCCTAC TATGATCCT TGAGCCTATA ATCTAATGAG	ATTOCACA TATOCACA TATOCACATO TOTACACATO TOCACATO TOCACATO TATOCACA ATTOCACA ATTOCACA
#B688888#	ADTIMANGO CONTRITION TECHCOTOT TECTOMANG TECTOMANGO COMMANDO CICOMORCA CACAMORCA CACAMORCA CACAMORCA CACAMORCA CACAMORCA		MTMC MTMC MTCAG MTCAG MTTA MCCTA		MGGTTGCA MGCTTATAT ANAGGTGCA GAMATTAA ACTACAGG CTCGAGGG TGGAGTTGG ACGAGGAC TGTAGGAAC TGTAGGAAC TGTAGGAAC	MICCICCTAC ATCCTCCTAC AGCAGATCA ACTACATCA ACTACATCA ACCACCTCT ACTACATCA ACCACATAAAGA ACCAATAAAGA ACCAATAAAGA	ATTOCCCT TO TO ANY OCCUPANT TO ANY OCCUPANT TO ANY OCCUPANT ACCUPANT ACCUPA
WO 02/086443 COCOCKO COCOCKO COCOCKO COCOCKO COCOCKOCKO COCCCCCCCCC COCCCCCCCC	GOMMAGGOA OATTECANO TEMBATECAT ANTOGETCAT ACAGTTAGCA TETEGATATO TETEGATATO TOGGAMGAC CAGTTOGANG	GGTGCTATTC TGCACTANTG ANTCCTGANC GANGAGGGAA ANCCAATCA ANGGTGANG GANGGTGATG ANGGTGATG ANGGTGATG ANGGTGATG ANGTGTGT ANGTGTGT ANGTTGTGGG		CANGONTA CANDOTTC TACTTAGAGG TACTTAGAGG ATTCAGATA CANGOTOTA CACAGAMTC	CTTGCTGAM ANGGGGAA TGGGAAGA ANGGAAGA TTCTGGTCA CTAGAAGA CTGGGTTG CAGATACTA ANGATATA ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC ANGATTCAC AN	CTOTCACCA OGCTTAACTO CGAACTTCTT GAAGCACAG ATCATTACCC CATAATGCCC GATTAACTGGC GTTTACTGGC	CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTINUES OF CONTI
5 10	. 15	30	35	\$	55 %	65	75 80 85

<sup>8</sup>eq 1D ND: 580 DNA sequence. Nucleic Acid Accession 8: 205 sequence Coding sequence: 148-1632

WO 02/086443

22 22 22 22 22 22 22 22 22 22 22 22 22	1100 1110 1100 1100 1100 1100 1100 110	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
CATATOTT CATATATA GAMATATA GAMATATA TIGITCAAI AMAAAMAA		S1   INCAMCADA MICHAGOAN THEAGAGANA MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICHAGOAN MICH
TCTAGTTCTG AGTTTTCTGA AACTTTCTGTG GCGATTAAAA	TOLAGORMO TOLAGORMO TOLAGORMO DE RESTREAN LONGERED FOR TOTATER POR	11 12 12 12 12 12 12 12 12 12 12 12 12 1
ACTCAACTT TTACTCTACC ATGTAATTT GATTACCCC TATAAATATTT	TATER THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP	11 11 11 11 11 11 11 11 11 11 11 11 11
TTACTACTO TTACCOCTC TTOTTCACC TTOTTCACC CAMATANA A Sequence: 08 sequence: 21	MACYPOOR EMECORITE EMECORITE EMECORITE EMECORITE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHIN MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHIN MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHIN MACHIN MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE MACHINE M	11   1   1   1   1   1   1   1   1   1
U86443 ATTTTATAT ACOTATTCA GTCATTAACT ATGGAATA AMMANAMA S81 Proteil serion [1:1]	TOTAL CONTROL OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T	
WU DZ/U86443 ATATTEK TATTEK TATTEK TATTEK TATTEK CAMBAN ANAMAMA AMAMAMA AMAMAMA BETGELI ACCESSION 1  1 11	HEROTICE OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTROLL OF CONTRO	Req ID NO. 543 DNA I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESSION I NUCLEI C ACID A CESTION

CCCCAAAAA AAGCATATA CACTAATAA TAACCTIATA CTGGTAAGT ATTGCTGGT ATTCTGTCC TATAGGAAAT O ATCCATATA COTTGAACC A TICTACCAA TICTGCTTCA O ATCTCCCCC TACTCCTCAT O CAATGAGA ATATGAACCA T CTTGTACAG TAATGAACA WO 02/086443
rooscertor Areacocc of retreective roosceroor of retreective roosceroor of actionate corrosing actionate and actionate actionates and actionates actionates actionates actionates of alterating offensive actionates corrosing offensive actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actionates actiona ATAGAGOTTA GGAATTCCAA A GTATTTGTAG CLATTATCAG TAAAACACTC TTCCATATGA I ATAATCTGT TACTTATTGT A ATAATTGTAG ATTTTTATAT T ATTECAACAG ន 

ТОТЛАСТИ ОТСИТАЛСТ ПОТПОЛО ЛОТИМИТЕТ МЕТИТОТО ВИМИТИВИ МИТЕТИТОТ ВИМОТИВИ ОТСИТЕЛИТЕ СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО СМОВИТО

WO 02/086443

Seq ID NO: 583 Protein sequence Protein Accession #: NP\_002842.

.0

2

2

22

II MATERIATE MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MATERIALE

II MAT ANDCOURT HERMANES CONDAIGNESS AND ACCOUNTS AND ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS TO ACCOUNTS AND ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUNTS ACCOUN 585 Protein sequence S 2 15 20 30 <del>\$</del> တ္သ S 23 45 25 5 2 8 35 73 8

HALLEROTTED COLLAWORTHOOR KUNESCORPT TOLLOGONG KKYPTCOLER GOSTHIEDEN TOWNINGER CORPHIEDEN TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER COMPANY TOWNINGER CO

3

35

<del>수</del>

45

Seq ID NO: 584 DNA sequence Nucleic Acid Accession #: NM\_005688.1 Coding sequence: 126..4439

တ္တ

55

8

જ

2

73

8

PCT/US02/12476														
900 900 1020 11140 1200 1320 1380	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	166044200		981		8	2000	0 0 0 0 0 0 0 0		021		120		9 1 2 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
TTTRONETS LFREILASPH POHTUNAUS GETLHRYGEL LAISTANGET GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GETTENAUN GET	51. 	TOACTICTA GCTGGCCA TOTCCGCA CCATCAGCT CCGTGTTTTT CCTAGGTCAT ACTGAGCTA		51 		51   CATGCAGGCC	CCCTOGCATA CCCGCGGGGT CAGCAGGCCG	CTTTCTGCCC CGCCCTTCC CATTGTGGGG GAAATAAAG		s1   arasoproga lbliam1toc		S1 CCTGCAGGG TGCTGCCTCT TGTGATTGCA	TCCAAOGT TCCAAOGT TCCAAOGT TCCAACGAA	ACCTCTACT ACCTCTACCT ACCTCTACCT ACCTCTACCT ACCTCTACTT ACCTCTACTT
STWIKGGGGR LAASBRUDB PPCVGRIADP LATIHAYNG RRQIPPDPVG RRIVELGGG ALERTENKE OTETDLLIQE RFYAMFAAAR	41 corrandeeer corrandeeer corrandeer corrandee	ACCEPTOR COCCEPTOR COCCEPTOR COCCECT MCTTCOC GOCCCCTT TTCATTORG TAGANATA		41 OGROPRGAGA EAELARRSLA WITGCFLPVP		41    -  -  -	GCCCAGGAGG GGGGGGGCGC CCTGCGGGGGC CCTGCGGGGGC	TCACCCAGTO CCCAGCCTGG GTGGCCAGTT TGTTTCTGTA		41 Geropranda Gleieschoo		41 OGCAGGBACE CTGGCTGGGC GAGGGAGTC	TOCCIACIA SATTOTAC SAACCAGO SAATOCOGO	ACCCAGTOR FACCCAGTOR CCATAAGATC FGGGTCTCCT ACGACTAGAC
GSTAFSTWL IRGVYFVKOP ERITTSSTOO TITOLATIVIA BOLSBALING BOLSBALING BOLSBALING FROYTEDOIN LILDSATAN PSYLEGINGS	31 	GOOGCCGAG AGCAGAGCTG OCTICTGAAG CCACCGCCAA GATCAGGCAG AGCCCAGCCT GAGTGGCCAG		31     AGGPQBAGAT   YLAMPPATPH   SCLQQLSLLM	esdnesse	11 CCGGGCAGAG	ATGCTGATO CCAGGAGAGG TCGGGGCCSA TGAAGGTGCC GCTGCAGACC	TTGATGTGGA GGCCCTAAG CCCAGCACGA CTTACATGTT		31     Aggpgragat   Rltaadhrqu	162.1	STANDARD CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENSION OF CONCENS	ATTOCOUTON OTTOCOCO GOTOCOGO ACATOCTCAC	TTACTOGACH CTGAGGGCT AATACAGTOT TCCAGGGCAA
MALFMLINY AVMLILKA DURELPROAD DURELSSPOAD DURELSSPOAD DURELSSPOAD TVRSNLDP ALLERCKI GOVVEFUT	addathc gangecat gangece gecamma	CACCCAGGGCCAG CACCCAGGGG TGCCAGGGG CTGCTGCAGA POTTGA TGTG AGAGGGGCTA GTCCCAGCAC	In mequence 4P_001318.1	21 		21   TCTCTGAGAG	TOCACGGGC TOCTOGCOGC AGCAAGGGCC TOCGCAGGAT CCGAACTGACT	GCTTCCCTO CTCAGGGCAG AGGGAATGGT AGGAGGACGG	in sequence Eos cequenc	11 21         STODADGPGG PGIPDGPGGN AQDGRCPCGA RRPDSRLLQP SOQRR	Bguence n 8: NM_005! 3671	21 AACCACCAAC GGCACCGCA GCACCCCCAA	ACTCTORAC AGGAACACT AACTCTOGAC CCAGGCTTCC	ANDCOACTO GONGOLAACC AOCTCTUCAO TOGAAGGCTG
086443  CONGOLARIA   coding sequence 19613  1 1 1 1  Actionogoac derivitors or creatabactor actionators concentrate concentrate or accordance or a	TOCTOCAGA COCTTCCCC ATCCGACTOA CACCTTTCCC CCCTCAGGGC TAGGGAATG	8eq ID NO: 587 Protein Protein Accession II NP	11       BTGDADGPGG   GLANGCRGA   NILTIRLTAA	Bed ID NO: \$88 DNA sequence Aucleic Acid Accession \$: Bos Coding sequence: 52459	11               	CAGGGGGGG CAGGGGGCA GCCCAGGGGC GTGCCGCTTC TGCTTCAGTT	OTCTCAGCA CTCAGGCTCC CTCCTCCCCT TTGTCGCTGG	Seq ID NO: 589 Protein sequence Protein Accession #: Eos sequenc		Beq ID NO: 590 DNA sequence Nucleic Acid Accession \$: NM_00552.1 Coding sequence: 901671	11 GCAGAGTGAG TGAGCGGCC CCTCCTGCCC	CACTGCAT CACTGCAT CCATGCAA TCATGTCAC	CTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO	
WO 02/0 VPMSVYGVTI VEDENGURE REPOTTPOR LUDGASPVAL LUDGASPVAL GLPOTTRIA GLPOTTRIA GLPOTTRIA GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENERGURE GENER	Coding eequ  Adchaaacca Craaaacca Cacaaacca TaacaaccaT	CCTCACTAGA CCTCACTAGA OATACTCCA CTOTCTCCAG GGCTCAGCCT GCCTCCTCCC OTTTOTCGCT	Seq ID NO: Protein Act	1 HOAEGROTGO PROPHOGAAS VLLKEFTVSO	Seq ID NO: Rucleic Ac Coding sequ	1             	GANGGCCAGG CCTGATGGCC OGTCCCCGGG CCGCATGGCG GACAGCCGCC	ATCAGCTCCT GTGTTTTTGG TAGOTCATGC GCCTGATTGT CTGAGCTA	Seq ID No: Protein Ac	1 MOAEGGGGG PROPHGGAS PLPVPLAGAP	Seq ID NO. Nucleic Ac Coding sequ	ACAGCOGAGC ACAGCOGAGC ACACAGAGAC ACACAGAGAC	TCOCTOCCT OCTTTACCO CTCTTACTOC CTCACATOCCA	ACCORDING CACCATACACA CACCATACACA CACCATACACA TACCATCACA AATGGTCACA AATGGTCACA
\$ 01	15	30		35	<u>:</u>	45	20	. 55	9	65	20	75	80	88

HINDAGGCE, CPELLIADARA ATBRENCOC INCLREGICED REMRICERO PICCLICUMET DISCUSSIONE CONTRACTOR DESCRICACION PROPERTINA CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION CONTRACTOR DESCRICACION PORTRACTOR DESCRICACION CONTRACTOR DESCRICACION PORTRACTOR D 8eq 10 NO: 591 Protein sequence Protein Accession #: NP\_005531.1 20 25 S 3 2 75 စ္တ 85 2 2 25 ಜ 35 <del>\$</del> 45 2

#15

S92 DNA sequer Beq ID NO: 592 DNA seque Nucleic Acid Accession # Coding sequence: 211.856

છ

WO 02/086443

	<b>5</b> _
	₹_
1,006160.1	<b>z</b>
Beq ID NO: 594 DWA sequence Nucleic Acid Accession 6: NM_006180.3 Coding sequence: 3522820	<b>z</b> –
No: 594 DN Acid Accem #equence: 3	=_
Muclaic Coding	٦-
~	,

•	Nucleic Ac	Nucleic Acid Accession 8: Coding sequence: 1522820	2620 NM 006160	160.1		
n		:	;	:	;	:
	<b>-</b>	==	<b>:</b> —	<b>:</b> _	;_	<b>1</b> _
	CCCCATTOD	CATCTACCA	OGNATICTOCO	CCCCAGAGAG	TCCCOOACGC	caccaarooa
2	100000000	GCCGGGCCAT	GCAGCGACGG	COCCOCCOCA	GCTCCGAGCA	OCCUTACCC
2	CHECKLOSTIC	COCACCACCT	CAGOCTCTGA	TAMOCTOGAC	TOOGCACOCC	CCCACAGO
	ACCOAGGAGT	TANGAGAGCC	GCAAGCGCAG	CONTROCCTC	CCCGCACGGG	TOGOGGAAAG
	coccoanac	Adecedoda	CAGGCACTCG	900700000	GOCTOCTAGG	GATOTCOTCC
15	OGCTTCTGGA	GGGCGCTTT	COCCATOCC	ACCTOCTOCA	AATGCAGTGC	CTCTCCCATC
	TGGTGCAGCG	ACCCTTCTCC	TOCCATCOTO	GCATTTCCGA	DATTEGAGCC	TAACAGTGTA
	. алтесталал	ACATCACCGA	ATTITICATE	GCAACCAGA	AAAGGTTAGA	AATCATCAC
	AAATTTCTTC	CTCRTAAAGC	ATTICIDATE	AGRANTETOR	TOTALIGICAL	CANTITACC
2	CGARACAAAC	TOACCAGTIT	GTCTAGGAAA	CATTICOUTC	ACCTTOACTT	OTCTOMETO
	ATCCTGGTGG	GCAATCCATT	TACATOCTCC	TOTOACATTA	TOTOGATCA	GACTCTCCAA
	DAGGCTAAAT	CCAGTCCAGA	CACTCAGGAT	TTGTACTGCC	TGAATGAAG	CAGCAAGAAT
	ATTCCCCTGG	CAMACCTOCA	ACCARACTO	ATCACATTAT	CCTGTAGTGT	OCCAGOTOAT
52	CCOUNTOCTA	ATATOTATIO	GGATOTTOOT	Accrognm	CCAAACATAT	GAATGAAACA
	AGCCACACAC	ADDGCTCCTT	AAGGATAACT	ACATTICAT	CONTRACAG	TOGGNAGCAG
	ATCTCTION	TOCCOGAAAA	TCTTGTAGGA	GANGATCANO	ATTCTOTCAA	CCTCACTOTO
	CATTITICACAC	TOWNSTATOR	ATTECTORAL	TCTCCACCT	CAGACCACCA	CICCIOCATT
30	TTGAATGAGT	CCAATACAT	CTOTACTAR	ATACATOTTA	CCAATCACAC	OGAGTACCAC
	OCCTOCCTCC	AGCTOGATAA	TCCCACTCAC	ATGAACAATG	GOGACTACAC	TCTAATAGCC
	ANGANTOAGT	ATCCCAACCA	TOAGAAACAG	ATTICTOCTC	ACTTCATOOG	CTGGCCTGGA
	GCGAATGACA	TORGODACAC	CACCAACACA	ACTAATGAAA	TCCCTTCCAC	AGACCITCACT
32	GATAAAACCG	GTCGGGAACA	TCTCTCOOTC	TATGCTOTOG	TOOTGATTOC	prenorong
	GGATTTTGCC	TTTTGGTAAT	generatera	CTTANOTTO	CAAGACACTC	CANGTITIOGC
	ATGAMAGGCC	CAGCCTCCGT	TATCAGCAAT	GATGATGACT	CTGCCAOCCC	ACTCCATCAC
	GGAATGACCA	AGATOCCTOT	CATTGAAAT	CCCCAGTACT	TTOOCATCAC	CACAGTOAG
9	CTCAAGCCAG	ACACATTTOT	TCAGCACATC		ACATTOTTCT	
	CTAGGCGAAG	CAGCCTTTOO	AMMOTOTIC		DCTATAACCT	
	CAGGACAAGA	TCTTOGTGGC	AGTGAAGACC	CTOMOGRIG	CCAGTGACAA	TGCAGGCAAG
	GACTICCACC	GTGAGGCCGA	GCTCCTGACC	AACCTCCAGC	ATOACCACAT	COTCAMENTO
45	TATOGOGICA	OCCITOCAGO	COACCCCTC	ATCATOORCE	TTGAGTACAT	TO COOC AC
?	COCCOCCOCCO	MCTGAGGA	GTCGCAGATG	CTGCATATAG	CCCIOCAGAI	200000000000000000000000000000000000000
	ATGGTCTACC	TGGCGTCCCA	GCACTTCOTO	CACCOCCIATT	TOGGGACCAG	оллетоссто
	GTCGGGGAGA	ACTTOCTOGT	GAMATCOOG	GACTITOGGA	TOTCCCGGGA	COTOTACAGC
9	ACTUACTACT	ACAGGGGGGG	TGGCGGGG	ATOCIOCES	TOTACHOON	CCTC CASA
3	TOGGRGATT	TCACCTATOO	CAAACAGCCC	TOTTACCAGC	TOTCAACA	TGAGGTGATA
	GAGTOTATCA	CTCAGGGCCG	AGTOCTOCAG	CGACCCCGCA	COTOCCCCA	GOAGOTOTAT
	GAGCTGATGC		асласалала	CCCCACATGA	GGAAGAACAT	CAGOGCATC
55	GATACCCTCC	TTCAGACTT	GGCCAAGGCA	TCTCCGGTCT	ACCTOGACAT	AGAGGATGAA
;	CATCTTTAA		AGGCCACCAA	OCTOCACAC	TTCACTCTOA	CAGTATTAAC
	ATCAAAGACT	CCGAGAAGCT	CTCGAGGGAA	GCAGTGTGTA	CITCHICATC	CATAGACACA
	GTATTGACTI	CTTTTCCCA	TIATCICITY	CTCTCTTTCC	ATCTCCCTTO	OTTOTTCCTT
9	ACCUMENT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACTCTGCAT	AGACAAAGC
:	CTTAACAAAC	GTAATTTOTT	ATATCAGCAG	ACACTCCAGT	TTGCCCACCA	CACTACCA
	TGCCTTOTTG	TATTECTOCC	TITIONIOTOG	ATGAMAMA	DOGANAACAA	ATATTTCACT
	TTATTATT	The Country of	TATACACA	CONTROLL OF	ACCOUNTS	TABABAGAA
જ	AACTTOTOTT	CANTCTOTON	AGCCTTTATC	TATOGGGGT	TAAAACCAGA	GAGAAAGAG
	ATTTATTA	AACCOCAATA	TOGGAGGAAC	AAAGACAACC	ACTODOATON	<b>ACTION OF THE P</b>
	CCTGAGGACT	ADGAMATACT TTTCTCAGGA	CAGCAACTOT	TACTOGCCTC	TOTOCCATOO	ATCATTCTT
5	TCCCATCACC		OCOTOCAGTA	GAGAGCANAG	ATGGCTT	

a equence	
£	5
Prote	4
398	To lead to
ē	
	-
Ÿ	ŝ

S		a_	<b>11</b>	Ħ-	<b>4</b> _	<b>15</b> —	
	MSSWIRWHOD	MESHIRHIGP ANARLMOFON LUNGFNRAAF ACPTSCKCSA	LVVOFWRAAP	ACPTSCKCSA	SRINCEDPEP GIVAPPRLEP	GIVAPPRLEP	
	NEVDPENITE	IPIANOXRLE		I INEDDVEAY VOLANLTIVD	BOLKPVAHKA	PLANSWLQH1	
	RPTRNKLIBL	SPIRNKLISL SREMPRALDL SELILVONPP TCSCDIMMIK	BELILVONPP	TCBCDIMMIK	TLOBAKSSPO TODLYCLASS	TODLYCLABB	
9	BYNIPLANTO		LAAPHLTVEB	IPROGLESAN LAAPKLIVES GKEITLSCSV AGDPVPRRYN DVGKLVSKIR	AGDEVERNIN	DVGULVBKHM	
⊇	NETGIITOGBL	ietentocal ritniseddb choiscvara Lycedodbyn Ltvnpaptit pleeptedhh	GKOISCVAEN	LVGEDQDSVN	LTVHPAPTIT	FLREPTSDAW	
	MCIPPTVKGN	PRPALOMPYN	CALLESKYI	PRPALOMPYN GALLHESKYI CTRIHVTRHT	BYRGCLOLDN PTHMMRGDYT	PTHORNGOYT	
	LIAKNEYGKD		MPGIDDGAMP	EKCIBAHPMO MPGIDDGANP NYPDVIYEDY GTAANDIGDT THRENEIPBT	<b>STANDIGDT</b>	THRENEIPBT	
	DVTDKTGREH		BUVOPCLLVM	LEVYAVIVIA SVIDPCLEVM LFLLRLARHS KPOMKOPASV	KINCHICOPASY	ISHDDOGASP	
,	LAH I SNOSNT	PESSECGPDA	PRSEEGGEDA VIIGMERIPY	IEMPOYPOIT !	NEGLKPDTFV	NBOLKPOTFV ORIKRANIVL	
2	KRELGEGAPO	KVFLARCYNL	CPEODKILVA	KVFLARCYNI. CPEDDKILVA VKTLKDABDN ARKDFHREAB LLTVILOKKHI	ARKOPHREAB	LLTWLOHERI	
	VXPYGVCVEG	DPLIMVPBYM	RHODLAKPLA	DPLINVPBYM KHIDLAKPLR ANGPOAVLMA	ECHPPTELTO SQNLHIAQQI	BONLHIAGOI	
	AAGWYTASO	AAGMYYLASQ HPVHXDLATR MCLVQENLLV KIGDPGMSRD VYSTOYTRVG GHTMLPIRWH	NCLVGENLLV	KIGDPGMSRD	VYSTOYTRVO	CHTHEPIRW	

FILAFLGNIG A LALESTLGAT R LALEVATAMY G TBYPTRRYYP K

MANAGLQLLO P Q1QCKVPDEL LI 1QANIFLLAG L LLCCSCPRKT T

Beq ID NO. 593 Protein sequence Protein Accession B: AAD16433.1

PCT/US02/12476

WO 02/086443
PPESIWRKP THEOWISLO VUMBIPTIO KOPYOLENN EVIECTIOGR VLORPRICEO
EVYELALICH GREPHRENT KOTHTLLOPL NASPVTLDI LO 6eq 1D NO. 596 DNA sequence Nucleic Acid Accession 8: AF410899 Coding sequence: 483..2999 . 55 જ ଞ

Beq ID NO: 597 Protein sequenc Protein Accession #: AAL67965.1 

	9	120	180	240
. 15-	<b>GIVAPPRLEP</b>	PLKNSPLOHI	TODLYCLINES	DVGNLVBROIM
₹	BRINCEDPEP	SOLKPVAHKA	K TLOBAKSBPD TODLYCLNES	ACCOPYPROMYN
<b>11</b> –	A LUNGPHRARY ACPTSCKCSA BRINCSDPSP GIVAPPRLI	INEDOVEAY VOLRNLTIVD SOLKPVAHKA PLKNSNLOH	TCBCUIMMI	OKSITLSCSV
<b>#</b> _	LUVOPHRAAP	1 INEDOVEAY	SELILVONPP.	PNCGLPBAH LAAPHLTVEE G
<b>s</b> _	NARLINGFO	IFIANOKRLE	GRICHFRALDL	
-	MASWIRWHOP	NSVDPENITE	NPTRNKLTBL	BRNIPLANIO 1
	;	3		

	WO 02/0 NETSHTOGSL WCIPTTYKON LIAKNEYGO	186443 Rithibodos Pedalgmpyn Ergigaaipmg	GKQI SCVARN GAILAIBEKYI WPGIDDDAARP	LVGEDQDBVN CTKIHVTHHT NYPDVIYEDY	LTVBPAPTIT EYHCCLQLON GTAANDIGDT	PLESPT SONH TYCONOMIPS TYRENE IPST
<b>v</b>	OVIDKIGKEH VGFASVISKD KPDTFVQHIK FHREAELLIY PTELTQSQML	LGVTAVVVIA DOBASPLAHI RHNIVLICKEL LGHENIVKFY HIAQOIAACH	SYVOPCLLYN SYGSNTPBS8 GEGAPGKYFL GYCYEGDPLI VYLASGHPYN	LFLLKLARHS ECOPDAVI IO AECYNICPEO AVPEYNONOD RDLATRINCLV	KTGHCDPSNP MTKIPVIEND DKILVAVKTU LMKFLANGD GENLLVKIGD	
10	DYYRVOGHTM	LPIRMMPPES PRTCPQEVYE	IMPREPTTES LALOCACREP	DVNSLGVVLM EMRKOJ KOTH	BI FTYGKOPY TLLGNLAKAS	Yolshing to Pvylding
7	Seq ID NO: Nucleic Aci Coding sequ	NO: 598 DRA ser Acid Accession sequence: 748	sequence on #: AB052906 .814	90		
2	-1-	11 -	11	:- I	41	51 -
20	CTCTGGGTCC GCTCCTGCTG	TTAATOGCAG TCCGGCTGGT ATCCCTAAGT	COGGGGCGGG CCCGGGCTGG TCAGACCTGG	TACCAAGATC OCCAGCCGAC ACCACGGTGG	CCTCACTCTC CCTCACTCTCTC TGTGCGGTTC	TCCCGCTTCT TTTGCTATGA AAGGCCAGGT
25	GGATGAAAAG CCTGGGGAAG GGTGGTGGAC GGAACCCCTC	ACCTGCAGG	ACTATORACTO TCACAACTOCO ACCAACTOCO CCAGGATGTC	TOGCARCAGO CTOGARAGOA TOACATTCAG TTOTGRAGOA	ACAGTERCAC CAGAACCCAG CTGGAGAATT AAAGCTGAAG	
ç	MATOTOGOCA GOTTOTOGOC COTTOTOGOC	CAGTTCAGTT ACGGTTCATC ATGTCCTTCC GGCATGGACA	CTGGAGCCAG CTGGAGCCAG ATTACTTCTC GCACCCTGGA		CTCTTTBACT GAAAAGTGGG TGTATAGGAT GGAGCACCAC	CAGAGAAGA AGAATGACA GGCTTGAGGA TCGCCATGTC
ર	CATCCTCCC CATCCTCCCC AAGCTGATAC	ACCCAACTCA TGCTTCATCC CAAAAGGCTC	GOGCCACAGC TCCCTGGCAT CTGTGAGCAC	CTCACCACCTC CTCACCACACAC OOTCTTCATC	ATCCTTTGCT TCCTTTAGAG AAACTCGCCC	TOACAGGTTA TOACAGGTTA TTCTOTCTO
32	TACCTACAT	AGCTCATTCA ATTATGCAAT CTAAACAAGA	CTGCCTTGAT TTTCTCTTGG TATATCATTT	TCCTTTTGCC TGCTACCTGA TCTTTCTTCT	ACATTTA TOOMTTCCT CTTTTOTTT	CCACCAGTTA
40	TAGACTICAG ATAGAAAAA TTAAATAAA	ACCTCTGGGG AFTTATATTA GAGTTCTATT	AFFCFFFCCO AFFCFFFCCO AFGAFFGFFF FCCCAAAAA	TOTCCTUAN CCTTTAGTAA AAAAAAAAA	TITATIOTIC AA	ALATTATTA TOTACTOATA
	Beq 1D NO: Protein Acc	O: 599 Protei Accession #: E	iin sequence BAB61048.1			
50	AAAAATKIL FLHYDCGHKT LQARMSCBOK SPHYPSMGDC	11 	21   GWERAGRADP LAVITAWKAQ FBFDOQIFLL WOSTLEPSAG	31 	41 	S1 AVOQQVDEKT ENTTPKEPLT KMENDKVVAM LCCLLIILPC
\$\$	Seg ID NO. Nucleic Act	NO: 600 DNA mequence Acid Accemion #: NM_ mequence: 57482	squence 1 #: MM_001 182	001698.1		
9	1   	11    -  - 	. 88	31   CTTTOTOCTC TGGCCACCT	41   TGCTCTGAG AGCTGTGGCC	s1    - 
. <b>.</b> 8	ACCCCANGA ACTACTACA ACTACTCTT ACACCTOTGC TCTACOANGT	GGAGGATAGG GCGTGCCCTT ACGTCCGCTG CGACGTAGAG CTTCCATGAA TCCCTGGAGG	ATATCCCOG CACTTOCCO COCOTACTA OTOOCCCCA CACCAGAAC AACAGAAGOT	TCAGCATETA TCAGCCAGTA GAGCCAGGCA CCATATOTAC TGCAGAAGAA	TAACAAGGC ACAGACCGTT CAAGTCCCAG ACAGTTGTGC ACAGTTGTGC	CTCAATOATG ACCAAAGATG GGGGGGTGA CCCAACTTGG TCTTTGGAGA CAAGAATCCT
70	AGGGATCTGT CCACCCCTGG GACAGACAGA CTTCCTTCTT AAACAGTAGC	ACTOSTOCCAT ACTOSTOCCA GAAGCTGCA OCTTCTAATA ATCGCC	TCGCACCCTGC GCACCCTTTT GCCCTGGTAC	CACCACCOAC GOGAGGCCTC GTTGCTCAGC ATGGTACACA	TCCCACCCC CCCATGTGCC AGGGGCTCT CCCCCCCACC	TOTAGTOCTC TOCOCCAGA OCCCTCCCTC TCCTGCAATT
75	Seq ID NO: Protein Act	601 Protes	Protein sequence in #: NP_001889.1			
08	1   	11 	21   WEPKEEDR11 VNYPFDVRVG 8	NI   PGOLYNADL# RIICTKSQP#	41   DENVORALHF LOTCAPHEGS	51     AISEYMATK   BLOKKQLCSF
\$	Seq ID NO: Nucleic Acid Coding sequent	602 DNA sequence id Accession #: NM tence: 299.961		003976.2		
1		=-	<b>4</b> –	<b>=</b>	<b>5</b> _	<b>5</b> -

9 2

2

13

GONDATION CONTRACTOR CONTRACTOR ON CONTRACTOR ON CONTRACTOR CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR ON CONTRACTOR O

20

421

		TCCCCAAOCC OCCTOCCCTO	cccacaaca accacaaca	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACACGACCTC CCGGCCCGTC CGTCAACAGC	CTGAOGGCTC GACCCTCCCO GAGAGGCCCC	TAGCAGCCC TATGAAGCCC GACCCCTCCT	TOGGCTOTAC		<b>:</b>	BSVAEABLOS	CRIMARSPHOL		22	TCTCCACGCT	AGCCTGCCCT CCCTGGCCTC	000000000000000000000000000000000000000	COCOGGGGTTO	CCCGGCCCT	acta A DOGCT	TOABAGGCC	CIATURANCE BOACCECTIC AGGACAGEA CTGCCCTOTA		<b>5</b> ~	baprspapre Graaraggpo Lelabligag		S1   TOCAGGGTTG	OCTOCHOATC CCTOCHOATC AGCCCTCATC	CANCOGCTC GTTGCAGATC CGGCAACCAC GCTCAATCTG
	<b>#</b>	AGOTECTTCC TCTCCGCGCA	CAGAGGCCTC TCCTGGCGTC GAGCCCGGCG	CAGCACTTCC CAGCAGGGCACCO	COCCOOCTCTCC CCCCOOOCTC CCTTCATOGA	TCCTGCCTGC TCCTGCCTGC CCTCAAAGCT	OACAACTGAC AGACCTCAGC TCGAACCTGG	OTOCTOOMC		<b>;</b>	HPTLAALALL Obgodabbod	LVRPRPCEGS TWRTVDRLSA		<b>\$</b> -	CTTOGAGGC	SCACAGOCTOC SCACAGOCCO STCCTOCCOCTO	AGAGCCCGGC	desabadada eradacesec	COCCODOCT	GOCTOCCTOD TTCCTOCCTO	GCCCCAAAGC	CAGGCCTOT TOTOCTGGAA		₹_	LBBVAEABLG PAPPBALPRG SCRRARBPHD ATACOCLG		41   	ACCCCATANG ACCCCATANG TCAATATCTC	CTGGGGCCTT AGGTTCTGCC GTACCAGCT TGCAGTTGCA GACTCACGAA
	<b>a</b> _	CCCCTCCTTC	AGCAGCOTCO CCCCCOCCTO TOCAGTGGAA	OCACCCCAT COCOCTCOGO OCOCTCOGCC		ACCACCTGCO COOTOGCTCT GOOACGAAGO	AAGACACCAG TGGCCAGGCC	annattace -		<b>1</b> -	PLGL8AQPAL	ALGLGHREDE EAVEPIOVNS	090.1	<b>1</b> .	COARCTTOCA	AND CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESSION CONCESS	TOCACCCCCA	COCOCTCO	CTGCGGCGG	CACCICCTOC	ACAGGTGAAG	AMMINICACION CTOSCCAGGC AGCCCCCGCC TQAMAGTGCC		<b>1</b> -	Laptlaalal Poperpapp Elvrfrpcso Stnrtvdrle	edneuce	31    -   	TOCTCCA000 CTGCCCTGGA TCCCCOTTCC	OSCATEACSC AACAAGCTGC CTTCTGTCCA CTCAAGGAGC CACCTGGTAG
. •	<b>a</b> -	CCCTGAGGCAG	OGCTCTGCTG CCGCGAAGGC OGCCCGCTGG	cccaccacca cccaaacaac accaaracac		GCTCTCCGCC GGACCCTTAC GCCTCAGCCA	CCCAGCTAA ACTCTGGGAC	TTGCTTGGTT	in sequence 19_476501.1	- 11	i Higalfipea Hibototasa	RLRSQLVPVR GOPCCRPTRY	quence 1 &: KM_057090.1	. ส.	TGATAGAGAT	TOCTCTOCT CCCGCGAAGG	COCCOCCOC	acccaaacha Taccaataca	9CA9CGGCTC	ACCTCTCCCC TOTALCCTTA	OCCTCACC TCATCCCCCAA	ACTICAGES CTGAGGESTE GTTGCTTGGT CC	Protein sequence on #: NP_476431.1	<b>#</b> -	APLGLØAGPA NCSGRARRPP RALGLØHRSD YEAVSPYDVN		21   CCTTTTGCT0	CCAOTOTACC GCCCACCCT ACTCAATGAG	TANGETOTOS CCTCGCCNC TANGETCTC TANGETCTC TANGETTCGNC
086443 ,	<b>:</b> -	TOTATOTO	TOGCCOCTCT GCCCTGCCCC GGGAACGCAC	GOCCCOCOCC GOOCTGOOOD COCAGCTGOT	TCCGCTTCTG GCTACTGGG GCTGCCGACC	CCOTOGACCO TTTOCAGACT CTAGCCAGCG	CCCTGCGGATAT CCCTGCGGAT CTTCTCACAG	CATATTOCAG	Seg ID NO: 607 Protein Protein Accession #: NP	11-	PLLEVLPPOA PDDVI.ASPAG	RARAAGARGC LRPPPGGRPV	8ag ID NO: 608 DNA sequence Nucleic Acid Accession #: NP Coding sequence: 29715	=-	стестоотот	CCCTGGCCTA CTGGCCGCTC AGCCCTGCCC	COCCCOCCO	COOCTOOO	AGCCTACTOG	ACCOTOGACC	ACTAGCCAGC	ACTICTORCA ACTICTORCA ACTIVORA ACATATTOCA GOAGCTOGOCC	609 Protes	=-	Lencenprrq GHLPGGRTAR CRLRSQLVPV VBQPCCRLPTR	Seg ID NO: 610 DNA sequence Nucleic Acid Accession #: Ex Coding sequence: 11746	11   AGCATTATCT	DCTGCCCTAG TTGTGGCGGT ACATCACTGA	TTUAGAAGAA GCTATCTCAG TQUCAGCCT ACTTCTCCCA
WO 02/086443 Coding sequence: 1		ATGCCCCCC	TOGCCCACCC GCGCCCCGCA CACCTGCCGG	CAGCCTTCTC CGCGCGGGCGC CGCCTGCGCT		ACCTGGAGAA GCTCCAGGGC CAGAGTCCCA	TACCOGTGGG AGAGCCCTCA TTCGGACCCA	TTGAAGGACA TCACTCATGG	Seg ID NO: Protein Acc	<b>-</b>	MPGLISARGO	RAARAGGPGS BLASLLGAGA	Seq ID NO: Nucleic Act		CTGATGGGCG	OTOGOCCACO OTOGOCCACO COCOCCOCO	CCACCTOCCO		CAGCCTGGC			CTTCOGACCC TCTCATGAAC TTTGAAGGAC CTCACTCATG	Seg ID NO: 609 Pr Protein Accession		Melgiggist Gppp/laspa Braraagarg Alrpppgerp	Beg ID NO: Nucleic Act Coding sequ	1   ATGCCACTGA	OCCTACCATO OGGOCACGCA CTCAACACGC	GCCTGAGGA GGCTCGCTGC TTCCAGGGCC CAGCGGGCC CTGGAATACA
		Ś	5	2	15		70	25	3	30	3	. %	3	9		45	!	Ş	3	;	S	9	ý	3.	70	75	6		88
						•																							

8 2 8 18 8

11 11 21 21 41 51
HECHORAR PRIMERLAND ALLOSVALM GARRERD EXPERTAS
SAGIRGOGIA RANCESTARR PROPERSER PERFERAN FROMENION POSINANA,
ROCINERAL PRIMERLANGE POSITIVAREN FORGERRAMS FIDILISASILO AGAIRPPERG
REVERECCEP TRYRANSFRO INSTRITURE LARKAGGIO

Seq ID NO: 603 Protein sequence Protein Accession N: NP\_003967.3

25

30

Beg ID NO: 604 DNA sequence Nucleic Acid Accession B: NM\_057091.1 Coding sequence: 783..1445

35

ACTOGCCCCT (

\$

S

55

8

65

2

6

THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO

O PLAFTLANI LILGGVARIA (ZGARREPA ESSPEVIAS I PEPUGERRA PEPUGERA EGGARANGO POSELACAGA I PEPUGERRA ESGGRANGE PUGELAGILO AGALREPEDG VISTNETVER LGATNOCLO

LEHCPMPRRQ PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRARR PARMCEGRAR PARMCEGRAR PARMCEGRARR PARMCEGRAR PA

MELGLGGLST L PACKLROCKT A ROCKLROCKP P RPV8QPCCRP T

8

Seq ID NO: 605 Protein sequence Protein Accession #: NP 003967.1

73

Seq ID NO: 606 DNA sequence Nucleic Acid Accession #: NM\_057160.1

WO 02/086443
sorotholon atoucoura matarathe atotat
Beg ID NO: 611 Protein sequence
Protein Accession 8: sass4587.1

PCT/US02/12476

PCT/US02/12																
	600 720 720 960 960 960 960	1260	12000	1240	1920 1980 2040 2160 2160	2460	2580 2700 2700	2820 2880 2940 3000	3120 3120 3160 3160 3160	3540 3540 3660 3660	33840 33840 33900 4020	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 6 2 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 4 8 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0 4 6 0	5100 5100 5160 5160	5280 5140 5460 5460 5520	5580 5640 5700 5760
		CAACGGGCTA CGGGAATGTC CAGACAGCTC GAACAACCAG GAACAACCAG	CANTOCCIOA TOTCCCTOAO TOACACCACA		AGAAGCAGGT AAAGCCCTGG AATCCTCCCC CTGTAGACTC GCCCCTCTGG	AACCOTCAAT CAOTTCCTGG GGAAGAAACA		TTTTCCCAGA GCCAGGACGG AATATGTGGG GGAGACCCTG GACTGCAGAG	COCAGOCCC TICATICITIC MATUTACO AGCIGOCACO OTCACACIOO	TCTSSCTTC GTGTGTGCTT ACGTCTSCCC CCCSATCCSC CCAATCCCSA	TACCACCANT TCCAGGGCCA TCCAGGGGCCA ATCTAGGAG	GGAAGTGAGC GOTGCCACA AGACCTGTG GCCAGGGCT AGACCCTTA AGACGCCTTA AGACGACCT GTAGGGGCC GAAGCCATTG GTGAGGAGC	TCAATTCTCA GTTCAGTTTT CTGGGAGTTA GTGCTTACTG GCACCCTGC	AGCTCATGGC GTTGCTCTCC TGTAACCACA TCATGGGAAT TTCTACTTAG	TATTGGGAM COGGACCCM CAMGATTCA AGTGGCCTTG COGGGGAMA	MOCCOCTGC CTGCMATCA GTAGAGTGTG TMATCCATTT
	MOCACETORS TOSCICETE SACTOCICETE ACACCOCAT TRACTICETE ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACTOCOCAT ACT ACTOCOCAT ACTOCOCAT ACT ACT ACT ACT ACT ACT ACT ACT ACT	ACATOTOTA ACATOTOTA ACATOTOTA ACTOTOTA ACTOTOTA	TCAGCCAGE CAAGCGTCCA CCAGTTACCC ACTACACTGA	CCCTGGCTGC AGATGAAGGC GACTGGAGGA COTGATTGCT	TCTCCOSTAG GGCCATGGCA TCTTCCTCCA CTCCGGGCCT CGCTGAGATA	TTCTGCTCCT GTTTCTTAAG TCATGCGCT ATCTGGAAAA	TTTGGACTTC TGCCTGGGG TGAAGTGTAC ACTGAACATA	CATCCTGGGC CCCCCATGA GGTGGAGGAG TATTATATCT GAAGCATCCT	TOCOGCICAT OTTITIANA ATTICANACO CATCACAGTIC ACACCGATOS TRAGONOTTO	ACCTGCCTTC TCATGGCAAC TCAGGTCTCC CACGACCCAAT	TCTGGAATC TGTGACATCC ACAAAAGTG TGTCCCAGGG GGTCTCCAAG	AGAGCCACA TIGCTOTOCCT GITTIOCCCAC GCACAMTIO ATCTTAACCC CTCCACCAG TAGGTGAGGG GTGGTGAGGG GTGGTGAGGG ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC ATCTTAACCC A	ATGCATTTGC GGGGTGCAGA GGAGTGGGAG TTTTAAAAA CTAGCCCTCA	TTTGTACAAG CCATTCCCT TCAAAGCTT TTTGTCCTC GATACAAGAG	AGAGATAACT ATAAACCACT GGAAGCCAGC	TCAGGGTTT TCAGGGTTTT ATGCGGCTTTA
•	AGGGGTCTTCC BATATCCCCA AACCAGATTG TACCTGTCCA CTCAACCGTC CCCATGCCA AATGTCTTCA	TTCATCTCCC AACOCACTGC TCCCTGGAGA CTCATGGCCA CTCATGGCCA	CCTOTOGRAPO OTTOCTOTTC CCAGACACA CCTOTOGRAPO	CTOCCTGATGC OTCCTGATGC GONATGATGC GONATGATCC	CTTGCCTGAT TCGAGAGGGC TCGAGAGGGC CCCAGGCCC AATAGTTCTC	CCCCTTGATT CATTTAACTG AGAAGGAAAA TGTGATTTTT	CATGTAGAAT AGAAATCTGG TTGAAGCATG ATTTTCACAA	ANATATCCCC CTOGGACCTG CCTOGCCAGG CACGAGATTT	GCAACTTOTC GCCTGTATCT AGATCCTTA TCTCCATCAA ACACGGCGGT TGTGGTCTGG	TCACACGAAT GAAGTTAGGC ATGGAGAATT TCTGGAAATC TGTGCTTTGG	ACAGAGAC ACAGAGAC CAGTTCCTGC TTTCACCCTC	AMGGCTTGCC CATGOTGGCC GGAGCCTGCA TTGTGCATAC GGCCCTGCT GGAGCCTCCT AGGAGCACC TCCCATCACA TCCCATCACA TCCCATCACA	CAACAGGATG AAGCTGGAGT ACGCCCATCT AGAACCACTA GATTCTCTCT TGGGGTACAG	CTCTTCUAC GAAATGGAAG ACCATATAGA AATAGAATAGA	TTCAANTGCT GCAGACAGCT GCTTTTAGGC TGCGTTGTTG GGTGGGCTGG	MAGAGAAT TTGCTAGGCC TTGTAGGCC CTTGTGGTGG
	CATCTCACCC CAGGACACCC CCAGGACACCC CCAGGACACCC CCAGGACCCCAG CCAGGACCCCAG CCTACCCCAG AATCTACCCGAC TCTACCCCACC	TCAGATCACC CCTCCACACC CCTCCACACC COTCAATGGC	GOACACTOTA CAATGTCAAC ACCATGGTAC GCTAACCAGC	CATTGTCGCC GAGCCAAGCT GCAGGGCTGG CTGGGTCCAT	CTCTTCCTGA TCAGGAAGAT TCAGGCTTCCT CTTCCCTGCG ACTTCGTGGGGA	TOWAGTTCT GACTTCAAC TATGAAGAG GTGTCTCACT	GGAATGAAAT GGATAGAGAA AAATTTTAA GGCTTGGTGG	ADDACTTAC GCAAGGCCC GTGGCCTGAA GTGGCCTGAA	TCCCTGCCA GACCTGATA CTCAGAGATG GTGGTAAAAT ACAGCAGGCG TCCTCCTGCG	COAGTCACAO TOGGGCTCAA TTACAGTGAA TCCACGGGGA ACAAGACACC	GCTCCACAAG TCCCCGCTCC TTTTCCCTTC CTTTGTAGCT	ATCACCOCT CCTCCAACA CCTCCAACA CCAATOTCT TCACCOTO ATCACTTOGA ACACCACCC TCTTCCTTTCC	OTCTCCTTTC OTCCCCAA TOACAGTCCC AAAGCCAATT ACTGGACGTG	TTTTATTAT TAMACCAMG CTCACTTOOT TCCCTTAMG CTTCCTCCTT		TAGATCATOT TAGATCATOT ATTTACAGAT OOGGOTCTOT
. 086443	DCCTCACCCA TOTATORAN AGANACTOC ACCACACCT TCTCATOCA TCTCATOCA TCTCATOCA	TTAGCCGCAA GCGAGCTGTC TGGCCAACCT TCTTGGCCAA	CCTGGAGGT OOTTAGGGAC TCATTATCAT ACCCAGAAAC CTACCACTGA		GTOTGCTACA CTTCCTACAA TTCATACCCC CAAGAACAGC CAGCCTGCTC	TCCCTCAAA CCTCAAAAAA TTGGGATCC GCCTCATCA		ACCCAGACCC OCTTCTGAAG GTCAGCCTGT ATGGAGACT	CCACACCCTC GCCTACTATO AGTCACATT ATCTCACTT TCCTGGAGC	TTCTCCTCCT CATATTCACA CTGGCCCAGT TTCAGCTGAC TCCCCGCTCC	TTAGCTCCCC TCTTATTAGC TGCTGACCAG CACTAGTGCA CGTCAGAGTC	GCACCTGGAG GCACATGAGC GCCCGTACC GGAAACCTCA GCACACCACA GCCTCAGAT ACCTCTGGAG TTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCGGG CTTCAGCCGG CTTCAGCCGGG CTTCAGGGGG CTTCAGGGGG CTTCAGGGGG CTTCAGGGGG CTTCAGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGG CTTCAGGGGGGG CTTCAGGGGGGG CTTCAGGGGGGGGGG			ACTCAGGAAG CAGATOTTAG CCCACAGTCA CCCACAGTCA CATGGCTGTCA	CCCAGOTTTC CCTTCAAAGC TTGGCGATGC GGCAGGGTTG
WO 02/086443	GOCAGAATA GTCTCCGGC GTTAACCTGC TTCCACACA CCACCCAGCA CCACCCAGCA CTGAAGCAGC TATGACAACC	OTCCTOATTC ACGCACCTTC TTCCGCATOT CCAGGGAATA CTGCAGAAACT	AACCAGCTA GGCCAGTCCC GTGCCTAGTT TCCGTCTCCTT		CTAGATAAAG COTGCCGGAC GGATTCCGA ACCTGTCCTC ACTTAGTCCA	ACCCAGCATG TGAGTTCTCT CAGCCTGGTT AGACAGAAGA		CAGCATCTAG GOAGATGGGG TCCCCCACA TOTCGACAGG	CTCCCTCCA TCCCCTCCA ACTTAGGGA GAATCTAGG TGAACTTCAGG	TCCAGGOTTA CTGCTATACA CTCTGGACAA AGGAAAGAAC TCTTATTAGC	TCGGCTCTTA CCCGATCGGC CAGGAGCACG TGTTTGCAAA AGATGAGGCC	ACTATTOGTO CCAGACCATO GCGGCATCCC GCGGCATCCCTG GATGCTCCTG GATATTCCTG GATATTCCTG CCTTATTGTA GCCTCTTTT	TACTACANAN COOCTGCAAT CCTCTCTOTT OTOTTOGACA TOCACACATA OCTACACATA	GOTGTTCAAT TTAGTCTTGG TTAGTCTTGG GOAAAAATA TGGGCTGTAT	AACTTTCAA GAACTTCCAA AGTTOGTCGA GCCCCCAGAT GGAAGGAAGC	CTCCTTCOSC CTTCATGCTO OCCCCACTOC AGCCCTGGTG
	~	10	15	50 .	25	30	35		45	20	55	8 8	8	75	80	82

^		#-	#-	· Ä-		18-	
0	MPLICHYLLLL LATHITELMB PQCLDSLESL GKNSLTHISP PHANNINLORL	UOCQANGAGE BPTLATBALT LLESNQLLQT RVPQHLGNLQT	AYHOCPSECT ALRIBENELS QPAHFSQCSN VLRLYENRLT PPSIPHOLDO		 Gripylsian Gripylsian Ley Ipdoap Uniqelalqo	LPMNAMBLQI NKLQVLPIGL HLVGLTTGATL NQIGLLSPGL	250000000000000000000000000000000000000
ς.	YDAHI BSLPD PRALANLONI YDAPARCOSD VPSYPETPAY IAAIVIGIVA	NYFSNLRQLO BLONNRLRQL ILPLRNWLLL POTPBYPDTT LACSLAACVG	VLILSRNGIS PONIFANVAG MQPRIGIDIV SV6STTELIS CCCCKKR8QA	PISPGAPHOL LAAIOLOHNO PVCPSPAIVR PVEDYTOLIT	TELRELGILHT LENLPLOITO GOSLI I INVN IQYTODRSVW C	NALGDLDGNV HLGKLCELKL VAVPØVNVPR GMTQAGSGLA	2555
20	Seq ID NO: Fucleic Ac: Coding seq	NO: 612 DNA seq Acid Accession ( sequence: 1447	equence n #: XM_098151 47	151			
		<b>#</b> _		a_	<b>=</b> _	25	;
3 8	ATGATGGATT AGTGGGGTAC TCTTGGAGTGG CAATTTTAA TCTCTAGCCC AACTTTGTAC AACTTTGTAC AACTTTGTAC	AGAGTICANT ANATICANT TOACACCC TOACACCCC TOACACCCC ANAMACTICAT ANAMACTICAT CCTOTTACTC	TOAGGGCTOO TTCCTCCT TCAGTGTOO CTGTGCAGA GCTGGTAGGA GCCTTAG	MIGAGECOG GITTACAGET MANAGETTECOT MINAGETTECOT MINAGETTECOT	CTGGTCCCC CCTGACAGT ACAMAGCA ACACTGGAC TACCCACTTG GAGTTTATT	AGAMAGETOG CCCCAGGCCA ATTAGAACCA GTGGÄTTCTC TGATGGGGTA TATCTCTTCA AAGGAAATGG	4 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
~	Bed ID NO: Protein Ac	613 Protes	in sequence XP_098151				
6	1 	11 	21   GUOSSVFLS SLALSTPAVG KPPPCCSP	31   VYBBLTVPRP VPPLPTCDGV	41  - SGVGAGSQCH QRHLLIPCAVP	si     Rrynkgolep   Nrlavlf188	120
\$	Seq ID NO: Mucleic Ac: Coding sequ	No: 614 DNA seq : Acid Accession sequence: 7713	Pence Parker 72	002658.1		•	
		<b>:</b> -	<b>:</b> -	<b></b>	<b>;</b> _	<b>3</b> _	
8	GCCCGCCTC CCCCGACCTC GAGCGACTCC	COCCOTCOCO GCCACCATGA AAAGGCAGCA	CCCTCCTGCC GAGCCCTGCT ATGAACTTCA	OCAGOCCACC OOCGCCCCTG TCAAGTTCCA	CTTCTCTGGG TCGAACTGTG	TCCTGOTCTAGOS ACTOTCTAAA	8233
S	GNANTICADA TCACTTTTAC CTCGGGGAAA GCAGGTGGGCAA		CTCAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTOTCCAAGA		ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCG		25555
9	AAAGCCTCC CCGCTTTAAG CATCTACAGG CCCTTOCTGC CATCGTCTAC	ATTATTOOOG AGGCACCOGG OTGATCAGCG CTGGGTCGCT		ATTTCAGTGT CACCATCGAG CACCTACGTG CACCTACGTG CTCCAACACG	GGCCAAAAA AACCAGCCT TOTGGAGGCA TACCCAAAGA CAAGGGGAGA		66255
S	GOTGGAAAAC CATTOCCTTG ACAGACCATC CACTGGCTTT TOTTOTGAAG	CTCATCCTAC CTGAAGATCC TGCCTGCCCT GGAAAAGAGA CTGATTTCCC	ACAAGAACTA GTTCCAAGA CGATGTATAA ATTCTACCGA ACCGGGAGTG	CAGCGCTGAC GCGCACGTGT CCATCCCCAG CTATCTCTAT TCAGCAGCC	ACCCTTGCTC CCCCACCAT TTTGCACAA CCCCACACCACC	ACCACACGA CCCGGACTAT OCTUTAAAA TGAAAATGA GCTCTGAAGT	1160
2	CTCAGGGCGT CTACCCTGG AGGAGGAAA TCCATCAGGT		OTTCCTCA OTTCCTCA TGAAGGAA ACACCAAGGA CCGCTTTCTT ACTCGGAAGA		ACTITION OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEMENT OF A STATEME	CAATTOTANO TCTCACACTT GAGGITCCCC TAGAGTCATC	20000
75	CACCACCAGG CAGACCCTCT TOTCTTTTTC GGCTCGAAGG				AGGCCTGGGT CATGTTACTG CAGGGCATCT TGTGAGGCC	ACCAGENACT CCTGTGCATO ATGGTTGAGA	1560 1620 1740
. 8	ANTGRAFIANT ANTGRAGGAG ANTGCANGAGG GCTGTGAGTG ANACTGTGTG CTGGGGCCTC		OGANGTOTAN GGGAGCAGAG AATATATATG TAAGAGCTGG CCACACAGAG CCACACAGAG	ACACTAACAA ACACTAACAA TOTOTOTATO TOTOTOTATO TOTOTOTATO TOTOTOTO		OMOCTTAGEC GEOCICTAAT FOTTOTOTOS ATATTECET TAGOTCACTE CTGCAGCATE	11920
~	ACCTOTOACC ATCCCTTCCT ACACTOAATA ATCAATAAAA	AGCACTOTICE TTTAGCCTAG TTTATATTTC TOTIGATTTTT		TTCACATAGA CCTCACTGGG TTTATATTTT	TOCOCTETC TOCOCTEACE TOTALTETA	TTGGCCAGTT ACCACTCCTT AATAMAGTG	2220

HALLARLIL C HCEIDKSKTC Y HCEIDKSKTC Y YCRNEDINRR B GOEFTTIEND P SHRUSSHYDED D PSHYNDED T CAADDOWTD S SHTKEBNGLA L

2

Beq ID NO: 615 Protein sequence Protein Accession #: NP 002649.1

Seq ID NO: 616 DNA sequence Nucleic Acid Accession #: NW\_024422.1 Coding sequence: 207..2907

ន

25

30

13

A MITTALE METALOGUE DE LETTER DE LE LETTER DE LE L'ESTANTE MEDITALE eq ID No: 618 DNA sequence Nucleic Acid Accession #: NM\_004949.1 Coding sequence: 202..1745 КИВНТКЕКИ, ВИМАВИМА Р РОБИДВИЕЛ РРВ
БРИМАТИКИ ОТВЕТИТЕТ 112 ВЕТИКИТИ УОБЕТИТЕТ 112 ВЕТИКИТИ ТИОДУСИТКИ ВЕТИКИТИ ТИОДУСИТКИ ВЕТИКИТИ ИЗГИБИТИКИ В ИТВЕТИТИ ИЗГИБИТИТИ ОТВЕТИТИТИ В ИТВЕТИТИ ОТВЕТИТИТИ В ИТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИТЕТ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИ ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТЕТО ОТВЕТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТЕТО ОТВЕТИТЕТО ОТВЕТИТЕТО ОТВЕТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТИТЕТО ОТВЕТИТЕТО ОТВЕТОТО ОТВЕТИТЕТО ОТВЕТИТЕТО ОТВЕТО 2 S 2 8 25 8 35 <del>\$</del> 65 2 73 8

20

25

8

65

2

73

<del>\$</del>

5

33

SKLDAZKLVO RVHLKBCPTA

ACTONITLATIVE

TLAILIPASD

11 | | NGALCRELLE

HEAARPSOSW

83

120

BKLDAEKLVG RVNLKECPTA TENGEKKKIP VPLEHQTKVL

ACKNYTLAND (

TLAILIPASD A

11 | | NGALCRILLL | PQILEDGSVY

83

NO: 617 Protein sequence

-			•											
11 12 13 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15		120	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	600 600 720 720 840		60 120 180		1180 1240 160 160		120			9 2 2 2 2 3	2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8
VFLERGTKVL YERRGEVOU IN IERROWY SPTLFERHET KTHEOVICKY CNP IGTYPH SAKIVERAET TVERRAET		51    -   CCTGGAGGGA   TGGGAAACAG	CTOGGRAGGG AGOGGGGGGG TCTGGGGGGGG AATGGGGGGG	TOCCCTOCG TOCCCTTC GCCTTTAATT TOGGTOBATA		S1 LANTEGIIFOR GRYCEHDORR SAGGAPELLA		11 		51   CODKIYNPLB NSQCH8SPIB		<b>s</b> –	ATGGGACCCC ACAGCCATTCA ACGCCATTCA ANTOGTATTG GGATATGTAA ATATACCCCA	ACCCTACAGA TACCCOGAGC GATGCTGTGG AATGGTGAGA
TENGEKKIP TPTALITIY TPTELEUTI KYBIIGUND KRBIIGUND KRBIIGUND TRIBIKYE TVIICETNA PROGYTVPI LIGIALECI UGABAGGYOG TIARET		41 	GARAGOTA GARAGOTA GCTTTCGGAG CTGGGCAGCT AGGCGCAGTG	CTACTOTAC CTTGGGCATC GCTGAAGCAC AMAMAAAA		4.1   Vatokerosp BPCVCyarpt DPLASHANGP HRL	_	41 		41   EPMLCQPAPR FVVYLKVQGV		₹_	AGCAGAGACC GOTCCTGCTC TATTGAATCC CCTGCCCCAG TCTAATTGTA	AGGATTCTAT OTTCCATOTA OCAGGACAAG OTGOTGOGTA CATGACCTC
KREPTILLEN PPLLLQOVG IIARATIPOO OPPOLGTIST OYPOLGTIST OYPOLGTIST OYPOLGTIST OYPOLGTIST OYPOLGTIST OYPOLGTIST IRANISTROP GGHTEVDNCH	545.1	31 		GCCCAGCCTO GCCCAGCCTO AAGCCGGGA TTTACCGTAA AGCCCCAAAA		HAGGREEVTK CRNOGTCVLG LOTPORCOPK RR PCGR PGLG	re PGENESH predicted	31 	licted	APAG8 3LTND	7	E -	CAGAGAAGA CCTOGAAGGA CCAAGCTCAC TCGCCCACAA ATGCCACACAG	AGNATORCAC CAACCOGACA CCAACCCCOT CAACCTACCT
TTYT I LLGSE PCSMLENEG UNRECTENE T VOOVCATOK LAK I KVOOPEO CLIVITANIE RESECIEYIK RESECIEYIK RESECIEVIK RESECIEVIK REMELALIO UDPR I COCOV	equence n &: NM_032545.1 718	21 ) AAGAGAAGGA CGGTCAGTTT	ACTGGACCTC AGCCGCTCCC GGAACGGCG GCTACTGCGA CCCTCCTCGC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	In sequence	21 NICHBYCREK GECABARPEC CIPCALACIP BLVPSVIQRE	equence n 6: FGENES 90	21 CATGAGGACC CCTCTTOTOT GGCACCCAGG CATGATOTOCC TCAGGGTCTOC TCAGGGTCTOC	ein sequence FGENESH predicted	21 YVSVCLALLC CTPWPCEALLC CTPWPCEALLC	squence 1 8: M18728 1085	-21	ANDAGOTOGA TTGCATGTCC CCCACCACTG GTTCTTCTAC GAAAGAGTGG CCAAGGGCCCG	AACOTCACCC AATOAAGAAG AOCAACACT GTTCAGAACA
02/086443  PD POILEGARY PD POILEGARY POILEGARY POILOGAR POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY POILEGARY	620 DNA sequence 1d Accession 8: N sence: 46718	TCANTGCACT CTTCTGTTTA	TCACCGCTCA GGGCCGAGG CGCTGCTGCA TTCACCGGCC GGAGCCTGCA	GGGCGGGGG GGCCTCCTG CGGAAGGGG TAATAATA GTAATAATA	Seq ID NO: 621 Protein Protein Accession #: NP	11 	MO: 622 DNA sequence : Acid Accession #: PC sequence: 1390	11 quaretead teratereer terateadee ACATAAGAE AGETAAGATAAGATAAGATAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAAA	O: 623 Prote: Accession 8: 3	11   DYPRBVLAP LBETRQCGP	Beg ID NO: 624 DMA sequence Nucleio Acid Accession 8: N Coding sequence: 511085	=_	CTCCTCTACA TCCCTGCAGA CTGGAAGCCA GGGAAGGA GTACAAAGGC ACAAGCTACC	ACTORATOCAG ACATOTTOTO CTCCATOTOC TCAACCTOAG
WO 02 AVLHSEDPD KORHTSENU EPRILFTVER PIFTEETTF POVITTSEQ VECKERAKO KEAKOTTS KEAKOTTS KEAKOTTS FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI FORDERINI GETTERINI GETTERINI	Req ID NO: 620 DI Nucleic Acid Acce Coding sequence:	AAACTGATCT CCATGTCAGG	GCACCACAG CCACCACAG CCCCACCACC CCCCACCACC	CCACGCTCAC ACTCCTCCAC COTCCTCCAC TTCTATTATTOG AAAAAA	Seq ID NO. Protein Acc	1 MTWRHIVELL VTGSAEGMGP BECGALENGA LLPCALLHEL	Seq ID NO: Nucleic Act Coding sequ	ATGAGGTTCA ATGAGGTTCA TATGTGGG GAACCATGG CAGGGTGTT TGGAGCTTT TGGAGCTTTT TGGAGCTTTT TGGAGCTTGTGGA AGTAAATGTG	Seq 15 NO: Protein Acc	1     MRPSVSGMRT   QCCYNDAIVS   SKCENGRIC	Beq ID NO: Nucleio Aci Coding sequ		OGAGCTCAAG CCTCAGCCC TICTAACCTT ATGTCGCAGA OTTACAGCTG	TCATAMABIC TGCCAMAGC CCTTCACCTA
. 00 5	3	20	\$2 £	33 25	40	\$ \$4	20	55 09		\$ 65	≥	25	80	85

C OCCUPANCE TO A CONTROCC TO A CONTROCC TO A CONTROCC TO A CONTROCC TO A CONTROCC TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL TO A CONTROL T	ACACAAAAC OCCCATAACT AOTOCTCCTO OTOCCTCTOA	NA ACANGGICTO 120 IT TANAGGAAA 120 IA CAGTCAACT 135 IC AAGATGICAA 136 IT TOCTTATGC 140	TAGCTTCAGA ATAMATAAG CCOTOTOTTC CACTCCCTGT AGCTGAACAG	NC ANTOGOTATO 186 DO CTACACTOAT 186 TO COTAGOTOAT 198 TO TOTAGOTOAT  CCCATCACA TEGTCACAC CACTCAAAT AANAAAAGA TACTTTAACT TACTTTAACT	AAAAGCAAT	E VILLAHNILPO (CO SVIÇUDIGEY II.  RE VONTTYLHEV II.  RE VANTYCEPUY II.  TE LAVLYCEPUY II.  TE LAVLYCEPUY II.  TE VANEGREWCO II.		S1 	C ACCCATTCA 11 AND AATCOTATTO 20 AND CONTACTCA 30 AND ATACCCCA 30 ATACCTACAAG 45	TA TACCOGAGG 40  TA CATGCTOTOG 50  TA ANTOTCAGA 60  TO ACTCTACTCA 60  TO ACTCTACTCA 60  TO ACTCTACTCA 60  TO ACTCTACTCA 60	ACCATTCCC OCACCTCTA ACACAAAAC OCCCATAACT AGTOCTCCTO	ACCAGACCT ACCAGACCT ACCAGATCTG TAAAGGGAAA CAGTCAAACT	TOCTTATOCC 140	AGENCATOR AGENCACAC ALTOCOTATC CTACACTCAT COTAGTCCAA	-	
ANTOTORANT ACAGAACCCA TCTATOCCC AGATOTOCCC ATCTORACCT CTCCTGCCAC	ATGGGAGGTT CCACCAATCC GCGGATCCTA TATGTGCCAA CAATGATCAC AGTCTCTGGA CVATTGGAGT GCTGGCCACG CAGTAGGAGT GCTGGCACG		CATTAGTATT TCACAGAGG TGTCAATCCC AACGTTTTAC TAGCAGCATC TTAACACAG CTTCTAGACT CACCTGTTCT TAATAGAATT GCTCCTACC	TOTTGACAT GOCTAAATAC OTOCTOCTTO GTTAAAATOO TTTOTATCTT GCCTAAOOTO TAGTAGTCAT ACTCCCTOOT		TTANTTCATA AATCACAAAT	11		1 41 1 41 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		CACCOGACA OTTCOATOTA CCACCCCOT GAGGACAAG CACCTACCT OTGOTGGGTA CCAATGGCAA CATGACCCTC AATGTGAAAT ACAGAACCCA		CGATTGGAG CAGGAAGACT GCCAGATTGG ATCCCATGGA ACCACTAAAA TGCCAACTC AATGAAATT AACTTGACC TAACTAGAGA			STATE STATE OF THE PERSON ASSESSED.
ACC CTGATCCTATG	TOUTTATCA GTGAATMIN ACCACAGICA GTGGCATCA TTCGATATTT	ATCCCATTTT ATCCTOGAGA TGCCACTCAG GACGACTTCA	ATGATGCTGT AGATCTATCT TGACTGACAT CAGAGTTGGA CAATGCCAAA	ATTACAAT ATTACAAT TITTACTOO ATACTCATAC	SACAMATOTO TAACTGATAA TGAGCCAGTO CATTAMAA CTTGAGTTAG	TOGTGCTGCT n sequence AAS9907.1	71 TABLLTPHNP GYVIGTQQAT YPELPKPSIB TLLEVIGNDA AAGNPPAQYS	sequence on #: M18728	21   	CCCACCACTO GITCTICTAC GAMGAGTOG CCAGGGCCCC	MATGAAGAAG AGCAACAACT GTTCAGAACA CTGCAGCTGT GGATCCTATG	CTGAATGTCC CCAGGGGAAA TGGTTTATCA GTGAATATA ACCACAGTCA	TTCGATATT ATCCCATTT ATCCCATTT ATCCCATTT ATCCCACTCAGA ACCCACTCAGAGA ACCCACTCAGAGA ACCCACTCAGAGA ACCCACTCAGAGA ACCCACTCAGAGAGA ACCCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	TAAGGCTCTT ATGATGCTGT AGATCTATCT TGACTGACAT	CAATGCCAA TOACACTTGT ATTAACAAT	
WO 02/086443 эсятемма амкалася коасматая сеситеме естеммая смятьесят	ACCACCTGC ACATACTCT TCTTTATCCC CACATCACT CACCACTGG CCTCAATAGG TCTCTCAGC TGTGGCCACC TATAGCAGC CTGGTGTATT	CANTECTICS ASSECTAT CICTOCICCS CANODISTS ACCETCAGG CEDADANTE GCANCCATO GENDANTE ANCANGACE CECATENTA	TOCCTCTTC OCTTOOCAGO OGOTACTTA ACAGAGTOTC AGATCCTTA GTGCACCCAO AAATGTACA TGGTCCTTT TTTAATTCAA CCCAGCCATG	GOAGGACTOT GTGCAGTTC GCTGAGACTA AGTTGTAGA CTGACCCATT CTTTATTCTA CTCTTGGTAT TACCCTCCTA CTCTTGGTAT TACCCTCTA		CTATCACTGT ACTIGIAGAG TAGCTCTATA ACT Seq ID NO: 625 Protes Protein Accession #: A	11 CR LHVPN KG ERVPO LV NEZATO PR LOLEN YR PGENL	Seg ID NO: 626 DNA : Nucleic Acid Accessic Coding sequence: 1355	1   1   GOAGCTCAAG CTCCTCTI CCTCAAGCCC TCCCTGCI		TCATAMATC AGATCTTOTO TGCCCAGCC CTCCATCTCC CCTTCACCTO TGACCTGAG GCCTCCGGT CAGTCCCAGG GCGTCAAAG GAACGATGCA	ACCOCAGTCA CCCAGTCACC CCTCAAAGGC CAATTACCGT ACCCACCTGC ACAGTACTCT TCTTTATCCC CAACATCACT CAGCCACTGG CCTCAATAGG	TICTICTICAGE TOTOGCACE TATACAGE CTGGTGTT GAATTCTTCT AGCTCCTCCA CTCTGCTCCT GAAGCCCTAT ACCCTCAGGC CTGAGGTGTT ACCCAAACTATI GTGAAAATT		TITATTCA CCAGCCATO OGAGGACT TROCATTC GCTGAGACT ANTITAGAA CTGACTAT CITATTCTA	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
888	~ 35955	2 283	23 58 4 4 F	88666	25 30 30 30 30 30 30	35 98 97		8 ¥ 8	88	SS FF AT	99899	65 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8			& \$	ŧ

8 8

÷	
ã	
=	
~	
9	
2	
2	
F	
U	
ے	
	į
	1
	-
	i
	ľ

PCI																															
•																															
24422		9			120	2 6 2	360	629	3	099	720	780	6	1020	1080	1200	1320	1380	1500	1560	1600	1740	1860	1920	50	2160	2220	2340	5	2520	
CNACTGALAT ANALALAGA TACTTTAACT TCTGTGGTTC CCAGGGGGAG		S1       ULTECQIYLV		iš	ATGGGACCCC ACAGCCTCAC	ACCCCATTCA	GGATATGTAA	ACCCTACAAG	GATOCTOTOO	MIGGICAGA	OCCAGTOCCA	ACCAPTICCC	ACACAAGAGC	Agracicorg	OTGGCTCTGA ACCAGACTCT	ACAAGGTCTG	CAGTCAAACT	AAGATOTCAA	TACCTICAGA	ATAMATAG	CACTCCCTGT	AGCTGNACAG	CTACACTCAT	COTAGECOA	OTCICION	TTOTTCACAC	CAACTGAAAT	TACTITAACT	retoroune	AAAAGCCAAT	
CTACATACTE CAATTAAAA AAGTEECETE TOTATTATT ATTOTATTOE AATCACAAAT		41   6160evased		<b>:</b> _	AGCAGAGACC	TATTOMATOC	TCTAATTOTA	AGGATTCTAT	GOAGGACAG	OTOCHCOUTA	ACADAACCCA	AGATOTOCCC	CCAGCAATOC	AGTOTOTOGA	GCTGGCCAGG	ACCACTAAAA	TAACTAGAGA	AGCTTTTCCC	TCACAAGAAG	AACOTTTTAC	CACCTOTACE	OCTCOCTACC GOTTABATAC	GTTAAAATOG	GCCTAAGGTG	ATACTCAATC	GCTTTAAGAT	CTACATACTC	AAGTCCCCTC	TOTATTTATT	ATTCACAAT	
GTGCTAAATG ANATTAAAC CATAATACAA TGTTAACCAA CTGTTGCTTGT		31   BPAMODDAVI VQMSPEBLDP	-:	<b>5</b> —	CAGAGAAGAC	CCAAGCTCAC	ATCOCAACAG	AGAATGACAC	CCAACCCCOT	CAACCTACCT	ATGTGAAT	ATCTATORCEC	ATCODACCTT	COATCATCAC	CACCARGAGE	ATCCCATOGA	TOGACAACTC	CACTATODAC	CATTAGRATE	TOTOMATOCC	CTTCTAGACT	TATAGAATT	отостостта	TATAMETER	CAGCCATCA	TAGCACTAAT	GTECTANATO	CATAATACAG	TOTTANCOA	TWITCHE	
TORRECAGTE CHATTARAN CTTGAGTTAG ACTAATCTCA ACAANACCO TOGTGCTGCT	627 Protein sequence seion A: AAAS9908.1	21   PPNLGLLMPA 81FNTAVCSN	MA sequence sssion #: M18728.1 23702501	<b>17</b> -	AAGAGGTGGA	GCCACCACTO	CCAGGGCCCG	AACOTCACCC	AGCACCACT	OTTCAGAACA CTGCAGCTGT	COATCCTATO	CCAGGGGAAA	TOGITIATOR	ACCACAGTCA	OTCOSCATCA TTCCATATTT	ATCCCATTT	ATOCTOGAGA	GACGACTTCA	ATGATGCTOT	AGATCTATCT	CAGAGTTOCA	CAATGCCAA	ATTAACAAAT	ATACHCATAC	TOCATOCAGE	TAACTGATAA	TOAGCCAGTO	CTTGAGTTAG	ACTAATCTOA	TOGTGCTGCT	
02/086443 AS STRAGGGAT AS ANGITABATC AN INCASTOR TO TECASTOR TO TECASTOR TO A ACT	627 Prote	11   RLLIMIRLLP PLVHPVTDIS	Req ID NO: 628 DNA sequen Nucleic Acid Accession N: Coding sequence: 2370250	<b>1</b> .	CTCCTCTACA	CTOGNACCCA	OTACAAAGC ACAAGCTACC	OCTOATCCAG AGATCTTOTO	CTCCATCTCC	CACTOCAGO	GACGATGCA	CAATTACOT	ACAGTACTET	CCTCAATAGG	CHEGIGANT	AGCTCCTCCA	CTCACCCTAT	GTGAGAAATT	GCTTGGCAGG	ACAGAGTOTC	TOTOCTITE	CCCAGCCATG	AGITTOTAGAA	TACCITICAL	TTAMATOTC	CAATGOTGO	CTCACCCCAT	TICCAGICTA	AGTAACCTGA	ACTTOTAGAG	Ţ.
WO 02 recented germanaka recented restrected centented restrected	Seq ID NO: 627 P. Protein Accession	1 	Seq 1D NO: Nucleic Act Coding sequ		GGAGCTCAAG	ATOTOGOADA	OTTACAGCTO TAGGAACTCA	ATOCATOCET	TOCCCANGCC	CCTTCACCTO	GCOTCAAAG	CCTCAAAGG	ACCCACCTGC	CAGCCACTGG	TECTICACAGE	GAATTCTTCT	ACCETCAGG	GCAACCATO	TOCCICITIC	GOOTAACTTA	AAATOTACAG	CONCORCIC	GCTGAGACTA	CTOACTCATT	CTCTAAAAGC	ATAMAGEC	TCTCACCTAG	ACACAGGAGA	TTACALLA	CTATCACTOT	MOCICIATA
8	0	S	٥	?	4		•	c	,		٠.	,			Ç			'n			0			S			9	2		4	,

8eq ID NO: 639 Protein sequence Protein Accession #: AAA59909.1

**=**\_ **12** – =-

	HLTHVPISVV	MITHVPISOV LPPCENLING TULVLYCPOO ALTVLVENCC PHS	TVLVLYCPOO	AITVLVENCC	- <del>2</del>	_
75	Seq ID NO: Pucletc Aci Coding sequ	Seq ID NO: 630 DNA sequence Proleic Acid Accession 8: NY_016639.1 Coding sequence: 40429	quence #: NH 016 29	17.60		
80	1    -  -	1 11 21 21 31 41 B1   CONTROLLE   CONTROLL	21   COODCOCAGO	31   ACOTOCACTA	4.1       TYGCTCGGG	B1   CTCCCTGCCC
88	AAGAAGTICA AAGTCAAGG BCTGCAGGAC CTGACCTTCG GAGAAGTICA	момитистве обистистия ститемовать письтомоги пислометь ситиосихов милисимос сывельское системоги сисиосих ститемоги сисиосих милисимоси системоги тисьовоги сисиосих сиси-тиз сигиоситем ститемоги тистовоги системоги ситиосих пистиомов соститию ститемогите тистовоги ситиосих титиогих вымисим сосывами миниситем техносскоги миниситем сосывального ситиосих миниситем техносскоги миниситем сосывального ситиосих миниситем сосиссовия миниситем сосионального ситиосих ситиосих миниситем сосиссовия миниситем сосионального ситиосих ситиосих миниситем сосиссовия миниситем сосионального ситиосих миниситем сосиссовия миниситем сосионального миниситем сосиссовия миниситем сосионального миниситем сосиссовия миниситем миниситем ситиосих миниситем ситиосих миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем миниситем минисит	CAGCICETOS GETUGOGETOS CAGGOGETOS TECNOGOGO TOCTOCOCOCE ETECNOGOGO TOCTOGOGOS GETECOGOSTO TOCTOGOGOST AGAGGAGACC CONCECCEAT AGAGGAGACC	ATRODOSCIE TROCTOSCOT TECTIONICES COTOCOCOS COCCUPIONE COCCUSACIONE CETURA ACCE CONCETURA TRECHOSCO COLCOSCULA CECUTATATO CETURA CONCETURA ETITOTOCO ETITIOSCO TECTIONOSO CECUTATORIO CETITOTOCO ETITIOSCO TECTIONICE COCCUSACIA MANDRAJARCE GIOCORDANDO ESTENCICACE PRODOCETA	TIGENGOCETE CONTOCCOSO CETECALACISC CALCETORAL GCALCETTETO CETECAGA TECHTOLOGO COSTETORAL GARACCATO COCAGAMA GETGCCELAC POPOCOCETO	COTOGOGOGO COTOGOGOGO COCTOGOGOGO COCTOGOGOGO TOTOGOGOGO

\$25555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$2555 \$255

41 | | BMBADLDKCM D | WRRCRREKF T POTAPCSROS BI Seq ID NO: 612 DNA sequence Nucleic Acid Accession #: NN\_001816.1 Coding sequence: 79.,2518 ATCHARGE ANTROCCC CTOCHACO GO THETHAGE ANTROCCC TECCHACO GO GOOTOGO GOSTIANT ACTURIAS CE ACHANGAC THOCATCH AND ACHANGAC THOCATCH AND ACHANGAC THOCATCH AND THOCATCHAIN GOSTICANN TOCACCAGO THACACHA GOSTICANN TOCACCAGO GO CCANAGGO GAGGARAIN TETATTOG GA MINANGAN TETTANCT THAMANAN AND MARGELREL HILVICIMEA LLREVADEDA BDPCCACCAAA PPAPTRILIMP ILGGALSLIF G GCPAVALIO Seq ID NO: 631 Protein sequence Protein Accession N: NP\_057723.1 2 2 ಜ 13 22 <del>수</del> 20 55 8 2 8 35 5 65 75 82

Š	
•	
	š
Ę	
5	
Ξ	
t	
	١
ò	

WO 02/086443
conservato accelente actualista transferia transcela 1420
conservato accelente actualista controlare attendado transcela 1420
amplicados estrocario alastraces controlare attendado transcelare 1420
amplicados preceptad alcabacha attalacest consecual attropados transcelare accelente 1740
amplication attalacest accelente attalacest 1540
amplication attalacest accelente 1840
amplication attalacest accelente 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 1840
amplication attalacest 18

PCT/US02/12476

Seq ID NO: 637 Protein sequence Protein Accession N: NP\_057606.1

								•						
3720 3786 3840	120 120 100 100	420 660 720 720 780		120 120 140 100	20222	720		120		25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 7 4 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1020 1140 1260	1340 1360 1560
CTTCALM! OTTTTGOTT OWNTICTEA	S1 LTRERREAPR CHICHYBGYV BPLKCGVBNK NOTAVREEMI FLITRRAEDS	AYSABGCONK TICRGKTSEC KAKAAPKOCP IQTPBRCTKC HCHOVONSHK VCAIPIFIKR NRPAVPTYAA		S1 daaccatigco cccoggagco caccacacaa cttctotttc	CTCAACCCAA TCAAAGATGT AAGAAAGGAA ACAAAACCCC TCCTTGTGCAA	AATTAATGCT CCATTCACAA		91     CKK#TGE698   WDSEDSGNPR		51 1 1111COMAGO OTCTOCOCOC COCCTCOCAMO CTCCCOGMOT OCCCTOCAMO	GCCCGTGCGC GGCGCAGAGC AAACCGCAGC CCTTCTGAGC CGAGGGCCCT	AGGCATCACA GCCCOTGGTA	CTCAGGAGAA CAAATOGAAC CTATOGGAAC OCTATTTOGT CGTCTOGCTG	CTTCCCCAC CCACACACAA AGAAATTGA TTGAAAATTG ACACACACAC
TTTCATAC TTTTAAAOT TAAAATACTT	41 	CLLAIPKEDB CKDCRFLPGG DAQCQVIFGS IPVFGIVPAI HYDCDVQKKC VPFFLIVPLI		41 CTTCCCOTCO TGCCTAGCGC AAGATGTACC GGGGAGTCTT AGGTGGGAAG	CACCAGCOAC AGCAGCAACT TCTCAACOTO AAAGAGAAAA CAACAAGATT	AGAGTCTTCC		41  - GNEMAVŒILM PKALŒNQQPB			CCACAGAAT COOTCCSOCA TOGCCTGGCT CTCCCOTGOT ATOTOTATA	CCATTANTOA COGTTACTTO TOCAAATTCA ACOTOOCCOC	CAGCAOTCCC AGAAAGGGT CTGAACATGA CCAGCATCAT GGGCAGGCTG	OTGANGGACA AATGGCACA CTCATGGGAC AAAAAAGAAA AACGGGAAGA
ACTAMAATT TTCATTAGT TTACATTAAA	31 RPGPOOTERL DEVVYTWAR PLONSSHPEH TRYVELFIVV INIVGGAGDV	EKLTLNKGEN FFAECAYGDC YCYNGMCQYY GKLQCENYGB NPQCYDASYL MYALKBGLL GSVPRHYSBY APPLYBBLT	091.1	11 CCTCCAAGGG OCTGGTCGC CCTGGTGACC AAAGAGGACA AAAGTACATC	DAACAGAAAC TTCAGAGGAT TGCTCCAGGT GCCTCCTCA TACGGATCAT TTGACTAAAT	ATTGTGGAAA TTCAAGGGG		31  - GTVLTKONPR GENRNHQPPQ	522.1		TTCCTTOTAC GACAACOTCA GTCACCCGGG TGCCTGGATC CAGAACOTGG	TCAGATATCT CCAGAGCCTA GACGAATACT GCCTCCAATG		AAATTTTGAT ACACAACAGC GAAACACAGC AAAGAGTTTT TCTTTTGCCA
AATTTTAAGC TTAACTGAAT AMTACACACAT AMMA n **quenc* P_003607.1	21 GLVGPVLGAA LERNKDLLPE HLENASYGIE LRRRRAVLPG GLEIWTNGNL VCSRSHAGGI	NPSCGAEDF CCEGSTCKLK MOYPCGNNKA KKCATGNALC TKCGAGKICR SVDGOPTYNE KNGANPSRQP GNLIPARPAP	sequence on #: NM_002091.1	21 	ANGCAAAGBA CTTCOTGGGA OTAGACTCTC GATAATBATO GCATCAGTTC FCTTTCATCC	actorance ottoottaa	Protein sequence m #: NP_002061.1	21  - GRAVPLPAGG GRAVPLGLIEA RHPLIGLIEA	Iquence 1 #1 NM_016522 1299	21 	CANGCTACTO CANAGCTATO TOACAACOGO TOACAACOGO CATCOAAGTOGO CATCOAAGTOGO	AGAGATTCT AACTOGTAGA TOTOAGTGAA COAGTGCAGT	GACACTGCAG CAAAAGACTG ACTCATCTTC CAAGCTGGGC GAGCACTGGGC	ACACCACA AAAATTAAA TTTCOGGGA AATGGAGTT
086443 rodarostaa aarascrita tacatataca aaaaaaaaaaaaaaaaaaaaaaaaa	11	ISCASIGN VECELOP OPDVPIO GESONEY POAVNEG PETROYOG OPTVESPO OPKVESPO	A DNA	11  -  -  - 	GCTCTCATAG AATCACCAGC GGCAAAGTTG AACCAGCAAT AGTTCTGCAA CTATTCTGTA	AAACTTGTTT TAAGCTACCT AACACAT	Mos 635 Protei	11 	No. 636 DNA sequence Acid Accession #1 NM sequence: 269.1299	11   cowdandan   cowdandan   cochanter   cochanter	TCOTOTCTCC CCACCTTCCC OOTOCACTAT ATCCTGGGAA OOCAGTACAG	CCAAATTOT CCTGCATAGC CCTGCATAGC CCGTTGGCTT	ACMARAGO ACMORTON TCCTCTCNA TOGCCTCCAA TCACCACOA	TOCKECACE ATATACAAT CAAGAATAC ATTTAGGTAC
WO 02/086443 AGATATORIA ARAGOT ANGITTARIA ARAGOT TOTOTARIA I TACAKIT ANAMANA ANAMA Seq ID 1001 633 Pr Protein Accession	1 HGGARPEG PYEKQVSYVI ECVHNSSIAL DIEKETAKDE LLANYLDSNY AQLVLKKGFG	NDCSCGARGC LVDAGESCOC	Seq ID No: 63 Nucleic Acid / Coding sequenc	1   AdTCTCTGCT CGGCAGTGAG AGCGGTCCCG CCACTGGGCG TGAGAGAGGG	GATTTGCTG GGCCTTGGGC AGGTTCAAAA CCCCCAGCTG TAAGAGACTG	CTTCTGGTTT TTTTATATC TAAAAGCTTA	Beq ID NO: Protein Acc	ARGSELPLVE VSERGSLKOO DVGSKGKVGR	Beq ID NO: 6 Nucleic Acid / Coding sequen	1 godsanacha crtsconnad itericenc crochecenc resconecen	ACCOCANA ACCOCACA  ACCOCACA ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC ACCOCACAC	CAMOTATOTO ATTAGCOTOA TOTOCCAAAQ COGGAACAOT		CONTRACTOR CONTRACTOR CONTRACTOR COTTOCAGAT
٧,	0 5	o		S %	0	\$		8 %	2	65 55	2	75	80	85

0		=_	<b>-</b> 2	<b>=</b> _	<b>7</b> _	S	
	MGVCGTLFLP NRVTRVAVLA NHPKTBRVHL BEDEYLBIQG LQCEASAVPS LGHTNASIML	WKCLVVVSLR RSTILYAGND IVQVBPKIVB ITREÇSGDYB ABPQWYKDDK PGPGAVSEVS	LIFLVPTGVP KWCLDPRVVL 189D181WEG CBASNDVAAP RLIEGERGVK WGTSRRAGCV	VRSGDATFP LSNTQTQY81 NNIBLTCIAT VVRNVKVTVN VENRPFLSKL WLLPLLVLHL	ANDNYTYROG ELONYDVYDB GRPEPTYTAR YPPY16BAKO 1FTNYSENDY LLKF	EBATLACTID GPYTCSVQTD HIGPKAVGEV TOVPVQQKOT GAYTCVABNK	22,22,5
20	Seq ID NO: Nucleic Act Coding sequ	638 DNA 1d Accessi Jence: 203	Tuence 8: MA	_012261.1			
		1-	- 33	<b>:</b> -	<b></b> =-		
53	ACAGAATAGG CACTCCAGGG	GCCAGCAGCT CGCTCCCTCC GCGACTTTGA	OCCCCCCTC OCOATTCCCT	COCTOSACAC TCTOTCCCCC CTCTGGCGGC	CONSTICCTAG GCCTCTCGCT CTCTGCAGCA	CTAGGGGCTC CACCCCGGCC GCACAGCCGG	823
	OCTCATTOGG ACTTCGAGTT	GOCACTGCGA CTCCTGATGT	GTATOGATCT TOTTCCATAC		<b>ATCATGGCAG</b>	GCATCGACAG AACAAGAAGT	2 2
3	GGANAATCTC TOGGACGACG GGCCAGCAAC	TCAGGCCTTT TGTCTCATGG TACGTAGATC	CAGAGTTTGC CAGAGTTTGC TGATCACAGA	TGAAAAGAT AGCCAAATTT ACAGGCCGAT	ATTOTACCTT ATTOTACCTT ATCGCATTOA	ATGATOTOTO CCCGGGGAGC	2 2 2 3
35	COCATATOCA	CTCANANTOC	TCTTTOTAM	GOALAGCCAC	AACATGTCCA	AGOGACCTOA	8 6 6
	CACCCCCCC	GICAGIACTO				TOCCTTOOT	720
6	TATCTCAGAT	TTTOTOTTCA	OTGANGAGCA TTTTGGGGCT	TAAATGCCA		GOGLOCALCT TOGTANCACT	6 6
	ATCCCAGTAT	MACACATOC	GCTAGAGGCC	TECCAACCAG	CACCCCCTAT	TCCTGCTCCC	201
45	CATAGCTACA	ATCAMCAG	CCTGGGTATC TCTTTCGGAT	TOTAGOCTTOC	TTOOCTION	TCCATGCTTA	222
	ATGCTGGGGA TGACTCTCCA	GOADGOGAGG		ACAGCTTTCG			138
20	TECHNAMACAT TECHNECOCOTTO TCATECTCCC	GACACAGCTO GACACAGCTO TGCAGCAAGA	GCTTATCCTA CCCCTGAAAG		CAGANGANTA AATGCACACA TTCTGGCTGG	DANTACAACC CATTCTGCAT	1500
	OTTTAGTGAT AAAACGACTA GOGGGACCTG	TOTCTTOGGA ATOTAACTAT AAGAATCAAT	ATOTITCACT OCADAOTIST CTSTOTOAST		TCCAGCGACT TCCTGTGCCA AAATGAAATA	GCAGCACCAG GGTCCAAGTC AAACACACTA	1620
55	FICTOTOGC	639 Protes	egnence				
	ein Ac	cession #: NP_036393.1	1P_036393.1				
9	et	=_	<b>12</b> —	<b>1</b> –	<b>;</b> _	ĸ_	
53	MDLQGRGVP8 EPAAKPIVPT PVKESHNMSK BCQAQQTISL LGLILGLVIM	IDRLRVLLML DVWASHYVDL GPEATWRLSK ABSDPQKTVT VTLAIYRVHR	PHTMAQIMAB ITEQADIALT VQPVTDSSEK MILGAVHIQP KMTANQVQIP	QEVENLAGLA RGAEVKORCO THPKDAVSAG PDISDEVFS RDASQTKOMO	Typeld) PVV Hegselqvpm KHTAISHHLS Kehkcpvder	RENGTICLAA VDRAYALIOU ALVIPAGKSY EQLEGITLPLI	3,626
9	Beg ID ZO: 6 Nucleic Acid Coding sequen	640 DNA 1d Accessi uence: 64.	requence on #: NM_002993	1,000			
	1       000ACGAGGC	11   	21  -  -  -  -	31               	+1           	51   TCTCTTGACC	٠
25	ACTATGAGCC GCCCTCCTCC GTCTCTGCTO CCCAAAACGA	TCCCGTCCAG CCCTGCTGCT TCCTGACAGA TTGGTAAACT	CCGCCGCGCCC CCTGCTGACG GCTGCGTTGC GCAGGTGTTC				2272
02	ACCATGCATC ACCATGCATC	TCCAGAAAT ATAMATTOC	TTTGGACAGT	GCGGAGCAGA		AACAAAAAA	2 4 3
	GAAGAGTOTO		TACGETTETE	CCTGAAGTTT	ACAGCTCAGC		2 3
82	CATTGACCA	TATTOTONOC	CTATCATACA	TECTTATA	TCTTACCOM	AACACTOTOG	22.0
	ACTCACTCT	CTCATABAT	AGGAAATATT	TTAGTTCTOT	111011000	AATATOTTAC	8

_
_
₹.
~
-
~
_
Ō
_
_
_
_
۲ ۱
~
•
_

PCT/US02/12476		·	*."					
960 1020 1140 1120 1120 1130 1130 1140	9	120 120 240 300	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			1 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	960 11080 11080 11140 11260 11360 11360 11640 11640
TOTCHACOS TOTOTAMOS GOCHANTS GARACTRA GARANTICO CAMATTAC TOTOTACAT TOTOTACAT TATOTCAT  S1 	51 dageceasca cceccacac ccertadera debagasca anacascac cracracaca	CCCGAGGGG CCCGTAGAG CCCGTCAGG GAGGTGGCC TCCGAGGGG GAGCTGCCC CCCGAGGAGCAG CCCTGGAGCAG	51   AETGAPRRFR RVMGAPRRSD YDDGPAGPDA PPEGVLGALL		BI AGCAGGACG AACTATGGT CAGACTTTT GAATGTACAT TGGCTCTTCGT	ACCOUNTS CUCCOCOCO CUCCOCOCO CUCCOCOCO CUCCOCOTO TOOOTOTTTO AATOCACCAT	AGCAAAGGCT GAAAATGAA GCCGAAGCTA TATCTTGTTG AACGATTTAT TATCTTGTTG AACGATTTAT TATCAATGATA ACGATGAACA GATACACAG GATACACAG GATACACAG GATACACAG GATACACAG GATACACAG	
ACATTOONS TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTANN TECTAN TEC	41   	41 ecrocretos orrroseco Augusteco Augusteco Calacoreso Calacoreso	GOACGACOAC ACCCOGOCC CUAGACCTO AGCCOGAC AGCCOCAC ATCCCCTTC CCCTGCCC	41   RGLSAASPE PE POARVIAGE   AAALRPRPPY N		CTCCTTGC GCAAGCTGC TAATGGGCA TAATGGGCA TAATGTGAT GAACAAAA	CCCCOTTOC OCTACCTOC CCTACCTOC CCCACCAO TITITITIAC CTOCOCAOC TICOTTTCA	CANTITATA A MACCOCCI GOSTICITATA I TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTTICA A TECOTOTICA A TECOTO
CECTATA A DAYTHCHA A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A OTTUNECT A O	Lasagev Peapfuk 1	OUTCOCC TOGOCCT TAAGCOC TOCCCCO TOGAGOC	COCACOCOCO COCACOCOCO MACACOCOCO TTCTTGCOO TTCTTGCOO CCAACOCOCO CATACOCOCO ACTTCTCCC OCATOCOCOCO ACTTCTCCC OCATOCOCOCO	31   ALCARPUKEP R ALCARPUKEP R ARACUPAPUP A GUVAAPRILER A	*	COCCAGCTTC AGACGGGCT CTGCGCTGT TOTTGGGTT COCCTGAT TOTTGGGTT COCCTGAT COCCTCAT COCCTC	ACCOCAGAC GCCCGGGCCC GCCCGGGAA GCCCCTGGAA GCCCCTGGATG CCCCCTGATGCT ACATAGATG	ATATTOTTIC CONTACTORY AND ATACCAGCT OF ANALTRAN 1 TOTOCTOT OF ANALTRAN 1 TOTOCTOT OF ACATCACT
AAGTTGTA TTTAGAT TTTAGATA TTTAGATA TTTAGATA TTTGAAA TTAGAGG TTAGAGG TTAGAGG TAAACCAA	21 LLALGULTP   VASLOGEGY Quence  #: NM_0132 09	21 adcadeatro dractocroto anacceroto Treconocat cronocate cronocate	TCTGATCCGG  OCTCTGCGCGCG  OATGCTGAGG  CTGGGACGA  CTGCGACCGA  CTGCTGCGC  CGCCCCCCGCG  CGCCCCCGCG  CGCCCCCGCG  CCCCCC		Nence #: NM_0022 :990	TTACTOCCAT  OCTOCACCA  OTTOCACCA  TACCOCTCC  TACCOCTCC  OAMOCCTT  OAMOCCCAC	CCTCCCCAN GCCAAGCCT GCTAGCCCT ATGTCCCCT CCAAGTCCCC CCAAGTCCAAG CTAGGTCCAAG	CCCCATORY  ANTATATA  ANTATATA  ANTATATA  ACCATORY  ACCATORY  ACCATORY  CCCCATORY  CCCCCATORY  CCCCATORY  CCCCA
**********	11 21   LANDERS   LANDER   LAN	11 66CTCGCTO COGCTTTTO 6CCGCTAAO 1CCTCGCCGC 1CCTCGCCGC 1CCTCGCCGC 1CCTCGCCGC 1CCTCGCCGC 1CCTCGCCGCC 1CCTCGCCGCC 1CCTCGCCGCC 1CCTCGCCGCCC 1CCTCGCCGCCC 1CCTCGCCGCCCC 1CCTCGCCGCCCCC 1CCTCGCCGCCCCCCCCC 1CCTCGCCGCCCCCCCCCC	COCCOGANE 1 COCCOGANE 1 COCCOGACCO COCCOGACCO COCCOCACCO COCCOCACO COCCOCACCO COCCOCACO COCCOCACCO COCCOCACCO COCCOCACCO COCCOCACCO COCCOCACO COCCO	643 Protein cession #: NP 11 2 1 RAGGVGLLVL I RAGGVGLLVL I RAGGVGLANALA POPELLANALA OPPARRLIPP	644 DNA Beq Accession Ince: 6812	CCTCCCCTO TO CTCCCCCTO TO CTCCCCCCTO TO CTCCCCCCCC	AGRACOTECT O GCCCTGAGAT GGGTCCCCCT TCGCCCOGGA GTTTGCATT AAACGACCCG GTGCCTTGCC	ATCAGANGT TTCATTAGA GANGTTCAT GANGTTCAT ATCATGCAC ATCATGCAC ACCATGCAT CTGCATGCT CTGCATGCT TAGANAGA TGAGANAGA TGAGANAGA TGAGANAGA
WO 02/086443 TCTTMCCCT AGGANATA TCTTMCCCT AGGANATA CANATATA ATTCTOTCA ANTANCTOTCA ANTANCTO	1 11 21 31 HSIDSSBARN WORDSSICA LIALLILLE PRINCESSBARN WORDSSICA LIALLILLE PRINCESSBARN WORDSSICA STANDOORN'S VASLANGAGOV CLD BRQ 1D NO. 642 DNA «equence CODING SEQUENCE 37. 809	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TCTGGGGGGG CTGCAGGTGT CCCAGGTTGT CCCAGGTGT CCCAGGTGT TGGCAGGCC TGGAGGGG TGGAGGGG TGGAGGGG TGGAGGGG TGGAGGGG TGGAGGGG CAGAGTGG CAGAGTGG	GATCHAGC  Seq In No. 443 Procein sequence Protein Accession N. NP_037403.1.  1	Seq ID NO: 644 DNA sequence Mucleic Acid Accession 8: NH_002214 Coding sequence: 681.2990	cccaaacca cccaaactr orraccactr orracctcc trocctrory ctraactarr	100000000 000000000 000000000 00000000 1000000	TITCAGGTGG A GCCCAGTGG A TITATAGCT A ATTITAGCT A ATTICAGC A ACAGATTAGA ACAGTTTAGA ACAGTTTAGA ACAGTTTAGA ACAGTTTAGA ACAGTTTAGA ACAGAGGTTAGA
5 5 5	n 0	30 25	35	× 0		8 %	5 5	85 %

		١	
		í	
		1	
		١	
			,
		•	
		1	
		i	į
		1	
		ì	
		:	į
		١	۱
		ı	
		1	
		i	i
		•	
		١	
		i	į
		۱	ľ

Beg ID NO: 650 DNA sequence Nucleic Acid Accession #: NN\_001506.1 Coding sequence: 259..2379

PCT/US02/12476

	3
	ş
	CHAMMAN
	TCCAATCAT
	ATAATAATA
/086443	AATTCTTTOT
WO 02	TOTATATTA

Seq ID No. 649 Protein sequence Protein Accession 8: NP\_056322

. 6

PCT/US02/12476		
111660 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 11160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160 1160	00000000000000000000000000000000000000	
THETHERE OF THE STATE OF THE ST	1 TYNGISOOUN ERGUYENEEK ERGUYENEEK ERGUYENEEK ENGEREEK ELAKKITEG IGGGGSEKY YELTOOTIN TELTOOTIN TELTOOTIN TELTOOTIN TELTOOTIN	11 AOCCOCAN AOCCOCAN AOCCOCAN ACCOCAN ACCOCAN ANTERCAN AN
ACTTOCACC ANOMOSTOR CONTENANT ANTENANT ANTENANT ANTENANT CONCOURT CONTENANT	1 ISANTTONISO DISANTTONISO DISANTTONISO DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DISANTESINA DI	14 coccorce coalcalact coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce coccorce cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco cocrco coccrco cocrco cocrco coccrco coccrco cocrco cocrco coccrco coccrco coccrco cocrco cocco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco coccrco cocco coccrco coccrco coccrco coccrco coccrco coccrco cocco coccrco coccrco coccrco coccrco coccrco coccrco coccrco cocco coccrco cocco coccrco cocco coccrco cocco coccrco cocco coccrco cocco cocco cocco coccrco cocco coccrco coccrco cocco coccrco coccrco cocco coccrco cocco cocco cocco cocco coccrco
TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG GENATION TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOLOG TECHGOL	11 DLTDELGLAK TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDDI TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDDI TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITALDE TEDJITA	OCCOCCA GACTGGA GACTGGA GAGTGGA GAGTGGA GAGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA AGTGA A
ACCESSES GUTTALAGO GUTTALAGO FOLGATARÍ FACCESA ACTITACO ACTITACO FOLGA TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO TOTACO T	In sequence P_003309.1	11 II III III III III III III III III I
(186443) octoritatio actoritatio actoritat	ession 8: 1)  1)  1)  1)  1)  1)  1)  1)  1)  1)	See of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total december of the total decem
WO 02/086443 ontrocho crrome arrocarre america control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre control arrocarre c	Seq ID NO. PTOLEIA ACCEPTORAN INTERNACIONAN INTERNACIONAN INTERNACIONAN INTERNACIONAN ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES ESTLAKLES	See ID NO Peritate Coding seque Coding seque Coding seque Code Code Code Code Code Code Code Cod

36	-1-	==	12	31	<b>;</b> .	22	
3	dragment.	100000000000000000000000000000000000000	PACCECTORIA	1	-		Ş
٠	TTAGACCOO	ACCOCIACO	ACAGCGGCCT	TOTACODOCC	CCCSAGTAAT	TOACCCAGGA	12 0
	CTCATTTTCA	COMMOCCTO	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TOMACATTET	180
۶	ATCTTTGGAT	OCCUPANT	TOAGGATGCA	AAGAGTGATT	CATCCAGGC	ATOTOGRAMA	2 6
3	ALCAGOANT CTCCTANGED	TOAMGAAAT	CAMPAIGITI	ACATITION	TUNCUTURAL	TI TICIACLE	9 5
	ATGGCCTACA	ACATGACTET	TTTCCCTAAT	CTCATCCCTC	ATTATOACCA	GAGTATIGGE	720
	GCGCTGGAAA	TOGACCATT	TCTTCCTCTC	9CANTETOO	AATOTTCACC	AAACATTOAA	9
į	ACTITOCTCT	<b>GCAMGCATT</b>	TCTACCMCC	TOCATAGNAC	AATTCATOF	GOTTCCACCT	940
3	TOTOSTANAC	<b>AMDADTOTT</b>	AGTATATICE	DATTOCAAA	ATTACTOR	CACTITIONS	909
	ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTOTOATOA	averanteer	99
	GIACTITIO	ATCCACACAC	AGAATETCET	OGTOCTCAGA	AGAMACAGA	ACANGROCA	25
	AGAGACATTO	GATTITION	TCCAAGGCAT	CTIMONCIT	CTOGGGGACA	AGGATATAAG	9 5
40	TTCTGGGAA	TIMECAGIG	TOCOCCICCA	TOCCCCAACA	TOTATTTA	AMOTOATOA	940
2	TOTAL PARTIES		A TTO A TOTAL	ACRECATION	Caracoraca	TAN CANADA	9
	ATATATTACT	CTOTCTOTTA	CAGCATTOTA	TCTCTTATGT	ACTICATION	ATTITIOCH	1020
	OCCUATACCA	CAGCCTGCAA	TAAGGCAGAT	CAGAAGCTAG	ACCITIONA	CACTOTTOTC	1080
7	CTAGGCTCTC	AAAATAAGGC	TTGCACCOTT	TTOTTCATEC	TTTTOTTT	TTTCACAATO	1140
2	GCTGGCACTG	TOTOTOTOT	GATTCTTACC	ATTACTION	TCTTAGCTGC	MOCANGRAMA	1200
	CONGRETATION	ANGCCATCCA	GCAMAGCA	OTTING THE	Argending	ATGOOGLACA	1260
	GOAGLITICA	Thomas	TTATGACCTC	GATGETTETE	OCTACTOR	ACTOTOCO	1380
:	CTOTOCCTTT	GIOTOTTIO	TOGGCTCTCT	CTTCTTTAG	CTOCCATTAT	TTCCTTAAT	140
တ္တ	CATOTTCGAC	AAGTCATACA	ACATOATOOC	COGNICONO	MANACTANA	GALATTIATO	1500
	ATTOCIANTIG	GASTCTTCAG	COGCTTOTAT	CITOTGCCAT	TAGTGACACT	TCTCCCATGT	1560
	TACGTCTATO	AGCANGTGAA	CADGATTACC	TOCOACATAA	CTTGGGTCTC	TOATCATTOT	1620
	COTCAOTACC	ATATCCCATO	TOCTTATOM	DCAMADCAA	AAGCTCGACC	AGAATTOOCT	1680
¥	TTATTTATOA	TAMATACCT	GATGACATTA	ATTGITOGCA	TCTCTGCTGT	CTTCTCTCTT	1740
2	GGWGCWAA	AGACATGCAC	AGAATGOGCT	COULTITIA	AACGAAATCO	CAGAGAGAT	000
	CCAATCAGTG	AMOTOMAG	AGTACTACAG	AAAACAIGIG	CACACAGO	AMAGCACAT	1020
	TOCARATOCA	TOTOTALCE	CACACACAC	ACAGCAAATC	ATOMORPH ST	TOCAGTAGCA	
;	ATTACTAGCC	ATCATTACCT	ACCACAGA	ACTITICAÇÃO	AAATCCAAAC	CTCACCAGAA	2040
0	ACATCARTGA	GAGAGGTGAA	AGCOGACOGA	OCTAGGACCC	CCAGGTTANG	AGAACAGGAC	2100
	TOTOGRAM	CTOCCTCOCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCCAC	2160
	GOGANGOOCC	AGGCAGGCAG	TOTATCTOM	AGTGCGCGGA	gravagava	GATTAGTCCA	3330
	AAGAGTGATA	TTACTGACAC	TOGCCTOGCA	CAGAGGAACA	ATTTGCAGGT	CCCCAOTTCT	2280
3	TCAGACCAA	CAUCCICA	ANGI TOCALO	rerenting	TACCAG	TICAGAGIG	
3	CAGAAGCAAA	AGGGGGTAC	ACTORAGO	ACCTATGOSC ACCTATGOSC	STATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	CAATCACTOT	2460
	TACOTTOTAL	TTTTGCACTT	AAAGTTGCAT	TOCCACTOR	TATACTOGAA	AAAATAGAGT	2520
	TCAAGAATAA	TATGACTCAT	TTCACACAAA	OUTTAINGAC	AACAATATAC	CTOMMOND	2580
۶	MATGROCAG	GTTATATA	TITITIME	AGTOTOGGAG	GACAGAGTTA	GAGGAATCTT	2640
?	CCTTTTCTAT	TTATOMOAT	TCTACTCTTG	GTANGAGTAT	TTTANGATET	ACTATOCTAT	2700
	GIATCITIT	ATACATATT	GAAAATAAGC	TATATOTAT	THEATTE	TTGARATCET	2820
	ATTCAAGTAT	TITTATCATO	CIATIOIDAI	ATTTTAGGAC	TITOGIAGO	TTACACTOR	2880
į	ATTTCTAGA	ANATIGIANA	ATAGECTICS	TITATACTOT	AAAAAAAA	ATACCAAAA	2940
c	STCTTATAT	ACCIVATITION	CTTTAAAAAC	CCACTTATTO	ATACCTTACC	ATCTMAAATO	3000
	TOTGATTET	ATAGLETOGT	TTAGGATT	TCCCCATCT	ANATTATOTA	ACTOMATA	8
	GOTOCITACT	CAMBAGTOT	CONCTATTOR	TIGINITATIO	CIGCICACIO	ATCCTTCTOC	2120
	GGCCAAGTGC	AATTON THE	TANAGED IN	TOTTOTAL	CACCELLE	ATTRIBUTA	1240
8	MCCACTTAC	AGTTGCTTAT	ATTITION	TIMETTIO	TTTCTTACA	TETAGASTAT	9
	TACATITION	ATTATACAGT	ACCTITICACA	GACATTITUE	94		
	200						
;	Protein Accession	ě	NP 003497.1				
8							

v
-
**
~
_
7
0
S
=
⋝
-
u
7

WO	WO 02/086443					
LITALIANZ	REMPTELLIC IPLPLLRGHS (	LFTCEP1TVP	LFTCEPITVP RCHONAYINT PPRINCHYD QSIAAVEHEE	PPPNIMOHYD	OSIAAVEMER	9
PLPLANLEC	LPLANLECE PNIETFLCION I	PVPTC1E01H	PVPTCIEGIH VVPPCRICKE I	RVY SDCKIQ, I	DIPOIRMPES	130
LECTRIQYOU		STVPVTPOPH TEPLOPOKKT EQUQROIGPN CPRHLATSGG QGYKPLGIDG	EQUORDIGIN	CPRHLATSOG	QOYKPLG1DQ	780
CAPPCPRINTE		KEDELEFAKS FIGTVEIPCL CATLPTFLTF LIDVERFRYP I	CATLETPLIP	LIDVERPRYP	BRPIITTBVC	240
YBIVSLAYF	BIVBLAYFI GYLLCOSTAC NICADBILLELQ	NKADEKLELG	DTWLGSQNK	DTWLGSQNK ACTVLPMLLY I	PPTHAGTVW	300
VILTITAR	ILTITHFLA AGREMECEAI EQUAVMPHAY	EDKAVMPRAV	ANGTEGPLITY	ANGTRGPLTV MILLALNIKVEG DNISGVCPVG	DISTRIBUTION	360
LYDLDASRY	YDLDASRYP VLLPLCLCVF VGLSLLLAGI	VOLSLLLAGI	ISLAHVROVI	OHDORNOBKE	KKPMIRIGVP	50
BGLYLVPLVT	T LIGENYROV	<b>WRITWRITWV</b>	SDHCROYHIP	CPYGAKAKAR	CPYQAKAKAR PBLALPHIKY	480
LATLINGIS	MILIVGISA VPNVOSKKIC IEMAGPPKRIN	TEXAGPPKIL	RXXDPISSR	RECEPT INTERPRETATION	LKHOMBKVKHK	940
KKHYKPSSH	KHYKPESHK LKVISKBMOT	STGATANHOT	BAVAITERDY	BAVAITENDY LEGETLIELO ISPETEMREV	TSPETSMREV	009
KADGASTPR	CADGASTPRL REGOCGEPAS PAASISALSG EQVDGXGQAG SVSRSARSEG RISPKSDITD	PAASISRLEG	EQVDGXQQAQ	SVBRSARSEC	RISPKSDITO	660

AUGUSTIAL VESESPESE KOSTSLAND BATTANAN SVESSAND TOLAGSHILA VESESPESE KOSTSLAND VEGTAKEOGG GENETT TOLAGSHILA VESESPESE KOSTSLAND VEGTAKEOGG GENETT SEQ. D. NO. 652 DNA sequence Nucleic Acid Accession, 5: NN\_014791.1 Coding sequence: 171.,2126

<sup>5</sup> Ξ. : 15

		:	;	<b>:</b>	;	<b>.</b>	
20	Tooccooco	-	CAACOOMO	) atmasaga	1	-	5
	OCCOCOTOTO	TCAGGACAGC	AGGCCCCTGT	CCTTCTGTCG	GGGGCCGCTC	AGCCGTGCCC	120
	TCCGCCCCTC	AGGITCITIT	TCTAATTCCA	AATAAACTTO	CAAGAGGACT	ATGAMGATT	180
	ATGATGAACT	TCTCAAATAT	TATGAATTAC	ATGAMACTAT	TOGGACAGGT	GOCTTICCAA	340
20	AGGTCAAACT	TOCCTOCCAT	ATCCTTACTO	GAGAGATOGT	AGCTATAAAA	ATCATGGATA	900
3	AAACCACT	ACCCACTCAT	TTGCCCCGGA	TCAAACOOA	GATTGAGGCC	TTGAAGAACC	360
	TGAGACATCA	<b>OCATATATOT</b>	CACTCTACC	ATOTOCTAGA	GACAGCCAAC	AAATATTCA	420
	TOGITCTICA	<b>GTACTGCCCT</b>	GGAGGAGAGG	TOTTTOACTA	TATAATTTCC	CAGGATCGCC	9
	TOTCAGAAGA	OGAGACCCOG	OTTOTOTIC	<b>OTCAGATAGT</b>	ATCTGCTGTT	<b>OCTTATOTIC</b>	540
,	ACAGCCAGGG	CTATOCTCAC	ACCORACCTICA	AGCCAGAAAA	THECTORE	DATBAATATC	909
2	ATAMATTAMA	CCTGATTGAC	TITOGECUCT	<b>OTTCCAMACC</b>	CAGGGTAC	AAGGATTACC	99
	ATCTACAGAC	ATCCTCTCOO	AGECTOOCTE	ATGCAGCACC	TGAGTTAATA	CAGGCAAT	120
	CATATCTT00	ATCAGAGGCA	GATOTTICGA	GCATGGGCAT	ACTUITATAT	GITCITATGE	780
	GTGGA TTTCT	ACCATTTGAT	CATGATAATG	TAATGGCTTT	ATACAGGAG	ATTATGAGAG	8
,	DAMATATOA	TOTTCCCAAB	TOCTOTO	CCAOTAGCAT	TCTGCTTCTT	CAACAAATGC	900
દ	TOCAGOTODA	CCCANADAM	COGATTTCTA	TOWNATCT	ATTGAACCAT	CCCTOGATCA	960
	TCCAGATTA	CAACTATOCT	отталотасс	AAAGCAAGAA	TCCTTTTATT	CACCTCGATG	1020
	ATGATTOCCT	MCACAACT	TCTGTACATC	ACAGAACAA	CAGGCAAACA	ATCCACCATT	1080
	TANTITICACT	<b>STGGCAGTAT</b>	GATCACCTCA	COCCTACCTA	TCTTCTGCTT	CTAGCCAAGA	1140
5	AGGCTCGGGG	MANACCAGTT	COTTIMBOC	TITCITCITI	CTCCTOTOGA	CARCCAGTO	1200
9	CTACCCCATT	CACAGACATC	MOTCHATA	ATTOGAGICT	COANCATOTO	ACCCCAAGTG	1260
	ATAMMATTA	TOTGGCGGGA	TTANTAGACT	ATGATTOOTG	TGAAGATGAT	TTATCACAG	1320
	<b>OTCCTOCTAC</b>	TOCCOCAACA	TCACAGITITA	CCAAGTACTO	GACAGAATCA	AATOGGGTGG	1380
	AATCTAAATC	ATTAACTCCA	<b>OCCTTATOCA</b>	GAACACCTGC	ANATANATTA	AAGAACAAG	1440
,	AMANTOTATA	TACTCCTAAG	TCTGCTGTAA	AGAATGAAGA	GTACTITATE	TTTCCTGAGC	1500
3	CUMBACTCC	AGTTAATAAG	AACCAGCATA	AGAGAGAMAT	ACTCACTACO	CCANATCGTT	1560
	ACACTACACC	CTCANAGCT	AGAMACCAGT	<b>GCCTGAAAGA</b>	MCTCCUATE	ANAATACCAD	1620
	TAMTTCAC	AGGNACAGAC	AUTTANTON	CAGOTOTCAT	TAGCCCTGAG	AGCOGTGCC	1680
	OCTCAOTOGA	ATTOGATOT	AACCMOCAC	ATATOGAGGA	GACTCCAAAA	AGAMAGOGAG	1740
9	CCAAAGTOTT	TOOGAGCCTT	DAAAGGGGGT	TOCATAGOT	TATCACTOTO	CTCACCAGGA	1800
2	DCANAGGAA	OCCUTATION	AGAGACGGGC	CCAGAAGACT	MANGCTTCAC	TATAATGTGA	1860
	CTACAACTAG	ATTAGEGAAT	CCAGATCAC	TOTTGAATGA	AATAATOTCT	ATTCTTCCAA	1920
	AGAAGCATGT	TOACTITIOTA	CAMAGGETT	ATACACTOM	STOTOMACA.	CAGTCAGATT	1980
	TTGGGALAGT	DACAATOCAA	TTTGAATTAG	AMOTOTOCCA	CCTTCAAAA	CCCGATGTGG	2040
22	TCGCTATCAG	GAGGGAGCG	CTTAAGGGCG	ATCCCTGGGT	TTACAAAAAA	TTAGTOGAAG	3100
S	ACATCCTATC	TAGCTGCAG	GTATAATTGA	TOGATTCTTC	CATCCTGCCG	DATCACTOR	3160
	COTOTOATAC	AGCCTACATA	AAGACTGTTA	Taktoochtz	CATTITANA	TTCATTOGAA	2220
	CANCOLACT	STATISTICAL SANS	AGCTATCTTA	AGACCIATAT	CICITIONIA	TAMACAMA	2280
	GATATTATT	TOTOTATORA	TCTAAATCAA	<b>GCCCATCTOT</b>	CATTATOTTA	CHORCETTE	2340
7	TAATCATOTO	GTTTTOTATA	TTATTATTO	TRACTICE	TABATTCACT	<b>TCCATATIOTO</b>	3600
3	AATGTAAGCT	CT-AACTATE	TCTCTTTCTA	ATOTOTAATT	TCTTTCTGAA	ATAMACCAT	2460
	TTOTOMATAT						

	_	_	_	_	_	_	
	MKDYDELLKY	INDYDELLINY YBLABTIOTO O	GPAKVKLACH	SPAKVKLACH ILIGEMVAIK IMDRAFLGSD LPRIKTEIEA	IMDIDITIOSD	LPRIKTRIBA	8
ç	LICHLRHOHIC	MULRICHIC OLYHVLETAN I	KI PWLBYCP	KIPWLEYCP GGELFDY118 GDRLSEETTR VVFRGIVSAV	<b>ODRLSZZETR</b>	VVFRQIVSAV	120
₹	AYVHEQOYAH	ROLKPENLLF	ROLKPENLLF DEYHILKLID FOLCAKPKON KOYHLQTCCO SLAYAAPELI	PULCAKPKIN	<b>FOYHLOTCCO</b>	SLAYAAPEL1	180
	<b>OCKBYLGSZA</b>	DVMSMQILLY	DESTLUSEA DVASHOILLY VLACOFLPPD DENVALYKK	DENVIOLYKK	IMRGKYDVPK	IMRGKYDVPK WLEPBSILLL	5
	<b>OOMLOVDPKK</b>	RIEMMONLLAN I	PWINCOYNYP	PHIMODYNYP VENOSIGNPPI	HLDDDCVTEL :	BVHHRNNRQT	300
	MEDLI BLAQY	DHLTATYLLL	LAKKARGKPV	RLRLÉSFECG QASATPPTDI	QASATPPTDI	KSNINBLEDV	360
,	TASDIDITIVAG		LIDYDWCEDD LETGAATPRI	SOPTKYWTES NGVESKELTP ALCRIPANKE	NGVESKELTP	ALCRIPANKL	<b>\$</b>
c	KINCENNYTPK			PEPKTPVNK NGHKREILTT PKRYTTPSKA RNOCLKSTPI	PRRYTTPSKA	RNOCLESTPI	9
	KIPWNBTOTD		KLATICVISPE RRCREVELDL NGARMEETPK RKGAKVFGBL	HOARMEETPK	RKGAKVPGBL	RRGLDKVITV	540
	LTRBKRKGSA		YMATTTREVIA	PDQLLMEINS ILPKKHVDPV QXGYTLXCQT	1 LPKKHVDPV	DXGYTLKCQT	909
	OSDPOKVTNO	PELEVCOLOR	PBLEVCOLOR POVVOTRROR LKCDAWYKR LVEDILBSCK V	LKGDAWYYR	LVEDILBSCK	^	

Seq ID NO: 654 DNA sequence Nucleic Acid Accession 6: NM\_000562 Coding sequence: 88..990 8

	9	120	
	THETCHOCCA	TIGCCTCCTA	
<b>4</b>	AGTTGCAGCC	TOATTTOCT	
<b>1</b> _	STCTCAGGCC	AGAATTOCAG TO	
<b>1</b> –	GACCAGACTC	CACTACCATO AG	
<b>1</b> _	OCATOOTOO	AAGGAAAACT	
<b></b>	GCAGAGCACA	MCGCCGACC	
85			

					,	
	WO 02/086443					
	GOCATCACCT OTOCCATACC	: AGTTANACAG	OCTGATTCTO	GANGTICTGA	GOLANAGCAG	180
	CTTTACAACA AATACCCAGA	TOCTOTOGCC	ACATOOCTAA	ACCCTGACCC	ATCTCAGAAG	200
	CAGAATCTCC TAGCCCCACA	A GACCCTTCCA	AGTAAGTCCA	ACGMAAGCCA	TOACCACATO	300
•	GATGATATGG ATGATGAAGA	A TOATOATOAC	CATOTOGACA	<b>GCCAGGACTC</b>	CATTGACTCO	360
^	AACOACTCTO ATGATOTAGA	1 TGACACTGAT	GATTCTCACC	AGTCTGATGA	91CTCACCAT	<b>4</b> 20
	TCTGATGAAT CTGATGAACT	I DOTCACTOAT	THEORYGOO	ACCTGCCAGC	ACCOMPT	480
	TTCACTCCAG TTGTCCCCAC	: AGTAGACACA	TATOATOOCC	GAGGTCATAG	TATTOOTOT	510
	GGACTGAGGT CANATCTAA	A DANGTITICOC	AGACCTGACA	TOCAGTACCC	TOATOCTACA	909
•	GACGAGGACA TCACCTCACA	A CATGGAAAGC	GAGGAGTTGA	ATOGTOCATA	CAGGCCATC	9
2	CCCGTTGCCC AGGACCTGAA	A COCOCCTTCT	DATTOODACA	OCCUTODOM	GOACAOTTAT	720
	GAAACGAGTC AGCTGGATGA	CCAGAGTGCT	<b>DAMACCCACA</b>	GCCACAAGCA	STCCAGATTA	780
	TATAAGCGGA AAGCCAATGA	1 TOAGAGCAAT	GAGCATTCCC	ATOTOM	TAGTCAGGIA	000
	CTTTCCAMO TCAGCCOTGA	ATTCCACAGC	CATOMATTIC	ACAGCCATGA	AGATATOCTO	006
:	GTTGTABACC CCAAAAGTAA	A GGAAGAAGAT	AMCACCTOA	AATTTCOTTAT	TTCTCATGAA	96
_	TTAGATAGIC CATCITCIGA	A GOTCAATTAA	AAGGAGAAA	AATACAATTT	20000000	1020
	ATTTAGTCAN ANGANAMAT	I DCTTTATAGE	AAAATGAAAG	AGAACATGAA	ATOCITICATA	1080
	CTCAGTTTAT TCGTTGAATG	TOTATCTATT	TOAGTCTOGA	AATAACTAAT	STOTTTON	1140
	ATTAGETETAG TETFOTGGCET	CATGONAACT	CCCTGTAMC	TAMAGCTTC	AGGGTTATGT	1200
	CTATGITCAT ICTATAGAAG	2 AAATGCAAAC	TATCACTOTA	TTANATATT	TOTTATICE	1260
2	TCATGAATAG AAATTTATGT	T AGANGCAMC	AMMTACTET	TACCCACTTA	AAAAAAAAT	1320
	ATAACATTTT ATGTCACTAT	-	TITITAAGTI	AGTGTATATT	TACTION	1380
	TAICTITITE TEGISTERAL	P. AMATCHITTA	TCTTGAATOT	AATAAGAATT	TOGTCOTOTC	1440
	AATTGCTTAT TIGITITICCC	: ACCONTICATOR	ACCUATTANT	AVACATAAC	CITITITACI	1500
2	GCCTAAAAA AAAAAAAA	1 AAAA	٠.			
3	4					

# Seq ID NO: 655 Protein sequence Protein Accession N: NP\_000573

	8	2	180	260	
15 —	KONLLAPOTL	HEDEEDELVT	TORDITSHME	LYKRKANDES	KLOSABSBVN
<b>=</b> _	QLYNKYPDAV ATMLAPDPSQ N	DOSHOSDESH I	RRPDIQYPDA 1	PETSQLODGS ASTRSHKQSR I	LVVDPKSKEB DKHLKFRISH SLOSASSBV
<b>=</b>	<b>QLYNKYPDAV</b>	STEEDSOOVED I	YOLRSKSKKP 1	YETSQLODGE	LVVDPKSKER
<b>1</b> -	QADSGBBEEK (	DHVDSQDSTD 6	TYDGRGDSVV	BOYDSRONDS	SHEPHSHEDM I
<b>=</b> _	LGITCAIPVE	MODIMODEDDD	VPTPVVPTVD	IPVACOLNAP	<b>ELSKVSRBPH</b>
	MRIAVICECL L	PSKENBSHDH	DEPTOLPATE	SEBLAGAYKA	OSCILACENTOSO
30				;	સ

### 7. 656 DWA seguence Sac ID NO.

		==		<b>1</b> -	<b>7</b> _	15 -	
4	OGGOTOGGAG	OCCCYCCCC	ACCTCCOCAC	androcovoc	00CCC000TT	валасатсся	9
2	COCOLAGO	TOCACACOCA	GCAGGGCGGAA	TTCATGGCTT	AAGCCCAGG	OCCUTGOC	3 3
	CAGAGCGACC	CAGACTOOTO	CAAGACGGCG	TOGGGCCACA	TCAAGCGGCC	GATGAACGC	~
:	AACGCCGAGA	TCTCCAAGAG	CCTGGGCAAG	COCTOONAL	TOCTOMAGGA	CAGCCAGAAG	2 %
ည	ATCCCGTTCA	Teccodage	GOAGCOGCTO	COGCITCAAGC	ACATGGCCGA	CTACCCCGAC	\$
	TACAAGTACC	OCCCCCCCAA	AAAGCCCAAA	ATOGACCCCT	COOCCANGCC	CAGCGCCAGC	\$
	CAGAGCCCAG	AGMAGAGCGC	0000000000	OCCOCCOCCOCA A A A TO COCCOCA	000000000000000000000000000000000000000	Addododdd	Z 6
;	00000000	AGGGGGGG	GOCCAGOCO	GCCAGTCCO	COCACTACGO	200000000000000000000000000000000000000	3
25	GACGACTACG	TOCTOGGCAG	cerdescore	AGCGGCTCGG	deadcodcad	COCCOOCIAG	Ę
	ACCCTCAAGT	<b>acordinates</b>	<b><i>GCATGAGGAC</i></b>	GACGACGACG	ACCACCACCA	COACOAGCTO	2
	CAGCTGCAGA	TCANACAGGA	accadacoad	GAGGACGAGG	MCCACCOCA	CCAGCAGCTC	2
	CTGCAGCCGC	COOCCACCA	accorcocka	CTOCTGAGAC	GCTACAACGT	caccuaata	2 3
Ş	CCCGCCAGCC	CTACGCTGAG	CAGCTCCCC	CAGTCCCCC	AGGGAGGAG	CCTCTACCAC	2 3
3	ANGARCATCA	CCASCACAC			STOREST OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PAR	arrest of the second	100
	TODOOCTOO	TOTOCACCTC	CTCGTCCAGC	AGCAGCOGCA	GCAGCAGOGG	CAGCAGCGGC	ä
	GAOGACGCCG	ACGACCTGAT	GTTCCACCTO	ADCTTOMATT	TCTCTCAAA	COCOCACAGC	120
Ų	GCCAGCGAGC	AGCAGCTGGG	0000000000	GCGGCCGGGA	ACCTUTOCCT	orcactaata	126
3	GATAAGGATT	TOGATTCOTT	CAGCGAGGGC	AOCCTOCOCT	CCCACTTCGA	OFFICECCAAC	3
	GACCIGOTOT	TCACATATTO	AAAGGCGCC	OCTOCTOCT	CHICAGO	GAGGETGCAG	3
	AGCTGGGTTC	CTTOGGAGGA	AGTTOTAGTO	GTGATGATGA	TOATGATGAT	AATGATGATG	250
ç	ATGATGGTGG	TOTTGATGGT	COCCOCTGOTA	GOGTOGAGGG	GAGAGAAGAA	CATOCTOATO	156
2	ATATTGATAA	ANTOTOTICA	COCANGAA	TTGGAAACA	TGATGAAAT	TTTCGTGGAG	25
	TOTTTATO	TOTOTOTOTO	TAGTTGCATA	CCTAGECTOR	AGTTOTOATT	ATTTTCCCAA	17
	MAATOTOTT	TITOTATIA	CTATTICETT	TTCCTCAAAT	TOSTOATTOC	AACAAAGGCA	180
į	DADGGGGGGG	CGCCGCCGAG	<b>OCCARGOTAGG</b>	ACCCOCTCCO	GAAGGCCCTG	TITIONAGETT	ä
c	OTCOOTCTT.	GAACTCTGGA	AGACGICTGC	NONDONCCCT	TTTGGCAGCA	COACTOTTAC	193
	TCTAGGGAGT	TOGTOGAGAT	ATTITUTE	CTTMGAGA	CTTANAGAAC	TOOTCATTIT	198
	****	Moderate					

## Beg ID NO: 657 Protein sequence Protein Accession #: NP\_003099.1 8

	KVWB 6(	_	CAKA 180	LO1K 240
<b>1</b> 8 –	RPHONAP	ADYPOY.	KAPAAAGA	DDDETG
<b>\$</b> _	WCKTASORIK	EAERLRLED	KOBBICKCOKE IO	PLOEDDDDDDD
	TEEDEFMACS PVALDESDED WCKTASCHIK RPMNAPWVM:	CALCICANOS. KOSEKIPPIR EAERLRIKUM ADYPOYKYRP	BAAGGGGSA GGGAGGAKTS K	GGAGKTVKCV
<b>#</b> _	TERGENACS	KALGKRYTOK	BAAGGGGGBA	<b>OSLRVSCSOO</b>
=-	WOOABSLEA ESNLPREALD	N SPONGWAEIS K	KPSABOSPEK	INGKAAQSOD YGOKODOYVL OSLKVEGBOO GOADKTVKCV FLORODODDD DDDRLQLQIK
	MVQQAESLEA	KIERRKIMED	RKKPKMDPSA KPSASQSPR	<b>GAGKAAQSGD</b>
	į	S		

Seq ID NO: 653 Protein sequence Protein Accession 8: NP\_055606,1

	WO 02/ OEPDREDERP ATSGAGGGR	086443 PHOQLLOPPC LYYSPIDATT	OOPBQLLRRY OHPPPLAQPA	OOPBOLLERY MVAXVPASPT I	SSSATSPEC	AGLYDEVRAD	300	PCT/US02/12	Ź
S	LEENIAGONL	KANFEDLVFT	Y	BLEEVUNGE	Kercerosa	PEPPOTCTPE	9		
	Seq 10 DO: 658 DNA Nucleic Acid Access Coding sequence: 12		sequence on #1 NM 001719	719					
0		=-	- 22	<b>=</b> -	<b>4</b> -	<b>8</b> –			
	GOGCOCAGCO	GOCCOTCT	GCAGCAAGTG	ACCOACOGC	GOTACCCCT	CCTGCCCCCT	120		
S	CCCTOTTCCT	deserteners dendeserte	CCAGCTGCGG	ACTTCAGCCT	CTTCGTGGGG	CTCTGGGCAC	180 240		
	CCATTITIOGO CCATTITIOGO CCATTITIOGO	CTTGCCCCAC	COCCOCOCC	AGCACCTCCA CGCACCTCCA Traccognega	GOCCAGCAC GOCCAGCAC	AACTCGGCAC	360		
0	OCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC		CCTCTGGCCA	180		
	TTTCCAGAT	CCCAGAAGGO	TTCCACCCAC	GCTACCACCA		CONTITUATO	0 09	·	
	ACATCCOOGA AGCACTTOGG	ACCCTTCCAC	AATGAGACGT	TCCGGATCAG TGCTCGACAG	COTTTATCAG	OTOCTCCAGG TOGGCCTCGG	720 780		
^	AGGACAGCTG	acrocracra agaccracAo	GACATCACAG	CCACCAGCAA	CCACTGGGTG	OTCAATCCGC ATCAACCCCA	9 0 0		
	TCTTCAAGG	CACCOLATICO	CACTTCCGCA	GCACACAA	CACGGGGGTTC	AACAGCGCA	1020	!	
o	AGAACAGCAG	CAGCGACCAG	AGGCAGGCCT	GTAAGAAGCA GTAAGAAGCA	CONGCIGIAL	OTCA OCTTOC	1140		
	AGGGGAGTG			ACATGAACGC	CACCAACCAC	GCCATCGTGC	126		
v	AGCTCAATGC	CATCHCOOTC		ATGACAGCTC	CACCICATO	CTGAAGAAT	963		
,	TTOGGGCCAA	CTTTTCCCC				AGCAGACCA	1500		
	MACATOAGC	TCAGACCTTC AGCATATOGC		TTTTCAGTO	AAAGGTGTGA GCAGCATCCA	GAGTATTAGG	1560 1620		
Q	DECCORCEAGE	OTCATTOOCT	AAACCTABCA		ACAGGGATA	AAGAAAATG CCAGAGGTAA.	1680		
,	TTATGAGGGC	CTACCAGCCA	GOCCACCCAG	COGTGGGAGG		GGCAAGGGGT	1800		
	CANTAMACO	AATUAATO							
δ	Seq ID NO: Protein Ac	O: 659 Protein Accession #: N	in sequence						
		=-	12	<b>1</b> -	<b>\$</b> -	51			
0	HONRELRANA	PHSPVALMAN	LPLLRSALAD	REDNEVHSS	PIHERLEGO	RREMORBILS	2		
	LQDSHPLTDA 18 FUTURE	HLQUKKONSAR DMVKBPVNLV P19VYNVA	CHOKEFEIPE	THREPRPOL	BKIPEGEAVT FORMATERITA	AAEPRIYKOY TENNENNYOO	180		
50	HNLGLOLSVB ONRSKTPICKO GECAPPLINSY	TLDOOSINPR EALRHANVAE MRATHRAIVO	LAGLICARGE MBESDQRQAC TLVHFINPST	JHKOP PHVAP KKHEL YVSPR JPKPCCAPTO	PKATEVHPRS DLGWQDWIIA LWAISVLYPO	IRSTGBKORS PEGTANYCE DSENVILKKY	\$20 \$20 \$20		
	RINKWRACGC	,							
Q	Seq ID NO: 660 DI Nucleic Acid Acces Coding sequence: 3	660 DNA set id Accession	DNA sequence cossion #: Eos se s: 2111895	ectrence		•			
		11-	ñ~	<b>a</b> _	5-	<b>5</b> -			
5	GOATCTOAGG GOOGCTTGGG	DOCCCCAGE	chertectee	ACOTTICATED CETATECACE	CACAGGITTT	AGGAGCGAT	60		
	CACCAATTAT	CCCTCGAAAA	TOACCTETE	ATATTTTAA	AAACGGAGAG	TTTTAMAA	180 240		
0	CACAGOTTCC	TTGAACAGCT	DGATTCTACO	ATMATGMA	CTATAGAGGA	AAGAAAAGG	360		
	CTTOTOCTOA	AAGCGAAAGT	ACMATOTOM ATGGGATGGA	CTCAACATCA	CAGCTCAACT	CCAGGAGGGA	420		
ų	AMATATOSS	CTOTTCCATO	CCCTCCTTAT	ATTTATCACT	TCACCATAA ACACCTTAAA	AGGAGTTGCT	540		
n	TICTITAME	CAGACTOCCT GCCTCTATOT	AATGTATACC	CAGCCAGATA	CCATCTCTT	TOTTCCTTO	120		
	CACATOCACT	TATTTOTOTC	TTCATOCTO	AGACCTACAA	OCATCTTOT	CANGACAGA	840		
0	CAMATTOCA	TOWOGCIAC	TICTOTOGAC	MATCACAT	ATATOGOTO	CAGATTOCT	960		
	TACCTOCATA	ATCTCATCT	TOTOGCTTTC	TTTCGGACA	CCAAATACCT	OTOGOGCTTC OTOGOGCTTC	0801		
2	ACTICTOOCTIC	ATGCGAGGTG	CTGGGAACTT	AGTGCTGGAG	ACATCAAGTG	CATTACA	1200		
,	CTABCTACCA	AATCGACACT	GACCAATGCA	оттороскто стаотстто	ACACMAGAA	CATCOTOTTC	1320	_	

11 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		200000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1000 1100 1200 1200	11111111111111111111111111111111111111	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	60 120 240
CTUTGAGGC CHATGGAGA CTGALANAG GALAGGAC CTGAGGAC CTGAGGAGA CCCAAACACT	S1  LULKAKVOCE  INULKAKVOCE  AVALITIOY  ONSIEATSVD  ILLIGMATPRA  ILLIGMATPRA  ILLIGMATPRA  SSCOONAST  OCODILMENS		S1 MATTINGTO COTCONDET TOTOCONTA COCCATAC	TTTATACATT ATTTATACA ACCAATAT TTGGCTACTC GACGATTGCA GACGATTGCA GACGATTGCA TTGGATTGCA ACCATTGCA ACCAATACA TTGGATTGCA TTGGA	TTCGGACAC TTGTTGCAGC GTGCTGGAGA TTATCTGTT TTGGGCATGA TAGTCTTTGG		TMINATAGT ANGIGTECALT TATGOSTATT CANTEGETG ANGIGTATC CENTECETG GANGATANA ANTATTCAC ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTANTOCAT ANTOCAT ANTANTOCAT ANTANTOC	CTTTTCTO	81   IITAQLQEGB PPHBLMKTWA RLHCTRHYIH BQYIGCKIAV
TCCCATCCA ACTICCTACTO ACTICCTACA CCACCATCACA TTATCTCTOCA CTOCCTATATATATATATATATATATATATATATATATAT	41 GTITIEDIV TYDINHKOVA VOYBIBYDBL PBETKTLAD PBETKTLAD PILFLATVRV GWEIRMEGEL SVLTTVTHBT		TACTOGOCAC TACTOGOCAC TOCTCCACO TOCTCCACO	THEORYTOCK CCTCCTTATA GUACATOCK ATTATACK OFTACTTCA TTCATOCKTA STANGOCK	OTOGCTTTCT CCAGCAGCAT TOGGAACTTA GOOCTGAATT ACCAATGCAG OTCCTGGTCC	ACTOGOCTCO TECHTIONS ANDTOGOCT ANDTOGOCT GCCAGCACA GCCAGCACA GACAGCCACA GACAGCCACA GACAGCCACA GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCCT GACAGCT GACAGCT TOTOGOCACA	AGETOTTACT ATGANATOC TAMITAMIO TAMITAMIO AMANGATT TAMITATATO TAMITATATO AMATATATO ACCTOMANAC CCCAMANAC	ACTICACTES ACTICACTES CONTINUATES	41   Vlkakvocel Rhcyphotyd Vailiotyr Nbieatbydk
GOOTGOMAN TCTATCATT CONTROLAT TCMATCTEA TCMATCTEA ATCATTAC CACAGGGCTA CTCTAA	11   HRFLEQLOSD   HRRLEQLOSD   PERLYWYT   VYHAHIGVE   YTHNLIFANE   VCLAHIGVE	8048	11 10CCCDTCOT TCTCCCDGC GCTGGGGCG AGCCCAGCTG	TOTOCOURA TOTOCOURA CCTCTATOTA TCTCATCAT TCTCATCAT TCACATAGOA	CCCATCTTT CCCAGGGTTT TGCGAGGTATT AGCAGCTATT AATCTGGAGG	TCACTCCTTC CTTTCAGGT GOTGAAAA TGGCGCCCC ACAGAGCCC CTGCCTGCCC CTGCCTGCCAAT ATTCTAATG AGAGAAACT ATTGGAAACT ATTGGAAACT	AATTCAGTTA TACTAACGAC AATTTGGGTAG AAATATAATG GAATCTAACT GAATCTAACT AATTGGCTGG	AATCHOOTH AATCHOOTH OTGGGATCAA	11 TITIERIUL YDFNHKOVAF GYBISPGELA GYBISPGELA ESLIMODOPO
CACTOGOCTC CACTOGOCTC CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG CACATOGOAG	21 INESISERE LICAPROTVO OPDISIONOS RATSIFYZOR HYPAILLYPOZY GADDIXNIYO LIVEGYNYIV RMIJSYDNOS LITLGOTVWSN	uence #: NM_00 795	21 	MAINTERS CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CO	ACCTGCATA CTCTGGTGG CTCTGGCTG CACCGATCT TAGCTACCA	TATACCTACT TETCAACT TETCAACT TETCAACTAT OCACCOCTAT OCAC	MAGGETGA CTCCTGTAAA ATTGGCATCA ATATCCCTT TALTCCTTA GGAGCAATTA CTGGAAAAATT	OCCUTATION OTGONANAT TATANTAGE TACATOGEAT In sequence The sequence	21 Laraqlosdo Igavpcppyi Perlywyty Vhahiqvkel
086443 creatrent creatrent adoration drocation drocation charter Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration Adoration A	11 VLPLPSPBT AVEDCRFL AVEDCRFL AVEDCRFL AVEDCRFL AVEDCRFL AVAGETURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA KLAKGTURA K	662 DNA e 1 Accessio snce: 143.	11 	ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAGEMICA A ACAG	GAAGTETET TOOGGETTEA GEACGAGEAA ATTTATEAAG GTTAGAGTTE CAATACAGGA	ATCOTOTTCO ATCOTOTTCO ATCOACACA ATCOACACACA CACACACACA CACACACACA CACACACA	ACTORATICO ATTACCTTCT TOTTCATTT TCTCTCATAT TAGMACTAO CCTOTOCATA TAGMACTAO CCTOTOCATA TAGMACTAO CCTOTOCATA TAGMACTAO CCTOTOCATA TAGMACTAO TAGMACTAO TAGMACTAO	ACCATOTICAT TIGITAATOTA TACTACATO TACTACATO 661 Protes 683 Protes	11 
WO 02/ OTATOACTO TTCTOACTO OTTOACCAT AGANCECAT AGANCECAT AGANCECAT AGANCECAT CACADAAN GANCEATO CACADAAN GANCEATO CACADAAN GANCEATO CACADAAN GANCEATO CACADAAN GANCEATO CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAAN CACADAA	1   HLRBSLETS!   HLRBSLETS!   DPHSTRACTENT!   RRLHCTENT!   PVAMMANAN   VGHDTRRQTH   VGHDTRRQTH   RHTLCCAGE   RHTLCCAGE   RHTLCCAGE   RHTLCCAGE   RHTLLSCAGE   RHTLLSCAGE   RHTLLSCAGE   RHTLLSCAGE   RHTLLSCAGE   RHTLLSCAGE	Bed ID NO: Nucleic Acto Coding seque	OGCCUTAGC TOTACCTACA TOTACCTACA GCTAATGCTC TATACAGGGAG	GCCGAGGG GCCGAGGGA GCCGAGGGA GCCTTANT CACCTTTT TTCCACTAGG CATCTTTTTTTTTTTTTC	CAMTACCTO ATGGGCTGTG CATCAGTGG CATCAGTGG TCTGAATACG CACAAGGAAG	AGTGCATTAC CCCCATGCAC CTGCTACTGG CTCCTGGGAC CACCGTGAC TATCTCTGG CAAGGAGAT GGAATCTAAC CAAGGAGAT	ATACTECTAT TITTAGGCTE GGAGTAGTTT GCTGTGGTT GCTGTAGCTT ATTACTTTG ATTACTTTG ATTACTTTG ATTACTTG ATTACTTG ATTACTTG ATTACTTG ATTACTAGAN	ACATICATORA TICATIONA TICATORA TITICAGE T T Beg ID NO: Protein Acc	1 HAGLGASLHV GNCPPEMDGL NYSDCLRFLQ MELPVSFNLR
\$ 10	15 20 25	30	35	45	20	55	65 07	27 80	88

PCT/US02/12476

			*											
00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		120	50000	120000	960 1020 1140		120 120 240 300		9778	29299	720 860 960 1020	1080 11200 11200 11360 1140	1500 1560 1660 1740	1980 1980 2040 2100
VAAMAVARAT GHDTRQYRK IIYCYCHGEV MVLISGRAAK RPMESIVEDTE	٠		CCCCTTCTAC TOTATTCCTG TCTCCOTCAG CGCCOTCAG GAGGGTGACA	TOTOGRADIA TOTOGRADIA TOTOTTAGO CCTCAACTOC	CCCTCCACA CCCCTCCACA CCCAAGTTGCA GGTCATTGACT		S1 VIAAVIMURK SBLTASLTNL CNISACSSLA RRTPNKLACT 11YSYKDEDM STS		51 TOCOGOSCCC COCCTGOOC CCGCCTGOOC ACCCAGACAO ACCCAGACAO	ACTGACANA ACTGACANA CCTOTACTCC CTTCATTCCC	COGCCACCTO CACCTTOCA GTGCTGCAC TTCTCAGCCC AACCGCAGG	TTTTAAGCCAC GOTCTGCCAG MAGGTCTACC OTCTACACCT GTGGCCACTG	AACCAGATGC ATCACAGCG GGCAGCATCG CCCCAGCCAC GGCCAGAGAGA	ACCTEGIAN
Ligmoppaap atkimetmav Pnspodpivs Sosqvaastr Godilmerps		41   CAATGAATGA ATACTOTGGA TCTGCCTGTT	AATTCATT GAATTGCTA ACCGCTGGTT TGCTGGTTAT TGACCAAAA	CCCCCATTA TCATCATGOT TOTCTCCGCA COOTOATGAC TCCTCCACGO	TOCTOGOST TOTATOGOS CCTCTCCON ATAGTATING GGCCACCCA		41 CLPIFFENGL RMFLRQGLLD AVPTLGRNCL BPHTSGSISR LALLHSVNN BISGGAVCNK		41 COOCTACTOC GROGORATIC OCTOGORATIC OCTOGORATIC OCAGGGGGT	CCTGAGCTTT GGATGATGTC TGAGGCAGT CCAGGTGACA AGATGGGACC	CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACTG	GOGGCAGAGO CATGCGGCAA TCCCCCAAG CACCCATGC TGATGCTGGT GAACATCACT GAACATCACT	CTOSTACASA GACCTTGGG CACCCCAGG CACACCAGGA TTCAGCCAGA TTCAGCCAGA TTCAGCCAGA	CCAGAATGGC CCAGAATGGC CCAGAATGGC
edtkylmopi Ilplatyrku Weirynickl Vletvyhstb Retkedsgro	2152	31 	MANACAGA TTCTTCGCTG TTCACCACT CTCACCACT CATAGCACC	ATGGCCTCC ACCACGTCT CTAATGAAGA GTGGTTCTGC	TOUTTICETOR GACGAGGACA GAGAGGCGTC TACATAGAGG GATGCCTCTC	·	11   I   U   U   UVLCVGTEP   UVMATATEN   VOHVKRMPLL   SOTGSQYIED	<b>:</b>	31 dereceaera conceaaera recaceraera receceeraeraeraeraeraeraeraeraeraeraeraeraera	AGGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCCACAGAC	AGGAGGGAA GCGCCACAG ATGAAAGCTT AGGCCATGTT AGGATGAGAC	AGATTAGOS AGATTGAAS TOCOGOTACO TTOCTGAAG GACAGATGT GCCAGATGT	CTACAGTTOT TCAMGAATGO GTATGAGCAG AGCTCAMGTT CGGTGCCCTG	GIGGECATGI GACTOTOTA COCTUNITICA TGCACATCIT
LHNLI PVAFP PILAAIGLNP CLPHSPTGLG PPCGSRCGS EGDCL PHSPH	sequence on:#: NM_012	21 	GGCAGTGATC TGCTGCCGAT TTCAAAACT GACTGCTTCC GATGCGGGTC	CTCTOCCTOC OTCCAACCTC CAAGAGGAAA ACCCATGAAG	TOTOMANOO CTCCTACAG GGAGAACCA AGGCAGCCAG CTAAACTCTG	ein sequence NP_036284	11 TODWIGHEL TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAT TREAVILLE TREAVILLE TREAVILLE TREAVILLE TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TREAT TRE	quence 1 11 134_002821 3362.	21 		OTCAGCAGCA TATTCCTGCT AGCATTGCTG AGCATTGCTG TGGCTCTTTG GCCACACGTGT	ATCTACCCCT CACCTAGGA GAGGACCTC CACCCGGGGAC TTGGCCATA GOTCAGCGA CACCCACACA CCCCAAGACA CCCCCAAGACA CCCCAAGACA CCCCCAAGACA CCCCCAACACACAC	ACACCAMAC TTCGAGGTCT TOGTACCGIT GTOCTGGAAA AAGAGGCCA CAGGCGAATG	GCCGGGGTA GGCCAGATTC CCAGAGCTTA GACCCCAGG
YOA VFV SNS	A DNA B Accessio	ACTITICIA MCTITITI	TOGTCATCGC CTAATTTAGC CAGGCCAGT ACAGTAGCTT CAATCATGAG	TCTGACAGT TCTGACAGT ACGTGTACGT GCCGGAGGAC TATGCTGGAC	CCNTCATCTA CCTTCTCTCA CCTTCTCTCA CCACTCATCA CCACTCACACACA	665 Prot Seeson #1	554545	No. 666 DNA seq Acid Accession sequence: 1503	11 TCGGGACGCC GCGTCCGCCT TTTCCCGAG GCCTCCCGAG GCCTCGCGCGCAGGAG	CACGGAGCG GGACTCTGC TGCCAACGC AGCTCGGAA	CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGCG GAGCCTGCAGA	CAATGCAGGG AGCCACACTT AGCTOGCAGC GTGGTOGGAG CGAGCTGGTTG CAACCTGGCT	GACCCAGGC GGACTCACG TGATGGGACA CCOTGTCCAA GGAGTTTGAC TAAGTGGGAA	CCTGCATTT CGGGCGCAG CAAAGTGGAA GGCCCAGGGG CACCAAGCTG
WO 02/086443 whetpelan typical addressed additive lakefivulu vychhty dogwych miscop additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dogwych typical additive dog	Seq ID NO: 6( Nucleic Acid A Coding sequence	CTTCTTTAAA	TCTAATTCTC TACCTOTTGG ATGTTTACA GGGCTTCTGG AGGCACATGT	TACCTIOTH CTGCSANTC TCATCAGC GCTTTTTTT	ATCATCTOCT OTCCTCACCA OTCCTCACCA OTCTTAGO	Beg 10 NO: Protein Acc		Bag ID No. 6 Mucleic Acid Coding sequen	AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGGTT CCCTCAGCTCC	CTOTCCAGA ACCGCCTCCA AAGCCCCCAG TGAAGCATCC ACATTGATGG	ATGOTCABAG GTCCTGAGGA GCAGCCAGAA CCCAGGAGGT AGCCACCCC	TCATCCAGA OCOTOTTAC AGCCCAGGA AGCCCAGGA AGAACGGCA GCCACGGCA TGCCCCCG	TOALTIGET TEATETENAN TOALGATOTA AGGCGENGE AGCCACTAT	ACCCTOGRAC TTATCACCTT TTATCACCTT TGCAGTGGGA TCCTGGACCC
~	0	S	0	8	0	S	0 %	-	, v,	0	ν,		0	۶2

	2280	9 5	0 0 0	90	1760	2880	000	. 000	1180	200	1360	1420	1540	009	200	9780	900	0961	020	97				9	120	. 250	300	2 2	540	9	720	780	200	960					3 6	180	200	360	9	009	099	9 2	840	096	0801	1140	1360
MCAGCTGCA			_		AGGATTTCCA		OCCTGGGCC							COCCIOCOAC					AGGAGGGTGG				18-	LACEVEAPOP	EARSANASTN	PODVVVARYE	VRPRNAGIYR	VPSICLKXPQD	VEVYDOTWYR	PITFKVEPER	AVAYLLAVL	GLGSGPAATN	KSKUEKLKSO	Lektovynsey				<b>1</b> -	TCTTTTTAT								ATTTACTOGC				
CATTGCAGGC	CATTOGGTTO	AGAAGAAGTG	CAGTCAGTTT	CACCACTTO	GENOTECCTO	CMGCAGMG	GAAGGTOTCT	CCAGGCCT00	GATGCCCAT	TAGACTTCCT	CACCOTGGAC	CATCTCTAGA	CTCACCCTCA	TOGGCAGTIT	ACTITION	TTCTCAGTT	CTGACCCAGA	GATGAAGGAG	CCTOGAGATI	1101111011			<b>=</b> -	CONTOGREAL	CVARDDVTGB	DESPARVILA	PANGSLLLTO	RODVIITVAT	PICACTLRING TVPCSATGRE	RAINGLTVAV	HIGH INTERNATION	AEIGEEVALT	GUARTLVLVK GDLKQFLR18	ORQVICYSALG THGENPHOOQ	LODSTVDSKP			<b>7</b> _	ACTURECTOC	CITATICAL	CCTACCAGTC	TTCAGTTTTT	ACTICATIAT	TAGCAMGET	TATTTOCALA	GCCTTATCCA	GATACTTOAC	TOGAATOCTT	TOATTOATTO	TTTTTATCAT	TCATGGCTAT
OCTACACCTO TOSTOGACAA	DOCTONION	CAGAGATECA	COCTOGODAA	TOCACTICCO	TOCHGGGGCT	CCCTCAGCAC	ACAGACAAGT	ACCACTTCCG	CACATGGAGA	AGGRETACTO	TOGRACAG	CAGGOGAGGA	CCTCCTCTC	GGCTTTGAGC	CTCATCTGCC	TTCCTTAATA	CTTOTOCACA	отосстваел	TATOCACCAC	COLTACATOR			<b>1</b> -	ATVPIKOPSE	DRLQDSGTFO	BEONFILBIA	RPPHLRRATV	CHANTAGOR	LIBEDGRFEV	IA SNGPQGQI	ILOPTKIGPR BOPGSPPPYK	BEDNOTED	PLAKAGGLEE HYNVLEYYDL	LAARNCLVBA	RPEPSELASA	epuanbes		a-	AAAACCTOTC	ATAGGATTGC	DOMACADATA	CTCTCTOTTC	ATTOOTOOCC	ATTCTTOOM	GACGCTTGGG	AGTOOTCC	GCTACATOTO	ACATACCCTA	AATCHTCA? OTOTCATTOC	ACTCCCCTCA	TTTGGATTCG
GACTCAGGCC	CCCTACAAGA	CAGCCCTCAG	CCCATCACCA	CAGCAGCAGC	OTOGATCTCC OTOGATCTCC	AAGTCACAGC	of character	AGTGAGTACT	GAAGTGTTTA	CONTINUENCE	accyacaccc	ATGCCCTGG	CCTOOCCTT	GGGCGACTAG	MCTCTGCCA	TTOTOGGGAG	CCACTCTOO	CTCATCCTAA	CATOGGAGGE	TTATTOTTOT	T Semistre	19 002812	17-	Librigator	OCSSLSTAAV	CABBAPGOAC	EDSTP! TNR8	IAEBDAGVYT	PTVVNYRNON KLKPTDPPOD	TREDAGNYTC	PLIQMEGROR VVDKPVPBBB	GEEPEMECLN	LICKBERGEV	LENNR PVH KD GD P ST K SD V M	QRCWAL8PXD	sequence ion N: Eos se	•	<b>z</b> –	GCTGTCATC	ATCTOGTATA	OCCUPATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	GIATCIGCIC	AAACOTOTTT	ACACTOR	AAAACAGAA	CACAGTAGCT	TATATTETT	TOTCATTTO	AGCCACGCTT	acterorace	COTOATGOTT
086443 овессетомо словаловес	CAGCCCTCCC	GCAGAACGGG	TAGCCTOCAG	GACCATOR	CCACCICCAC	TOAMAATTO	TAACTGCCTG	TOTOTACAAC	CCTGATGTGG	ACTACTOGGA	CACTCACATT	CCCCCCCCAGG	CTGAGCAGO	GACCCAAACT			TOMOTOCTOC	CTCTCCTTTC	TATATAAACC	CCCCACACTT	667 Protes		11-	PREL'DLLAVI.		UNITABLASI OPERSOLYBC	ATMOTE AAAD	OKCHREVLAN	LOCITOATPK	NACTURFARY	NINHTEAPLY NINHTEAPLY	KAKRLOKOPE	PPRESLAPIT	CTOVALCHEH	GCPSKLYRLM	≨Ĩ.	•	<b>1</b> _	AGAGGCAGGA CTGAACATGA	CGATTATAGG	TOGGAATATT	OCTTCCA00	TTAATCCTGA	CINCAGGITT	CACACATACC	TAGANGNACC	TATTATCTO	ATGGTGTCAC	COATOTOT	TCAATOOTOT	Tracroctor
WO 02/0 recardacar acaremaca	Адаассства	GAGGGCCTTT	TCCCACGOTC	OCCTO CAGAC	ACTACATGOT ACTACATGOT	AGAGCAAGGA	TOGCTOCOCO	TCAGCAAGGA	CCTTCOOTOT	CAGATGATGA	GOCCCTCCTT	GAGGAGGGAG	TTGCTGAGGT	OCCTCACTTO	TICHCCCT	AGOCTTOOGA	ACACAGCAAG	CCCCACCCTT	TOCAGOTTOG	OCCATCOTTA	00 CT D48	Protein Acc		MCAARCEDAR	VHVYWLLDGA		EAMPRICOPEA	VRLPTHGRVY	SOLEEGKPGY	GEST,PENVTD	RYTCIAGNEC	GLMFYCKKRC	LOPRRELEMP	PLSTKOKVAL YHPRQANVPL	AGKARLPOPE	Seq ID NO: Mucleic Adi			ACCCTTOTET	GTTGTCACT	OTTTATTO	ANANCTITCO	ATCCCAGGAG	TOCCIONICI	TCACTOGGTC	TACAGITACIC	OTGATTICTO	AGATTTTOTT	ACAGTGATTO	GTTCTAGNAC	ATGCTTCCCA
	•	•		2			15			20	, 		;	3			30			35	3		40			42			20	}		34	ว		09		;	S		5	2		ž	2		ć	8		;	82	

PCT/US02/12476

WO 02/086443 смактот с гистостто стаксмят стопстока макастега састемат темесана какаметт стастим вытально

Seq ID NO: 669 Protein sequence Protein Accession #: Eos sequence

S

v	Protesh Acc	cession #1	Protein Accession #: Eos sequence				
,		=-	12	<b>5</b> -	<b>\$</b> _	11	
	MOYOROSPVI	PPOPRLVLLI	MOTOROGENI PROPRINTI KOGALSOTDY YOSLVNKTPG PROYLLLSVL OPLYPFIAMI	YOSLVNKTPG	PPOYLLLSVL	OPLYPPIAMI	9
,	SYNIIAGDTL	BKVPGRIPGV	INNIAGDTL BKVPQRIPGV DPENVPIGRH PIIGLSTVTF TLPLSLYRNI AKLOKVSLIS	PIIGLBTVTP	TLPLSLYRNI	AKLGKVBLIB	120
2	TOLITAILGE	TOLITLINGI VMARAIBLOP I	HIPKTEDAWV I	PAKPNAIQAV	PAKPNAIGAY GVHBPAFICH HNSPLYYSSL	HNSPLVYSSL	91
	EEPTVAKWSR	LIMMSIVIEV	SEPTVAKWSR LIHMSIVISV PICIPPATCS YLTPTGPTQG DLFENYCRND DLVTFGRPCY	YLTPTOPTOG	DLFENYCRUD	DLVTFGRPCY	240
	GVTVILLTYPM	ECFVTREVIA	SVIVILLYPH ECPVIREVIA NVPPGGNLSS VPHIVVIVMV SIVATLVSLL IDCLGIVLEL	VHUTVVIHW	ITVATLVSLL	IDCLGIVLEL	300
	NGVLCATPLE	PLIPSACYLK	HGVLCATPLI PIIPSACYLK LSEEPRIHSD KIMSCYMLPI GAVVMVPGPV MAITHTGDCT	KIMSCVMLPI	DAVVMVPGPV	MAITHRODGE	360

Seg ID NO: 674 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..1140 2

HOGEMPYCEP DNFBLINTSE SHVQQTTQLS TLAIBIFQLE

240 240 350 420 420 420 420

0

15

Eos sequence

Seq ID NO: 670 DNA sequence Nucleic Acid Accession #: Eo Coding sequence: 1..1284

2

25

30

8

A MESSICENCE ASAGCAGGA GCCTUTCARE COCCOCCAGO TOLANALAC TITCOGCTTT 6
COLAGOTAN TO STOTEMENT OFFICETED ATTENDAGE TITTOGACCT COTTANANC TITCOGCTTA ATTENDAGE TITTOGACCT TOTATANCE ASAGCAGGA AND TATANCE AND ATTENDAGE TITCOGCTTANA TOCTTANAN COCCUTANAN COCCUTANAN COCCUTANAN COCCUTANAN COCCUTANAN AND ATTENDAGE AND ATTENDAGE AND ATTENDAGE AND ATTENDAGE AND ADDRESS AND ATTENDAGE AND ADDRESS AND ATTENDAGE AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND AD ဓ္က 35 22

숙

a constitucina cocconomia \*\* Treatmont reconomia \*\* Treatmont production \*\* Treatmont production \*\* Treatmont production \*\* Treatmont correction \*\* A conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*\* Conscious anamana \*

ANGOGRADO GENTECTE COCCOGOA ANA
ANGOLACIO GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECTE GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT GENTECT

35

<del>수</del>

HOTOROGENI PROVAKTEDE POTLILIENIO PLYPPIANIE WHITAGDELE KVEOKIEGUO BENYTZAGENE ILGUESTET LEJEKTAKIK KAGKELES GUTTLIJOH WAANELDEN ILGUERAKOP KENNIGANO WERAYICHE NEPVYELEE GUTTAKHEL INSULTEUR PROGALES FILLYWAY IVATLUELLE DCADTUZZHA GYLLITENE CYTTEUIA VPROGALES FILLYWAY IVATLUELLE DCADTUZZHA GYLCATEJE ILBENGTUZZ BESERVEREN LABOVALDIO AVWAYOTWA AIRYOGCHE GOMPICCEPO FEBLINTEED HVOOTIGLET LAISIPQLE 5, င္တ

922229

Sag ID NO: 676 DNA sequence Nucleic Acid Accession #: NW\_006851.1 Coding sequence: 26..874

55

HOTOROGENT PORGLETOR KOACPELDIG LIPWOSYTD PELVILINGO ALGOTOTTORS
LIMETORING TO VANCHISTEL TILLIGANS PORELONDE NUTZOANTI
CALTITITO ESCINDIARA, CHURCHERTO, TILLIGINA ALGOTOTTO
PRANCANOMA REALTORISE TUVARELETO TATLIGINA ALGOTOTTO
PROPERTORION SERVICIONION TRADECTOTT VILITAMECA VERMINANT PORGLEGORI
INTIMULIAN VANFORMAI THIODOCTINGO ENTOFFIJFII PRACTILLIGE ENTERSINI OPTIVICIBLE
SERVICIONION PARTICIPALINO SERVICIONIONI TERROPORTO
PROPERTORIONI THIODOCTINGO ENTOFFIJFII PRACTILLIGE ENTERSINI OPTIVICIBLE

25

8

Seq 1D NO: 671 Protein sequence Protein Accession #: Eos sequence

20

45

Beq 1D NO: 612 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..1203

65

2

73

8

. 88

AGGANITETE CECEGRATE COCUMATO AGGITTANA TAGETICODA ACTEGRATE ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEGRATA ACTEG 8 2 72 8 જ

ANGOCIACE MANGOLAGA GENERARE GEOGRADAR TITOCHUR TITATARA AMITICAR I AMAGAGA GENERARA ANGOCIACA MANGOCIACA ANGOCIACA 
WRILGLISLA LATGLVGGET RIIKGFECKP HOGPHQAALP EKTRILCGAT LIAPRWILITA 8

WO 02/086443

WO 02/086443

	1777CO(1)
v	ANGLARBYIV HLOGORIGAR EOCOTAKAT ESFFRIPARN SIPRICHRAD INCURANSPY 110 SITRANDRUT LESSCHTAGT SCLISSMOST SEPGREBET INCURRICE EQCERATYO 110 HITTOWNCAS VORSCHESC GESGGPLACH GSLOGIISHG GEDCELATRAF GYTINCKIV 210 PMIGETHANN
,	Seq ID NO; 678 DNA sequence Nuclaic Acid Accession %: Eos sequence Coding sequence: 1?)3
0	11 21 51 51 
15	GTGATGAGAA GAGATGCCCC AAGGCTAAGT GGAAATGTGG GCCGACTTC CCAGGGGAT (CATTGCATC ATGGTGGCT TCCGGTGCAA TGGGTTGAG TTGGCAGGGA TGAAAGAAA TGCACAGGAA ACCCTCTGCT TTGTCCAAC
	астосьада, соосстетот аттаськая осттейтей соятояско акалемент сизгаваты местатамы еттесьма коссовом тестате акалассы, стототят коссовом сыстатос
70	GENECATEAT TITTETIONED OTHOROGICC THETOGOLAGT OUTCITUCAL AGEOGRACIA CENTRATAGE CONCECUTION ACCORDINGLY ACCORDINGLY OF CONCENTRATE OCCUPANCIAL OF CANCELLANGIAL ACCORDINGLY OF CANCELLANGIAL ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGLY ACCORDINGL
. 25	ACTIONATED CONTROLOGICAL OCONTROLOGICAL CONTROLOGICA CHOROCACO CONTROLOGICA CHOROCACO CONTROLOGICA CHOROCACO CONTROLOGICA CHOROCACO CONTROLOGICA CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGONO CICCARGON
30	Bed ID NO., 679 Protein sequence Protein Accession 8: Eos sequence
35	11   12   21   31   41   51   51   51   51   51   51   5
Ę	RECISARSAS QARSELLEVE DISHSPOOPO POEGTARPRD
}	Seq 10 NO: 680 DNA sequence Nucleic Acid Accession 8: 378103.1 Coding sequence: 11190
45.	31 4 51
50	TECHANAM TRACECHA GANACTETT TTECKETOT CTCANTANA CTEGACCIC TRACETCA AGAMACAN TECHOGAGO CTTTECTAN TRACENTOC CTTANTOT GTANATAN TECHOGAGO CTTTECTAN MACTINET ANTECTANAN TECHORAL GANTANANAN
	TECCTICAGO AGCELCIATA ATTITACTES CALCUMANA OTTOGRANA TCALCATACTO CECTTOGTO CANATECTOS AGGACANTO
55	TCCTATCATT BATCGGCCTO AGTCTANTAG CTTTGGGGGC AGAGGGTTC TGGGGGCTT TGGTGGAGC CAGTTGGAG ANAACATGG AGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
9	смастист сътемати сестития изтичани обамбам. миссиссте тамками типиотет мититизм климета смититити диамисти типиотет тисмимот климета сметами обистами обистами обистами обистами тистими тоситеми обистами.
65	CTTOCAGE CATGOGRAD ANAGORAT TOSOGRATT TOCAGATES ANACCHT COGNITICAL TECHNICOS ANGORETOS CONTICAS TECHNICOS ANGORETOS CONTICAS TOCAGATOS TOCAGATO COCAGAGA TITUCANA TOCAGATO ANACCHOS CONTICAGA COCAGAGA TITUCANA ANACCHOS CONTICAGA COCAGAGA TITUCANA ANACCHOS CONTICAGA COCAGAGA TITUCANA ANACCHOS CONTICAGA COCAGAGA TITUCANA ANACCHOS CONTICAGA COCAGAGA TITUCANA ANACCHOS CONTICAGA COCAGAGA CONTICAGA COCAGAGA CONTICAGA CONTICAGA CONTICAGA COCAGAGA CONTICAGA CONT
8	ATRIOTICAL OCTRICATO PRESENTA PANDATE TECTIVATA ATRICTITCA GAMACIAC CICTATICA AGRICIACTI GAMACIAA TECCITICA CAMACIAC GEOATITUT CECTICACI TEGOLITE AGANTICATICA CATRATIATO ATRICATAMA ATRIOAGAGE TETECCAGE AGANTICATA CATRATIATO ATRICATAMA ATRIOAGAGE TETECCAGE ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA TOROCAGOTI GAGOTITUT ATRIACIAE AGEOANICA ACCANTOGA AGEOANICA AG
75	ADMINIST CANCACTICS CEGARACIA ATACETETES GEOGREGIC TRANSAMES STOCKAMBAS GARATICOS AGARAMAS CITTICICE MATTIGOSOT ETCHANCE TRATEACTA TACACCANT CAGAGETTE AGGETTERA ACAMATICA CATTIGOTOS CAGAGETTE AGGETTERA ACAMATICAS CATTIGOTOS CAGAGETTERA ACAMATICAS CATTIGOTOS CAGAGETTERA ACAMATICAS CATTIGOTOS
80	COSTGORAN STECATORS ANTICATES STATECTSC ACTACANOS SCACASTANAS ACATICAGOS GAACATGATC
82	8eq ID NO: 681 Protein sequence Protein Accession #: AAB34388.1

ဓ္က

35

Seq ID NO: 683 Protein sequence Protein Accession 8: NP\_057161.

Seq ID NO: 682 DNA sequence Nucleic Acid Accession B: NM\_016077.1 Coding sequence: 128..667

20

23

2

15

gansabb Qaabblene Dtshbpqpd Pqegtabprd	VE DISHSPOOP	POEGTAEPRD			
ence :: \$78203.1					
<b>#</b> -	· =-	<b>s</b> _			
_	•••	_	9		
ACCEPTED ANGUAGEST	NT CTCCGACAAT	CTITICCIAL	130		
-		_	240		
-	_	-	90		
-	MA TCATCTATCT	CTCCTTOGTG	920		
AGREETTO GOINECTIAC			9		
-	_		540		
	u	-	009		
-	_	-	9 9		
		_	120		
_	TC MOTTITON	ATGTATCTOG	097		
AGAACCUT TCTGGAAACA			006		
-	٠.		96	-	
		•	1020		
MATCCOTT CTOSTICITA	•	_	1080		
•	-		9		
•	-	-	1200		
CASTCAGOT CCCCAGGAGG	AGO TITICCIACA	TOTAL	1320		
STURCHES STURGARDS	•	•	1380		
, .			1440		
			1500		
AGCAAACA ACCAATGOGA	-	_	1560		
			1620		
TATAGAACT GTGCAAAGAG	GAG GAGAATACCC	TOCAUTOCAC	1740		
TITICICIO ANTIGORICA		• 0	1800		
_		_	1960		
_	CTT ATTCTCAGGC	•	1920		
-		-	1980		
		_	2040		
			2100		
ACADATANG CACATTCCTC	CTC ACATCCAGGO	GAACATGATC	277		
ANACTOTON					
sequence					
1 000710					

11 21 31 HERSELWRY LARBSTLOLA VOVACOMCIO MELRYCPONI DEGRIFMALIN VANDLOMENO KVAAOCHRAA VENKROLORR PDEZTLIALLA MANOMCLIV EUIQDAGRIQ TAPOSCTVLO HOOGELETWI GOOGLAYLAV LENLERGOAL STARLGROOT POLLERLAN GOFFENSTEIN DAPANALITI PEPULSEGG HALVELST ARBENOTER LENGLSCARP GALMILLERS ELHERODAR GREARANNE DECKLOFGEC CHITTRAN HONGERSTAN ANSENGINTS LINLEDTER ACCUPATIN LIONGROOT Seg ID NO: 684 DNA seguence Nucleic Acid Accession #: NM\_004864.1 Coding sequence: 26..952 Seq ID NO: 685 Protein sequence Protein Accession #: NP 004855.1 COGAACGAGO TCAGATOCTC OCCCGAGOCO 45 25 ଓ જ 2 75 8 85 6 20

686 DMA sequence Seq ID NO:

Nucleic Acid Accession #: NM\_003423.2 Coding sequence: 48..851

8 35

ID MO: 688 DNA sequence atc Acid Accession 8: NM\_005221.3

<del></del>

45 20 55

ප

65

WO 02/086443

PCT/US02/12476

PCT/US02/12476

sequences of accession numbers, and patent applications cited in this specification are herein It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, ncorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WO 02/086443

# WHAT IS CLAIMED IS:

A method of detecting a lung cancer-associated transcript in a cell

from a patient, the method comprising contacting a biological sample from the patient with a

polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence

as shown in Tables 1A-16.

The method of claim 1, wherein the polynucleotide selectively

hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.

The method of claim 1, wherein the biological sample is a tissue ۳.

2 sample.

The method of claim 1, wherein the biological sample comprises

isolated nucleic acids.

The method of claim 4, wherein the nucleic acids are mRNA.

The method of claim 4, further comprising the step of amplifying

nucleic acids before the step of contacting the biological sample with the polynucleotide.

The method of claim 1, wherein the polynucleotide comprises a

sequence as shown in Tables 1A-16.

The method of claim 1, wherein the polynucleotide is labeled.

The method of claim 8, wherein the label is a fluorescent label. o;

The method of claim 1, wherein the polynucleotide is immobilized on <u>6</u>

a solid surface.

The method of claim 1, wherein the patient is undergoing a therapeutic

regimen to treat lung cancer.

The method of claim 1, wherein the patient is suspected of having lung 12

cancer.

A method of monitoring the efficacy of a therapeutic treatment of lung 13.

cancer, the method comprising the steps of:

WO 02/086443

PCT/US02/12476

(i) providing a biological sample from a patient undergoing the therapeutic

treatment; and

(ii) determining the level of a lung cancer-associated transcript in the

biological sample by contacting the biological sample with a polynucleotide that selectively

hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,

thereby monitoring the efficacy of the therapy.

The method of claim 13, further comprising the step of: (iii) comparing 7.

the level of the lung cancer-associated transcript to a level of the lung cancer-associated

transcript in a biological sample from the patient prior to, or earlier in, the therapeutic

treatment,

The method of claim 13, wherein the patient is a human.

A method of monitoring the efficacy of a therapeutic treatment of lung . 19

cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic

treatment; and

(ii) determining the level of a lung cancer-associated antibody in the biological

sample by contacting the biological sample with a polypeptide encoded by a polynucleotide

that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in

Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated

antibody, thereby monitoring the efficacy of the therapy.

The method of claim 16, further comprising the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated

antibody in a biological sample from the patient prior to, or earlier in, the therapeutic

treatment.

The method of claim 16, wherein the patient is a human. <u>..</u>

A method of monitoring the efficacy of a therapeutic treatment of lung . 61

cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic

treatment; and

PCT/US02/12476

(ii) determining the level of a lung cancer-associated polypeptide in the

biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to

a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby

monitoring the efficacy of the therapy.

The method of claim 19, further comprising the step of: (iii) comparing

the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated

polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic

treatment.

The method of claim 19, wherein the patient is a human.

An isolated nucleic acid molecule consisting of a polynucleotide 55

sequence as shown in Tables 1A-16.

The nucleic acid molecule of claim 22, which is labeled. 33 The nucleic acid of claim 23, wherein the label is a fluorescent label 24.

An expression vector comprising the nucleic acid of claim 22. 25.

A host cell comprising the expression vector of claim 25. 26.

An isolated polypeptide which is encoded by a nucleic acid molecule 27.

having polynucleotide sequence as shown in Tables 1A-16.

An antibody that specifically binds a polypeptide of claim 27. 89

The antibody of claim 28, further conjugated to an effector component. 29.

The antibody of claim 29, wherein the effector component is a ဗ္ဗ

fluorescent label.

The antibody of claim 29, wherein the effector component is a 31.

radioisotope or a cytotoxic chemical

The antibody of claim 29, which is an antibody fragment. 33

WO 02/086443

PCT/US02/12476

The antibody of claim 29, which is a humanized antibody 33. A method of detecting a lung cancer cell in a biological sample from a

patient, the method comprising contacting the biological sample with an antibody of claim

The method of claim 34, wherein the antibody is further conjugated to 35.

an effector component

The method of claim 35, wherein the effector component is a 36.

fluorescent label.

A method of detecting antibodies specific to lung cancer in a patient,

the method comprising contacting a biological sample from the patient with a polypeptide

encoded by a nucleic acid comprises a sequence from Tables 1A-16.

A method for identifying a compound that modulates a lung cancer-

associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a lung cancer-associated polypeptide, the

polypeptide encoded by a polymucleotide that selectively hybridizes to a sequence at least

80% identical to a sequence as shown in Tables 1A-16; and

(ii) determining the functional effect of the compound upon the polypeptide.

The method of claim 38, wherein the functional effect is a physical 39.

effect.

The method of claim 38, wherein the functional effect is a chemical 6.

effect.

The method of claim 38, wherein the polypeptide is expressed in a 41.

eukaryotic host cell or cell membrane.

The method of claim 38, wherein the functional effect is determined by

measuring ligand binding to the polypeptide.

The method of claim 38, wherein the polypeptide is recombinant.

WO 02/086443 PCT/US02/12476

44. A method of inhibiting proliferation of a lung cancer-associated cell to

- treat lung cancer in a patient, the method comprising the step of administering to the subject a
- therapeutically effective amount of a compound identified using the method of claim 38.
- 45. The method of claim 44, wherein the compound is an antibody.
- 46. The method of claim 45, wherein the patient is a human.
- 47. A drug screening assay comprising the steps of
- (i) administering a test compound to a mammal having lung cancer or a cell
- isolated therefrom;
- (ii) comparing the level of gene expression of a polynucleotide that selectively
- (11) comparing the revei of gene expression of a polynucicotude that selective; hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
- treated cell or mammal with the level of gene expression of the polynucleotide in a control
  - 7 cell or mammal, wherein a test compound that modulates the level of expression of the

    - polynucleotide is a candidate for the treatment of lung cancer.
- 48. The assay of claim 47, wherein the control is a mammal with lung
- cancer or a cell therefrom that has not been treated with the test compound.
- 49. The assay of claim 47, wherein the control is a normal cell or mammal.
- 50. A method for treating a mammal having lung cancer comprising
- administering a compound identified by the assay of claim 47.
- A pharmaceutiPcal composition for treating a marmal having lung
- cancer, the composition comprising a compound identified by the assay of claim 47 and a
- physiologically acceptable excipient.

### This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

#### **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

□ BLACK BORDERS
□ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
□ FADED TEXT OR DRAWING
□ BLURRED OR ILLEGIBLE TEXT OR DRAWING
□ SKEWED/SLANTED IMAGES
□ COLOR OR BLACK AND WHITE PHOTOGRAPHS
□ GRAY SCALE DOCUMENTS
□ LINES OR MARKS ON ORIGINAL DOCUMENT
□ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

#### IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.